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                  zzp700836283.h1
Seq. ID
Arabidopsis thaliana
                  116379
Seq. No.
                  0 1.R1010
Contig ID
                  LIB3234-001-P1-K1-F7
5'-most EST
                  BLASTX
Method
                  g4105262
NCBI GI
                  1176
BLAST score
                  0.0e + 00
E value
                  479
Match length
% identity
                  73
NCBI Description (AF044573) actin [Brassica oleracea]
Seq. No.
                  116380
                  0 2.R1010
Contig ID
5'-most EST
                  jC-atXP73CF3B10T7d2
                  BLASTX
Method
                  g1669387
NCBI GI
                  1547
BLAST score
                  1.0e-173
E value
                  355
Match length
% identity
                  89
                  (U41998) actin 2 [Arabidopsis thaliana]
NCBI Description
                  116381
Seq. No.
                  0 3.R1010
Contig ID
                  jC-atXLIB327409P3a11b1
5'-most EST
Method
                  BLASTX
                  g1669387
NCBI GI
BLAST score
                  801
                  1.0e-85
E value
                  194
Match length
                  85 .
% identity
NCBI Description (U41998) actin 2 [Arabidopsis thaliana]
                  116382
Seq. No.
                  0 4.R1010
Contig ID
5'-most EST
                   j\overline{C}-atXLIB327407P1e12b2
Method
                  BLASTX
NCBI GI
                  g1669387
                  897
BLAST score
                  9.0e-97
E value
                  178
Match length
                  98
% identity
NCBI Description (U41998) actin 2 [Arabidopsis thaliana]
```

```
116383
Seq. No.
                  0 7.R1010
Contig ID
5'-most EST
                  LIB3176-002-Q1-K1-D3
                  BLASTX
Method
NĊBI GI
                  q1669387
BLAST score
                  637
                  3.0e-66
E value
                  141
Match length
                  89
% identity
                  (U41998) actin 2 [Arabidopsis thaliana]
NCBI Description
                  116384
Seq. No.
Contig ID
                  0 8.R1010
                  jC-atXP22C114O13T7074a1
5'-most EST
                  BLASTX
Method
                  g1703108
NCBI GI
BLAST score
                  2.96
                  2.0e-26
E value
                  57
Match length
                  100
% identity
                  ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis
NCBI Description
                  thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
                  thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
                  thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                  thaliana]
Seq. No.
                  116385
                  0 10.R1010
Contig ID
5'-most EST
                  LIB22-027-Q1-E1-D10
Method
                  BLASTX
                  q1669389
NCBI GI
BLAST score
                  527
                  1.0e-53
E value
Match length
                  99
                  97
% identity
                  (U42007) actin 8 [Arabidopsis thaliana]
NCBI Description
                  116386
Seq. No.
                  0 11.R1010
Contig ID
                  jC-atXLIB327408P1f10b1
5'-most EST
Method
                  BLASTX
                  g1703115
NCBI GI
BLAST score
                  610
                  2.0e-63
E value
Match length
                  113
% identity
                  ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis
NCBI Description
                  thaliana >gi_1145695 (U39480) actin [Arabidopsis thaliana]
                  >gi 3236244 (AC004684) actin 3 protein [Arabidopsis
                  thaliana]
                  116387
Seq. No.
                  0 12.R1010
Contig ID
                  LIB25-027-Q1-E1-F4
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1703129
```

```
757
  BLAST score
  E value
                    1.0e-80
                    158
  Match length
  % identity
                    ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis
  NCBI Description
                    thaliana >gi 1002533 (U27981) actin-11 [Arabidopsis
                    thaliana]
                    116388
  Seq. No.
                    0 13.R1010
  Contig ID
                    LTB3176-048-P1-K1-C11
  5'-most EST
                    BLASTX
  Method
                    g1703115
  NCBI GI
  BLAST score
                    613
                    7.0e-64
  E value
                    113
  Match length
                    100
  % identity
  NCBI Description ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis
                    thaliana >gi 1145695 (U39480) actin [Arabidopsis thaliana]
                    >gi 3236244 (AC004684) actin 3 protein [Arabidopsis
                    thaliana]
                    116389
  Seq. No.
                    0 14.R1010
  Contig_ID
  5'-most EST
                    LIB22-085-Q1-E1-H2
  Method
                    BLASTX
  NCBI GI
                    g3420239
  BLAST score
                    578
                    9.0e-60
  E value
                    106
  Match length
  % identity
                    100
                    (AF059484) actin [Gossypium hirsutum]
  NCBI Description
                    116390
. Seq. No.
                    0 18.R1010
  Contig ID
                    jC-atXLIB327407P1e12a2
  5'-most EST
  Method
                    BLASTX
                    g1531674
  NCBI GI
  BLAST score
                    296
  E value
                    1.0e-26
                    57
  Match length
  % identity
                    100
                    (U68462) actin [Striga asiatica]
  NCBI Description
                    116391
  Seq. No.
                     4 1.R1010
  Contig ID
                    LTB3175-058-P1-K1-G5
  5'-most EST
  Method
                    BLASTX
  NCBI GI
                    g1002803
  BLAST score
                    1798
                    0.0e + 00
  E value
  Match length
                    358
  % identity
                    (U33932) flavanone 3-hydroxylase [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                    116392
```

4 2.R1010

Contig ID

```
5'-most EST
                   jC-atXP25C123O11T7009a1
Method
                   BLASTX
                   q1002803
NCBI GI
BLAST score
                   467
                   1.0e-46
E value
                   107
Match length
% identity
                   86
                  (U33932) flavanone 3-hydroxylase [Arabidopsis thaliana]
NCBI Description
                   116393
Seq. No.
                   5 1.R1010
Contig ID
5'-most EST
                   LIB35-039-Q1-E1-E4
Method
                   BLASTX
                   g117238
NCBI GI
                   1830
BLAST score
                   0.0e + 00
E value
                   424
Match length
% identity
                   MAGNEŞIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN
NCBI Description
                   CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE)
                   >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast
                   - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411)
                   protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana]
                   >gi 2832653 emb CAA16728_ (AL021710) protein ch-42
                   precursor, chloroplast [Arabidopsis thaliana]
                   >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein
[Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene
                   [Euglena gracilis]
                   116394
Seq. No.
                   5 2.R1010
Contiq ID
                   jC-atXLIB327417P3g11b1
5'-most EST
                   BLASTX
Method
                   q117238
NCBI GI
                   1000
BLAST score
                   1.0e-108
E value
                   338
Match length
% identity
                   MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN
NCBI Description
                   CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE)
                   >gi 81656 pir S12785 protein ch-42 precursor, chloroplast
                   - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411)
                   protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana]
                   >gi 2832653 emb CAA16728 (AL021710) protein ch-42
                   precursor, chloroplast [Arabidopsis thaliana]
                   >gi 4490290 emb_CAB38561.1_ (X51799) chloroplast protein
                   [Arabidopsis thaliana] >gi_228771 prf 1811226A ccsA gene
                   [Euglena gracilis]
                   116395
Seq. No.
Contig ID
                   5 3.R1010
                   jC-atXP102CE4F4T7b1
5'-most EST
                   BLASTX
Method
                   g3334150
NCBI GI
BLAST score
                   298
E value
                   2.0e-51
                   165
Match length
```

```
% identity
                  65
                  MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR
NCBI Description
                   (MG-PROTOPORPHYRIN IX CHELATASE) >gi 2129847 pir JC4312
                  chlorophyll magnesium chelatase (EC 4.99.-.-) - soybean
                  chloroplast >gi_1732469_dbj_BAA08291 (D45857) Mg chelatase
                  subunit (46 kD) [Glycine max]-
                  116396
Seq. No.
                  5 4.R1010
Contig ID
                  jC-atXLIB327415P4b04b1
5'-most EST
                  BLASTN
Method
                  g16241
NCBI GI
BLAST score
                  330
                  0.0e + 00
E value
                  386
Match length
                  99
% identity
                  Arabidopsis thaliana cs/ch-42 gene for a chloroplast
NCBI Description
                  protein (cs)
                  116397
Seq. No.
                  6 1.R1010
Contig ID
                  jC-alXLIB327434P3a04b1
5'-most EST
                  BLASTX
Method
                  g1046373
NCBI GI
BLAST score
                  1829
                  0.0e + 00
E value
Match length
                  346
                  100
% identity
                  (U37336) SAG12 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  116398
                  7_1.R1010
Contig ID
                  LIB23-039-Q1-E1-H7
5'-most EST
Method
                  BLASTX
                  g1170203
NCBI GI
BLAST score
                  2383
                  0.0e+00
E value
                  539
Match length
% identity
                  88
                  GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi 454359
NCBI Description
                   (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]
                  116399
Seq. No.
                  7 2.R1010
Contig ID
                  LIB3175-018-P1-K1-F10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1346263
BLAST score
                  2530
                  0.0e+00
E value
                  530
Match length
% identity
                  95
NCBI Description
                  GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR)
                  >gi 2146736 pir S65773 glutamyl-tRNA reductase 2 precursor
                  - Arabidopsis thaliana >gi 1049057 (U27118) glutamyl-tRNA
                  reductase [Arabidopsis thaliana]
```

Seq. No. 116400

Method

```
7 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P1d01b2
Method
                  BLASTX
                  g1170203
NCBI GI
                  796
BLAST score
                  4.0e-85
E value
Match length
                  183
% identity
                  89
                  GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi_454359
NCBI Description
                   (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]
                  116401
Seq. No.
                  8 1.R1010
Contig ID
                   jC-atXLIB327403P3c03b2
5'-most EST
Method
                   BLASTX
                  g2497886
NCBI GI
                   300
BLAST score
                   6.0e-27
E value
                   54
Match length
                  100
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B)
NCBI Description
                  >gi 1361999 pir _S57862 metallothionein 2b - Arabidopsis
                   thaliana >gi 1086463 (U11256) metallothionein [Arabidopsis
                  thaliana]
                   116402
Seq. No.
Contig ID
                   8 2.R1010
                   j\overline{C}-atXLIB327437P3e11a1
5'-most EST
                   BLASTX
Method
                   q2497886
NCBI GI
BLAST score
                   145
                   7.0e-09
E value
Match length
                   24
                   96
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B)
NCBI Description
                   >gi 1361999 pir S57862 metallothionein 2b - Arabidopsis
                   thaliana >gi 1086463 (U11256) metallothionein [Arabidopsis
                   thaliana]
                   116403
Seq. No.
                   8 4.R1010
Contig ID
                   jC-atXLIB327438P3f04a2
5'-most EST
                   BLASTX
Method
                   q2497886
NCBI GI
                   300
BLAST score
                   5.0e-27
E value
Match length
                   54
                   100
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B)
NCBI Description
                   >gi 1361999 pir S57862 metallothionein 2b - Arabidopsis
                   thaliana >gi 1086463 (U11256) metallothionein [Arabidopsis
                   thaliana]
                   116404
Seq. No.
                   8 6.R1010
Contig ID
                   g2722104
5'-most EST
```

BLASTX

```
g2497886
NCBI GI
                  186
BLAST score
                  1.0e-13
E value
                  51
Match length
                  76
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B)
NCBI Description
                  >gi 1361999 pir__S57862 metallothionein 2b - Arabidopsis
                  thaliana >gi 1086463 (U11256) metallothionein [Arabidopsis
                  thaliana]
                  116405
Seq. No.
                  9 1.R1010
Contig ID
                  jC-atXmonuni27Ce09b1
5'-most EST
Method
                  BLASTX
                  q1352458
NCBI GI
BLAST score
                  2555
                  0.0e + 00
E value
                  498
Match length
                  100
% identity
                  INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE)
NCBI Description
                  (IMPDH) (IMPD) >gi_2117507_pir__JC4999 IMP dehydrogenase
                  (EC 1.1.1.205) - Arabidopsis thaliana >gi_1100063 (L34684)
                  IMP dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  116406
                  10 1.R1010
Contig ID
5'-most EST
                  PLN g1800113
Method
                  BLASTX
                  g1100253
NCBI GI
                  11567
BLAST score
E value
                  0.0e + 00
                  2254
Match length
                  99
% identity
                  (D34630) acetyl-CoA carboxylase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  116407
                  13 1.R1010
Contig ID
                  jC-atXP59C196D17T7d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q115486
BLAST score
                  762
                  6.0e-81
E value
                  149
Match length
% identity
                  CALMODULIN-2/3/5 >gi 99671 pir S22503 calmodulin -
NCBI Description
                  Arabidopsis thaliana >gi 1076437 pir S53006 calmodulin -
                  leaf mustard >gi_2146726_pir__S71513_calmodulin -
                  Arabidopsis thaliana >gi_166651 (M38380) calmodulin-2
                   [Arabidopsis thaliana] >\overline{gi}_1166653 (M73711) calmodulin-3
                   [Arabidopsis thaliana] >gi_474183_emb_CAA47690_ (X67273)
                  calmodulin [Arabidopsis thaliana] >gi_497992 (U10150)
                  calmodulin [Brassica napus] >gi_899058 (M88307) calmodulin
                   [Brassica juncea] >gi_1183005_dbj_BAA08283_ (D45848)
                  calmodulin [Arabidopsis thaliana] >gi 3402706 (AC004261)
                  unknown protein [Arabidopsis thaliana] >gi 3885333
                   (AC005623) calmodulin [Arabidopsis thaliana]
                  >gi 228407 prf 1803520A calmodulin 2 [Arabidopsis
```

Match length

128

thaliana]

```
Seq. No.
                  116408
                  13 3.R1010
Contig ID
                  LIB23-063-Q1-E1-B4
5'-most EST
                  BLASTX
Method -
                  q3913191
NCBI GI
BLAST score
                  301
                  6.0e-27
E value
                  151
Match length
                  29
% identity
                  CALMODULIN >gi 1296524_emb_CAA66215_ (X97612) CaMF-1 [Fagus
NCBI Description
                  sylvatica]
                  116409
Seq. No.
                  15 1.R1010
Contig ID
5'-most EST
                  q397203
Method
                  BLASTX
                  q2144183
NCBI GI
BLAST score
                  528
                  1.0e-53
E value
                  122
Match length
% identity
                  86
                  DNA-directed RNA polymerase (EC 2.7.7.6) chain III -
NCBI Description
                  Ecotype Columbia >gi 1184686 (U35049) RNA polymerase I(A)
                  and III(C) 14 kDa subunit [Arabidopsis thaliana]
                  >gi 1184688 (U35050) Arabidopsis thaliana RNA polymerase
                  I(A) and III(C) 14 kDa subunit [Arabidopsis thaliana]
                  >gi 3980382 (AC004561) RNA polymerase I(A) and III(C) 14
                  kDa subunit (AtRPAC14) [Arabidopsis thaliana]
Seq. No.
                  116410
                  16 1.R1010
Contig ID
5'-most EST
                  PLN g1335996
Method
                  BLASTX
NCBI GI
                  q2498329
BLAST score
                  7288
E value
                  0.0e + 00
                  1451
Match length
% identity
NCBI Description
                  PATTERN FORMATION PROTEIN EMB30 >gi 2129665 pir S65571
                  pattern-formation protein GNOM - Arabidopsis thaliana
                  >qi 1209633 (U36433) GNOM gene product [Arabidopsis
                  thaliana] >gi 1335997 (U56140) similar to the Saccharomyces
                  cerevisiae Sec7 protein, GenBank Accession Number J03918
                   [Arabidopsis thaliana] >qi 1335999 (U56141) similar to the
                  Saccharomyces cerevisiae Sec7 protein, GenBank Accession
                  Number J03918 [Arabidopsis thaliana]
Seq. No.
                  116411
Contig ID
                  16 4.R1010
5'-most EST
                  jC-atXLIB327411P3f08b1
Method
                  BLASTX
NCBI GI
                  g2498329
BLAST score
                  226
                  2.0e-39
E value
```

NCBI GI

```
% identity
                  75
                  PATTERN FORMATION PROTEIN EMB30 >gi 2129665 pir S65571
NCBI Description
                  pattern-formation protein GNOM - Arabidopsis thaliana
                  >gi 1209633 (U36433) GNOM gene product [Arabidopsis
                  thaliana] >gi 1335997 (U56140) similar to the Saccharomyces
                  cerevisiae Sec7 protein, GenBank Accession Number J03918
                  [Arabidopsis thaliana] >gi 1335999 (U56141) similar to the
                  Saccharomyces cerevisiae Sec7 protein, GenBank Accession
                  Number J03918 [Arabidopsis thaliana]
                  116412
Seq. No.
                  17 1.R1010
Contig ID
                  jC-atXLIB327408P4c10b1
5'-most EST
Method
                  BLASTX
                  q1213594
NCBI GI
BLAST score
                  2176
                  0.0e + 00
E value
                  419
Match length
                  100
% identity
                  (X93080) responsible for fatty acid elongation from C28 to
NCBI Description
                  C30 [Arabidopsis thaliana] >gi_1655786 (U40849) CER2 gene
                  product [Arabidopsis thaliana] >gi_4220539_emb_CAA23012_
                  (AL035356) CER2 [Arabidopsis thaliana]
Seq. No.
                  116413
                  17 2.R1010
Contig ID
                  jC-alXLIB327434P4d08b1
5'-most EST
Method
                  BLASTX
                  q3212879
NCBI GI
                  1051
BLAST score
                  1.0e-115
E value
                  241
Match length
% identity
                  (AC004005) putative ribosomal protein L7 [Arabidopsis
NCBI Description
                  thaliana]
                  116414
Seq. No.
                  18 1.R1010
Contig ID
                  PLN g1254989
5'-most EST
Method
                  BLASTX
                  q1254990
NCBI GI
                  2318
BLAST score
                  0.0e+00
E value
                  488
Match length
                  93
% identity
                  (U26542) 1-aminocyclopropane-1-carboxylate synthase-like
NCBI Description
                  protein [Arabidopsis thaliana] >gi_1254992 (U26543)
                  1-aminocyclopropane-1-carboxylate synthase-like protein
                  [Arabidopsis thaliana] >gi_1586513_prf__2204225A
                  aminocyclopropanecarboxylate synthase [Arabidopsis
                  thaliana]
                  116415
Seq. No.
                  20 1.R1010
Contig ID
                  jC-atXP73C223G19T7b1
5'-most EST
                  BLASTX
Method
```

q1702987

```
BLAST score
                  1199
E value
                   1.0e-132
Match length
                   263
                   90
% identity
                  14-3-3-LIKE PROTEIN GF14 PHI >gi 1493805 (L09111) GF14
NCBI Description
                  protein phi chain [Arabidopsis thaliana] >gi 2232146
                   (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis
                   thaliana]
                   116416
Seq. No.
                   20 2.R1010
Contig ID
                   jC-atXLIB327424P1b02b2
5'-most EST
Method
                   BLASTX
                   g1702987
NCBI GI
                   1195
BLAST score
                   1.0e-131
E value
                   246
Match length
                   96
% identity
                   14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14
NCBI Description
                   protein phi chain [Arabidopsis thaliana] >gi_2232146
                   (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis
                   thaliana]
Seq. No.
                   116417
                   20 3.R1010
Contig ID
                   LIB22-052-Q1-E1-B11
5'-most EST
Method
                   BLASTX
                   g1702986
NCBI GI
BLAST score
                   1242
                   1.0e-137
E value
Match length
                   267
                   93
% identity
                   14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi
NCBI Description
                   isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14
                   chi chain [Arabidopsis thaliana]
                   116418
Seq. No.
                   20 4.R1010
Contig ID
                   jC-alXLIB327435P2a10a1
5'-most EST
                   BLASTX
Method
                   g421836
NCBI GI
BLAST score
                   553
                   2.0e-94
E value
                   189
Match length
                   92
% identity
                   G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040
NCBI Description
                   (M96855) GF14 [Arabidopsis thaliana]
                   116419
Seq. No.
                   22 1.R1010
Contig ID
5'-most EST
                   PLN g1277089
                   BLASTX
Method
                   g2129677
NCBI GI
BLAST score
                   2052
                   0.0e + 00
E value
Match length
                   402
% identity
                   97
```

```
NCBI Description
                  probablel N-acetyltransferase hookless 1 - Arabidopsis
                  thaliana >gi 1277090 (U50399) putative N-acetyltransferase
                  hookless1 [Arabidopsis thaliana] >gi 1277092 (U50400)
                  putative N-acetyltransferase hookless1 [Arabidopsis
                  thaliana] >gi 4468983 emb CAB38297 (AL035605) probable
                  N-acetyltransferase hookless 1 [Arabidopsis thaliana]
Seq. No.
                  116420
Contig ID
                  23 1.R1010
5'-most EST
                  PLN g1279211
Method
                  BLASTX
NCBI GI
                  g4455256
BLAST score
                  929
E value
                  1.0e-100
Match length
                  258
% identity
                  100
                   (AL035523) protein-methionine-S-oxide reductase
NCBI Description
                   [Arabidopsis thaliana]
                  116421
Seq. No.
Contig ID
                  23 2.R1010
5'-most EST
                  PLN g1279211
Method
                  BLASTX
NCBI GI
                  q4455256
BLAST score
                  1358
                                                           . . . . . .
E value
                  1.0e-151
Match length
                  258
% identity
NCBI Description
                   (AL035523) protein-methionine-S-oxide reductase
                   [Arabidopsis thaliana]
Seq. No.
                  116422
Contig ID
                  24 1.R1010
5'-most EST
                  g2047389
Method
                  BLASTX
NCBI GI
                  g2500192
BLAST score
                  954
E value
                  1.0e-103
Match length
                  198
% identity
                  RAC-LIKE GTP BINDING PROTEIN ARAC3 >qi 1304413 (U43501)
NCBI Description
                  Rac-like protein [Arabidopsis thaliana] >qi 2645643
                   (AF031427) Rho-like GTP binding protein [Arabidopsis
                  thaliana] >gi 2924513 emb CAA17767.1 (AL022023) Rho1Ps
                  homolog/ Rac-like protein [Arabidopsis thaliana]
                  116423
Seq. No.
Contig ID
                  24 2.R1010
5'-most EST
                  LIB25-110-Q1-E1-A3
Method
                  BLASTX
NCBI GI
                  g2801769
BLAST score
                  153
E value
                   6.0e-61
Match length
                  196
% identity
                  (AF042330) rac-like small GTP binding protein [Brassica
NCBI Description
```

% identity

```
116424
 Seq. No.
                    28 1.R1010
 Contig ID
                    PLN g1353769
 5'-most EST
                    BLASTX
 Method
                    g2499810
: NCBI GI
                    695
 BLAST score
                    3.0e-73
 E value
 Match length
                    131
                    100
 % identity
                    PROFILIN 1 >gi_2981657_pdb_1A0K_ Profilin I From Arabidopsis Thaliana >gi_1353763 (U43322) profilin 1
 NCBI Description
                    [Arabidopsis thaliana] >gi_1353770 (U43325) profilin 1
                    [Arabidopsis thaliana] >gi_1835878_bbs_179026 (S82691)
                    profilin isoform 1 [Arabidopsis thaliana, Columbia,
                    flowers, Peptide, 131 aa] [Arabidopsis thaliana]
                    >gi_3687242 (AC005169) profilin 1 [Arabidopsis thaliana]
                    116425
 Sea. No.
 Contig ID
                    28 3.R1010
                    LIB35-039-Q1-E1-C9
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g2499810
 BLAST score
                    238
                    6.0e-20
 E value
 Match length
                    46
                    98
 % identity
                    PROFILIN 1 >gi 2981657 pdb 1A0K Profilin I From
 NCBI Description
                    Arabidopsis Thaliana >gi 1353763 (U43322) profilin 1
                     [Arabidopsis thaliana] >\overline{gi}_1353770 (U43325) profilin 1
                     [Arabidopsis thaliana] >gi_1835878 bbs 179026 (S82691)
                    profilin isoform 1 [Arabidopsis thaliana, Columbia,
                     flowers, Peptide, 131 aa] [Arabidopsis thaliana]
                    >gi 3687242 (AC005169) profilin 1 [Arabidopsis thaliana]
                    116426
 Seq. No.
 Contig ID
                    29 1.R1010
                    jC-atXLIB327414P1c09a1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                     g2499811
 BLAST score
                     664
 E value
                     2.0e-69
 Match length
                     126
 % identity
                    PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis
 NCBI Description
                     thaliana] >gi \overline{1}353772 (U43326) profilin 2 [Arabidopsis
                     thaliana]
                     116427
 Seq. No.
                     30 1.R1010
 Contig ID
 5'-most EST
                     jC-atXLIB327419P2h07b2
                     BLASTX
 Method
 NCBI GI
                     g2499813
 BLAST score
                     637
                     1.0e-66
 E value
 Match length
                     134
```

```
NCBI Description PROFILIN 4 >gi_1353768 (U43324) profilin 4 [Arabidopsis
                   thaliana] >gi_{\overline{3}687241} (AC005169) profilin 4 [Arabidopsis
                   thalianal
                   116428
Seq. No.
                   32 1.R1010
Contig ID
                   jC-atXP100C251L10T7b1
5'-most EST
                   BLASTX
Method
                   g2117424
NCBI GI
                   585
BLAST score
                   3.0e-60
E value
                   113
Match length
                   100
% identity
                   thioredoxin - Arabidopsis thaliana >gi_992962_emb_CAA84611_
NCBI Description
                   (Z35474) thioredoxin [Arabidopsis thaliana] >gi 1388076
                   (U35640) thioredoxin h [Arabidopsis thaliana]
                   116429
Seq. No.
                   32 2.R1010
Contig ID
                   g1054346
5'-most EST
                   BLASTX
Method
                   g2117424
NCBI GI
BLAST score
                   345
                   4.0e-32
E value
                   117
Match length
                   47
% identity
                   thioredoxin - Arabidopsis thaliana >gi 992962_emb_CAA84611_
NCBI Description
                   (Z35474) thioredoxin [Arabidopsis thaliana] >gi_1388076
                   (U35640) thioredoxin h [Arabidopsis thaliana]
                   116430
Seq. No.
                   32 4.R1010
Contig ID
                   g2446030
5'-most EST
                   116431
Seq. No.
                   32 5.R1010
Contig ID
                   g2\overline{5}96490
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2117424
                   300
BLAST score
                   3.0e-27
E value
                   73
Match length
% identity
                   thioredoxin - Arabidopsis thaliana >gi_992962_emb_CAA84611_
NCBI Description
                   (Z35474) thioredoxin [Arabidopsis thaliana] > \overline{gi}_1 \overline{13}88076
                   (U35640) thioredoxin h [Arabidopsis thaliana]
                   116432
Seq. No.
                   33 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327425P3c05b1
                   BLASTX
Method
                   g2129752
NCBI GI
BLAST score
                   674
                   1.0e-70
E value
Match length
                   132
                   100
% identity
NCBI Description thioredoxin - Arabidopsis thaliana >gi_992964_emb_CAA84612_
```

(Z35475) thioredoxin [Arabidopsis thaliana] 116433 Seq. No. 34 1.R1010 Contig ID 5'-most EST PLN g16551 BLASTX Method NCBI GI g267122 590 BLAST score 4.0e-61 E value 114 Match length 100 % identity THIOREDOXIN H-TYPE (TRX-H) >gi 478400 pir_ JQ2242 NCBI Description thioredoxin h - Arabidopsis thaliana >gi 16552 emb CAA78462 (Z14084) Thioredoxin H [Arabidopsis thaliana] >gi_1388080 (U35827) thioredoxin h [Arabidopsis thaliana] 116434 Seq. No. 35 1.R1010 Contig ID 5'-most EST jC-atXLIB327414P3a10a1 Method BLASTX NCBI GI q3738287 BLAST score 1075 1.0e-117 E value Match length 210 100 % identity (ACO05309) glutathione s-transferase, GST6 [Arabidopsis NCBI Description thaliana] 116435 Seq. No. Contig ID 35 2.R1010 5'-most EST q958209 Method BLASTX NCBI GI g3738287 BLAST score 541 E value 3.0e-55 Match length 186 % identity 65 NCBI Description (AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana] Seq. No. 116436 35 3.R1010 Contiq ID 5'-most EST jC-atX25094Q1E1F09b1 Method BLASTX g3738287 NCBI GI BLAST score 142 9.0e-09 E value 70 Match length % identity NCBI Description (AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

. 116437

BLASTX

35 4.R1010

jC-atXLIB327431P1e09a1

Seq. No. Contig ID

Method

5'-most EST

```
NCBI GI
                  g3738287
BLAST score
                  551
E value
                  2.0e-66
Match length
                  138
                  96
% identity :
                  (AC005309) glutathione s-transferase, GST6 [Arabidopsis
NCBI Description
                  thaliana]
                  116438
Seq. No.
                  36 1.R1010
Contig ID
                  LIB22-005-Q1-E1-B12
5'-most EST
                  BLASTX
Method
NCBI GI
                  g619751
BLAST score
                  1384
                  1.0e-154
E value
                  275
Match length
                  99
% identity
                  (U18970) phosphoribosylanthranilate isomerase [Arabidopsis
NCBI Description
                  thaliana] >gi 1403668 (U34756) phosphoribosylanthranilate
                  isomerase [Arabidopsis thaliana]
                  116439
Seq. No.
                  37 1.R1010
Contig ID
5'-most EST
                  LIB3234-095-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q2499236
BLAST score
                  1521
                  1.0e-170
E value
                  348
Match length
                  88
% identity
                  NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST
NCBI Description
                  >qi 1419474 emb CAA66944 (X98298) ndhA [Arabidopsis
                  thaliana]
                  116440
Seq. No.
Contig ID
                  38 1.R1010
5'-most EST
                  LIB23-067-Q1-E1-F2
                BLASTX
Method
                  g1483218
NCBI GI
BLAST score
                  1852
E value
                  0.0e + 00
                  374
Match length
                  94
% identity
NCBI Description
                  (X99793) induced upon wounding stress [Arabidopsis
                  thaliana]
Seq. No.
                  116441
                  39 1.R1010
Contig ID
5'-most EST
                  PLN g1497986
Method
                  BLASTX
NCBI GI
                  q1497987
BLAST score
                  2802
E value
                  0.0e + 00
Match length
                  653
                 85
% identity
                  (U62798) SCARECROW [Arabidopsis thaliana]
NCBI Description
```

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```
116442
Seq. No.
Contig ID
                   40 1.R1010
                   PLN g1507700
5'-most EST
Method
                   BLASTX
                   q1507699
NCBI GI
BLAST score
                   1814
E value
                   0.0e+00
                   347
Match length
                   100
% identity
                   (L81119) COL2 [Arabidopsis thaliana] >gi_1507701 (L81120)
NCBI Description
                   COL2 [Arabidopsis thaliana]
                   116443
Seq. No.
                   41 1.R1010
Contig ID
                   LIB23-046-Q1-E1-B1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3913379
                   3143
BLAST score
E value
                   0.0e + 00
                   604
Match length
                   98
% identity
                   CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR)
NCBI Description
                   >gi 1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis
                   thaliana]
                   116444
Seq. No.
                   42 1.R1010
Contig ID
5'-most EST
                   PLN g166769
                   BLASTX
Method
                   q418904
NCBI GI
BLAST score
                   3116
                   0.0e+00
E value
Match length
                   689
                   90
% identity
                   heat shock protein 83 - Arabidopsis thaliana >gi 166770
NCBI Description
                   (M62984) heat shock protein 83 [Arabidopsis thaliana]
                 116445
Seq. No.
                   43 1.R1010
Contig ID
                   jC-atXLIB327426P2g03b1
5'-most EST
Method
                   BLASTX
                   g1173194
NCBI GI
BLAST score
                   719
                   6.0e-76 ·
E value
Match length
                   163
                   91
% identity
                   30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13)
NCBI Description
                   >gi 2119093 pir S59594 ribosomal protein S13 precursor,
                   chloroplast - Arabidopsis thaliana >gi_16767_emb_CAA79013
                   (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis
                   thaliana] >gi_662869 emb_CAA88028_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana]
                   >gi_1107483_emb_CAA63021_ (X91955) 30S ribosomal protein
                   S13 [Arabidopsis thaliana] >gi 1515107_emb_CAA60413_
                   (X86734) plastid ribosomal protein S13 [Arabidopsis
                   thaliana]
```

```
116446
Seq. No.
                   43 2.R1010
Contig ID
5'-most EST
                   LIB24-025-Q1-E1-D8
                   BLASTX
Method
                   g2760183
NCBI GI ·
                   277
BLAST score
                   5.0e-24
E value
                   106
Match length
% identity
                   54
                   (AB010082) ribosomal protein S13 [Bacillus halodurans]
NCBI Description
                   >qi 4512429 dbj BAA75296.1 (AB017508) rpsM homologue
                   (identity of 84% to B. subtilis ) [Bacillus halodurans]
Seq. No.
                   116447
Contig ID
                   43 3.R1010
5'-most EST
                   jC-atXLIB327431P3g02a1
Method ·
                   BLASTX
NCBI GI
                   g1173194
                   790
BLAST score
E value
                   3.0e-84
Match length
                   154
% identity
                   100
                   30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13)
NCBI Description
                   >gi 2119093 pir S59594 ribosomal protein S13 precursor,
                   chloroplast - Arabidopsis thaliana >gi 16767 emb CAA79013
                   (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis
                   thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana]
                   >gi 1107483 emb CAA63021 (X91955) 30S ribosomal protein
                   S13 [Arabidopsis thaliana] >gi 1515107 emb CAA60413
                   (X86734) plastid ribosomal protein S13 [Arabidopsis
                   thaliana]
                   116448
Seq. No.
Contig ID
                   44 1.R1010
5'-most EST
                   PLN g2258115
Method
                   BLASTX
NCBI GI
                   g1502428
BLAST score
                   2625
E value
                   0.0e+00
Match length
                   524
% identity
                   97
NCBI Description
                   (U62330) phosphate transporter [Arabidopsis thaliana]
                   >qi 2258116 db; BAA21503 (D86591) inorganic phosphate
                   transporter [Arabidopsis thaliana]
                   >qi 2258118 dbj BAA21504 (D86608) inorganic phosphate
                   transporter [Arabidopsis thaliana]
                   116449
Seq. No.
                   46 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327410P4a11b1
Method
                   BLASTX
NCBI GI
                   g3913418
BLAST score
                   1718
E value
                   0.0e + 00
Match length
                   346
% identity
                   96
```

Method.

BLASTX

```
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                  (SAMDC) >gi 1531763 emb CAA69073 (Y07765)
                  S-adenosylmethionine decarboxylase [Arabidopsis thaliana]
                  116450
Seq. No.
Contig ID
                  46 2.R1010
5'-most EST
                  jC-atXLIB327412P1f06b1
                  BLASTX
Method
                  g3913418
NCBI GI
                  1097
BLAST score
                  1.0e-120
E value
Match length
                  227
                  92
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                  (SAMDC) >gi 1531763 emb CAA69073 (Y07765)
                  S-adenosylmethionine decarboxylase [Arabidopsis thaliana]
                  116451
Seq. No.
                  46 3.R1010
Contig ID
                  jC-atXP24C123D4T7059d1
5'-most EST
Method
                  BLASTX
                  g4581162
NCBI GI
BLAST score
                  440
                  3.0e-43
E value
Match length
                  117
% identity
                  72
                  (AC006220) putative symbiosis-related protein [Arabidopsis
NCBI Description
                  thaliana]
                  116452
Seq. No.
Contig ID
                  46 4.R1010
5'-most EST
                  q2581666
Method
                  BLASTX
                  g1490554
NCBI GI
BLAST score
                  106
E value
                  3.0e-04
Match length
                  136
% identity
                  ·74
                  (U63633) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  116453
Contig ID
                  46 6.R1010
                  jC-atXLIB327414P2f02a1
5'-most EST
Method
                  BLASTX
                  q4581162
NCBI GI
BLAST score
                  344
                  6.0e-35
E value
Match length
                  113
% identity
                  (AC006220) putative symbiosis-related protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  116454
                  46 7.R1010
Contig ID
                  LIB3175-026-P1-K1-E11
5'-most EST
```

```
q1531762
NCBI GI
                   195
BLAST score
E value
                   1.0e-14
Match length
                   51
                   75
% identity
                   (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                   thaliana] 🚁
                   116455
Seq. No.
Contig ID
                   46 8.R1010
                   jC-atXLIB327403P3e11b2
5'-most EST
Method
                   BLASTX
                   g1490554
NCBI GI
BLAST score
                   562
E value
                   1.0e-64
Match length
                   150
% identity
                   86
                   (U63633) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                   thaliana]
                   116456
Seq. No.
                   46 10.R1010
Contig ID
5'-most EST
                   g934989
                   BLASTN
Method
NCBI GI -
                   g2244991
BLAST score
                   316
                   1.0e-178
E value
                   366
Match length
% identity
                   97
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   116457
Seq. No.
                   47 1.R1010
Contig ID
                   jC-alXLIB327435P4h07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1402906
BLAST score
                   1626
                   0.0e + 0.0
E value
Match length
                   329
                   95
% identity
                   (X98314) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >qi 4468977 emb CAB38291 (AL035605) peroxidase, prxr2
                   [Arabidopsis thaliana]
                   116458
Seq. No.
Contig ID
                   47 2.R1010
                   jC-atXP60C198K22T7039d1
5'-most EST
                   BLASTX
Method
                   g1402906
NCBI GI
BLAST score
                   292
E value
                   4.0e-38
Match length
                   160
% identity
                   67
                   (X98314) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >qi 4468977 emb CAB38291 (AL035605) peroxidase, prxr2
```

[Arabidopsis thaliana]

Seq. No.

116463

```
Seq. No.
                   116459
Contig ID
                   48 1.R1010
5'-most EST
                   LIB3234-049-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   q543712
BLAST score
                   2593
                   0.0e + 00
E value
Match length
                   496
                   100
% identity
                   1-AMINOCYCLOPROPANE-2-CARBOXYLATE SYNTHASE 2 (ACC SYNTHASE
NCBI Description
                   2) (S-ADENOSYL-L-METHIONINE METHYLTHIOADENOSINE-LYASE 2)
                   >gi_476924_pir__A47199 1-aminocyclopropane-1-carboxylate
                   synthase (EC 4.4.1.14) - Arabidopsis thaliana
                   >gi_16148_emb_CAA78260_ (Z12614) 1-aminocyclopropane
1-carboxylate synthase [Arabidopsis thaliana] >gi_166580
                   (M95595) 1-aminocyclopropane-1-carboxylate synthase
                   [Arabidopsis thaliana] >gi 2505881 emb CAA73310 (Y12776)
                   ACC-synthase [Arabidopsis thaliana]
Seq. No.
                   116460
Contig ID
                   49 1.R1010
5'-most EST
                   jC-a1X24100Q1E1F09b1
Method
                   BLASTX
NCBI GI
                   g113171
BLAST score
                   588
E value
                   6.0e-61
Match length
                   122
% identity
                   ACYL CARRIER PROTEIN 1 PRECURSOR (ACP)
NCBI Description
                   >gi 81596 pir S03267 acyl carrier protein precursor -
                   Arabidopsis thaliana >qi 16152 emb CAA31991 (X13708) acyl
                   carrier protein [Arabidopsis thaliana]
Seq. No.
                   116461
Contig ID
                   50 1.R1010
5'-most EST
                   PLN g16159
Method
                   BLASTX
NCBI GI
                   g444790
BLAST score
                   771
E value
                   0.0e + 00
Match length
                   427
% identity
                   43
NCBI Description nucleotide translocator [Arabidopsis thaliana]
Seq. No.
                   116462
Contig ID
                   50 2.R1010
                   jC-atXLIB327431P2f12a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q444790
BLAST score
                   1866
E value
                   0.0e + 00
Match length
                   403
% identity.
                   nucleotide translocator [Arabidopsis thaliana]
NCBI Description
```

```
52 1.R1010
Contig ID
                   LIB3234-058-P1-K1-A2
5'-most EST
                   BLASTX
Method
                   q135858
NCBI GI
                   1129
BLAST score
                   1.0e-124
E value
Match length
                   268
% identity
                   TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                   >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -
                   Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
                   tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein
                   [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast
                   intrinsic protein alpha [Arabidopsis thaliana]
                   116464
Seq. No.
                   53 2.R1010
Contig ID
                   LIB3177-016-P1-K1-E9
5'-most EST
                   BLASTX
Method
                   g132090
NCBI GI
                   118
BLAST score
                   2.0e-13
E value
                   87
Match length
                   55
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   Bl precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
                   116465
Seq. No.
                   53 3.R1010 -
Contig ID
                   jC-atXLIB327427P1e02b1
5'-most EST
                   BLASTX
Method
                   g2500381
NCBI GI
                   138
BLAST score
                   3.0e-34
E value
                   104
Match length
                   66
% identity
                   60S RIBOSOMAL PROTEIN L44 P (L41) (L41 P-TYPE)
NCBI Description
                   116466
Seq. No.
                   53 4.R1010
Contig ID
                    jC-alXLIB327435P4g04b1
5'-most EST
                   BLASTN
Method
                   g2264320
NCBI GI
                    92
BLAST score
                    1.0e-43
E value
                    230
Match length
% identity
                    66
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXI10, complete sequence [Arabidopsis thaliana]
                    116467
Seq. No.
```

54 1.R1010

Contig ID

BLAST score

```
jC-atXLIB327408P3q07b1
5'-most EST
                   BLASTX
Method
                  q1168607
NCBI GI
                   942
BLAST score
E value
                   1.0e-102
Match length
                  179
% identity
                   100
                  AUXIN-INDUCED PROTEIN AUX2-11 >gi 16197 emb CAA37526
NCBI Description
                   (X53435) Aux2-11 protein [Arabidopsis thaliana] >gi 454285
                   (L15450) auxin-responsive protein [Arabidopsis thaliana]
                   116468
Seq. No.
                   57 1.R1010
Contig ID
                   jC-atXLIB327420P3e01b1
5'-most EST
                   BLASTX
Method
                   g119143
NCBI GI
                   2268
BLAST score
E value
                   0.0e + 00
                   434
Match length
                   100
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi 81606 pir__S06724 translation elongation factor eEF-1
                   alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                   (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi_1369927_emb_CAA34454_ (X16431) elongation factor
                   1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                   >gi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                   >qi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
                   116469
Seq. No.
                   57, 2.R1010
Contig ID
                   jC-alXLIB327434P4h03b1
5'-most EST
Method
                   BLASTX
                   g119143
NCBI GI
BLAST score
                   2268
                   0.0e + 00
E value
                   434
Match length
                   100
% identity
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi 81606_pir__S06724 translation elongation factor eEF-1
                   alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                   (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi 1369927 emb_CAA34454_ (X16431) elongation factor
                   1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455
                   (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                   >gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                   >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
                   116470
Seq. No.
                   57 3.R1010
Contig ID
5'-most EST
                   g1268526
                   BLASTX
Method
                   g4455192
NCBI GI
```

```
3.0e-37
E value
Match length
                  88
% identity
                  88
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  116471
Seq. No.
                  57 4.R1010
Contig ID
                  jC-atXLIB327417P1g09b1
5'-most EST
Method
                  BLASTX
                  q99688
NCBI GI
                  972
BLAST score
                  1.0e-140
E value
Match length
                  264
% identity
                  98
                  translation elongation factor eEF-1 alpha chain (gene A4) -
NCBI Description
                  Arabidopsis thaliana >gi 295789 emb CAA34456 (X16432)
                  elongation factor 1-alpha [Arabidopsis thaliana]
                  116472
Seq. No.
                  57 7.R1010
Contig ID
                  LIB3176-084-P1-K1-E9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g126766
BLAST score
                  733
E value
                  0.0e+00
Match length
                  403
                  94
% identity
                  MALATE SYNTHASE, GLYOXYSOMAL >gi 68216 pir SYRPMA malate
NCBI Description
                  synthase (EC 4.1.3.2), glyoxysomal - rape >gi 167150
                  (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]
Seq. No.
                  116473
Contia ID
                  57 10.R1010
                  jC-atXLIB327421P2d02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g99688
BLAST score
                  423
E value
                  3.0e-41
Match length
                  137 ·
% identity
                  72
                  translation elongation factor eEF-1 alpha chain (gene A4) -
NCBI Description
                  Arabidopsis thaliana >gi 295789 emb CAA34456 (X16432)
                  elongation factor 1-alpha [Arabidopsis thaliana]
Seq. No.
                  116474
Contig ID
                  57 11.R1010
5'-most EST
                  jC-atXP80C240N4T7d1
Method
                  BLASTX
NCBI GI
                  g99688
BLAST score
                  700
E value
                  7.0e-74
Match length
                  137
% identity
                  99
                  translation elongation factor eEF-1 alpha chain (gene A4) -
NCBI Description
                  Arabidopsis thaliana >gi 295789 emb CAA34456 (X16432)
```

elongation factor 1-alpha [Arabidopsis thaliana]

```
116475
 Seq. No.
 Contig ID
                    57 12.R1010
                    jC-atXLIB327401P3a03b2
 5!-most EST
                    BLASTN
 Method
                  .. g1532162
 NCBI GI
 BLAST score
                    46
 E value
                    1.0e-16
                    353
 Match length
                    55
 % identity
                   Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3,
 NCBI Description
                    AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14
                    genes, partial cds, AT.I.24-7, ascorbate peroxidase
                    (ATHAPX1), EF-lalpha-A1, -A2 and -A3 (EF-lalpha) and AT.I
                    116476
 Seq. No.
                    57 16.R1010
 Contig ID
                    LIB3234-079-P1-K1-A7
 5'-most EST
                    BLASTX
 Method
                    q99688
 NCBI GI
                    593
 BLAST score
                    1.0e-102
 E value
                    244
 Match length
                    78
 % identity
                    translation elongation factor eEF-1 alpha chain (gene A4) -
 NCBI Description
                    Arabidopsis thaliana >gi 295789 emb_CAA34456_ (X16432)
                    elongation factor 1-alpha [Arabidopsis thaliana]
                    116477
 Seq. No.
                    57 26.R1010
 Contig ID
                    LIB3176-095-P1-K1-G2
 5'-most EST
                    BLASTX
 Method
                    g119143
 NCBI GI
                    184
 BLAST score
                    3.0e-14
 E value
 Match length
                    49
                    92
 % identity
                    ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
 NCBI Description
                    >gi_81606_pir__S06724 translation elongation factor eEF-1
                    alpha chain - Arabidopsis thaliana >gi 295788 emb CAA34453_
                    (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                    >gi_1369927_emb_CAA34454_ (X16431) elongation factor
                    1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455
                    (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                    >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                    >gi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                    >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
                    116478
 Seq. No.
                    60 1.R1010
 Contig ID
                    jC-atXLIB327409P1b07b1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g2982454
 BLAST score
                    613
· E value
                    0.0e + 00
 Match length
                    356
                    92
 % identity
                    (AL022223) fructose-bisphosphate aldolase [Arabidopsis
 NCBI Description
```

NCBI GI

thaliana]

```
116479
 Seq. No.
                    60 2.R1010
 Contig ID
                    jC-atXLIB327409P1b04b1
 5'-most EST
                    BLASTX
 Method
                    g2982454
 NCBI GI
 BLAST score
                    701
                    8.0e-74
 E value
                    156
 Match length
                    91
 % identity
                    (AL022223) fructose-bisphosphate aldolase [Arabidopsis
 NCBI Description
                    thaliana]
                    116480
 Seq. No.
                    60 3.R1010
 Contig ID
                    LIB3177-046-P1-K2-G7
5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g2982453
                    617
 BLAST score
                    1.0e-125
 E value
                    263
 Match length
                    87
 % identity
 NCBI Description
                    (AL022223) fructose-bisphosphate aldolase-like protein
                    [Arabidopsis thaliana]
                    116481
 Seq. No.
                    60 4.R1010
 Contig ID
 5'-most EST
                    LIB3168-062-P1-K1-D2
 Method
                    BLASTX
                    g113617
 NCBI GI
 BLAST score
                    298
                    1.0e-31
 E value
                    138
 Match length
 % identity
                    63
                    FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
 NCBI Description
                    >gi_68199_pir__ADMU fructose-bisphosphate aldolase (EC
                    4.1.2.13) - Arabidopsis thaliana >gi_16284_emb_CAA37226_
                    (X53058) fructose 1,6-diphosphate aldolase [Arabidopsis
                    thaliana]
                    116482
 Seq. No.
                    61 2.R1010
 Contig ID
 5'-most EST
                    LIB3177-044-P1-K2-D6
 Method
                    BLASTX
 NCBI GI
                    g1072480
 BLAST score
                    524
                    2.0e-53
 E value
 Match length
                    100
                    98
 % identity
 NCBI Description
                    cruciferin 1 precursor - rape
                    116483
 Seq. No.
                    61 3.R1010
 Contig ID
 5'-most EST
                    LIB3168-098-P1-K1-C11
 Method
                    BLASTX
```

q1628583

```
BLAST score
                   238
E value
                   7.0e-20
Match length
                   157
% identity
                   74
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                   116484
Seq. No.
Contig ID
                   61 4.R1010
5'-most EST
                  LIB3168-036-P1-K1-H11
                   BLASTN
Method
NCBI GI
                  q4159706
BLAST score
                   107
E value
                   3.0e-53
Match length
                   111
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGL6, complete sequence
Seq. No.
                   116485
                   61 5.R1010
Contig ID
5'-most EST
                  LIB3234-081-Q1-K1-H9
Method
                   BLASTX
NCBI GI
                  q4006924
BLAST score
                   1609
E value
                   1.0e-180
Match length .
                   295
% identity
NCBI Description
                   (Z99708) beta-galactosidase like protein [Arabidopsis
                  thaliana]
                   116486
Seq. No.
Contig ID
                   61 6.R1010
5'-most EST
                   LIB3177-044-P1-K2-E8
Method
                   BLASTX
NCBI · GI
                   g461840
BLAST score
                   183
E value
                   1.0e-148
Match length
                   276
% identity
NCBI Description
                  CRUCIFERIN CRU1 PRECURSOR (11S GLOBULIN) (12S STORAGE
                   PROTEIN) >gi 17801 emb CAA44042 (X62120) cuciferin subunit
                   [Brassica napus]
Seq. No.
                   116487
Contig ID
                   61 7.R1010
                   jC-alXLIB327435P3g05a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4159712
BLAST score
                  156
E value
                   2.0e-82
Match length
                  156
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
```

ċ

MWI23, complete sequence

BLAST score

```
116488
Seq. No.
Contig ID
                  61 8.R1010
5'-most EST
                  LIB3234-065-P1-K1-F4
Method
                  BLASTX
                  g3808062
NCBI GI
BLAST score
                   406
E value
                   6.0e-39
Match length
                  388
% identity
                  25
                  (AB019195) PV100 [Cucurbita maxima]
NCBI Description
                  116489
Seq. No.
Contig ID
                  61 9.R1010
5'-most EST
                  LIB3168-017-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  211
E value
                  6.0e-16
Match length
                  522
                  28
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  116490
Seq. No.
Contig ID
                  62 1.R1010
5'-most EST
                  LIB3234-095-P1-K1-G12
                  BLASTX
Method
NCBI GI
                  g1628622
BLAST score
                  1788
                  0.0e + 00
E value
Match length
                  336
% identity
                  (U72631) flavonol synthase [Arabidopsis thaliana]
NCBI Description
                  >qi 1805305 (U84258) flavonol synthase [Arabidopsis
                  thaliana] >gi 1805307 (U84259) flavonol synthase
                   [Arabidopsis thaliana] >gi 1805309 (U84260) flavonol
                  synthase [Arabidopsis thaliana]
                  116491
Seq. No.
Contig ID
                  63 1.R1010
5'-most EST
                  PLN q16292
Method
                  BLASTN
NCBI GI
                  q4757392
BLAST score
                  130
E value
                  2.0e-66
Match length .
                  432
% identity
                  21
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K14A17, complete sequence
Seq. No.
                  116492
Contig ID
                  64 1.R1010
5'-most EST
                  g1159026
                  BLASTX
Method
NCBI GI
                  q1169519
```

```
E value
                  1.0e-47
Match length
                  92
% identity
                  100
                  EM-LIKE PROTEIN GEA6 >gi 486680 pir S34802 embryogenic
NCBI Description
                  abundant protein - Arabidopsis thaliana
                  >qi 16295 emb CAA46821 (X66023) late-embryogenesis
                  abundant protein [Arabidopsis thaliana]
                  >gi 298075 emb CAA77981 (Z11923) Em protein homologue
                  [Arabidopsis thaliana] >gi_298077_emb_CAA77982_ (Z11924) Em
                  protein homologue [Arabidopsis thaliana]
                  >qi 4587991 gb AAD25932.1 AF085279 5 (AF085279) ATEM6
                  [Arabidopsis thaliana]
Seq. No.
                  116493
                  65 1.R1010
Contig ID
                  LIB24-114-Q1-E1-D8
5'-most EST
Method
                  BLASTX
                  q81630
NCBI GI
                  439
BLAST score
                  5.0e-43
E value
                  222
Match length
% identity
                  47
                  glycine-rich protein atGRP-8 - Arabidopsis thaliana
NCBI Description
                  >gi 16297 emb CAA77895 (Z11869) Glycine rich protein
                  [Arabidopsis thaliana] >gi_16309_emb_CAA77883_ (Z11858)
                  Glycine Rich Protein [Arabidopsis thaliana]
Seq. No.
                  116494
                  66 1.R1010
Contig ID
                  jC-atXLIB327414P3f02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3688799
                  1209
BLAST score
                  1.0e-133
E value
Match length
                  253
% identity
                  (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  116495
Contig ID
                  66 2.R1010
                  jC-atXLIB327416P2f11b1
5'-most EST
Method
                  BLASTX
                  q135860
NCBI GI
BLAST score
                  1286
                  1.0e-142
E value
Match length
                  251
% identity
                  100
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic
                  protein gamma - Arabidopsis thaliana
                  >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                  protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732
                  (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                  >qi 445129 prf 1908432B tonoplast intrinsic protein gamma
```

[Arabidopsis thaliana]

5'-most EST

```
116496
Seq. No.
                   66 3.R1010
Contig ID
                   q2\overline{5}97253 ·
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2246621
BLAST score
                   1320
                   1.0e-146
E value
                   273
Match length
                   95
% identity
NCBI Description
                  (AF004393) salt-stress induced tonoplast intrinsic protein
                   [Arabidopsis thaliana]
                   116497
Seq. No.
                   66 4.R1010
Contig ID
5'-most EST
                   LIB3176-035-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   a3688799
                   487
BLAST score
E value
                   7.0e-86
                   253
Match length
% identity
                  (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
NCBI Description
                   thaliana]
                   116498
Seq. No.
Contig ID
                   66 5.R1010
                   q2\overline{4}13850
5'-most EST
Method
                   BLASTX
NCBI GI
                   q135860
BLAST score
                   509
E value
                   2.0e-51
Match length
                   113
% identity
                   51
                   TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi 99761 pir S22202 tonoplast intrinsic
                   protein gamma - Arabidopsis thaliana
                   >gi 16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                   protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi 166732
                   (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                   >gi 445129 prf 1908432B tonoplast intrinsic protein gamma
                   [Arabidopsis thaliana]
Seq. No.
                   116499
                   66 6.R1010
Contig ID
                   q9\overline{3}3503
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3688799
BLAST score
                   506
                   4.0e-51
E value
                   133
Match length
% identity
                   (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
NCBI Description
                   thalianal
                   116500
Seq. No.
Contia ID
                   66 9.R1010
```

jC-atXLIB327401P4g01b1

Method

BLASTX

```
g135860
NCBI GI
BLAST score
                  709
E value
                  6.0e-75
Match length
                  182
                  56
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic
                  protein gamma - Arabidopsis thaliana
                  >gi 16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                  protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi 166732
                  (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                  >gi 445129 prf 1908432B tonoplast intrinsic protein gamma
                  [Arabidopsis thaliana]
                  116501
Seq. No.
Contig ID
                  66 14.R1010
5'-most EST
                  g936021
Method
                  BLASTX
NCBI GI
                  g3688799
BLAST score
                  144
                  2.0e-08
E value
Match length
                  220
% identity
                  47
                  (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  116502
Contig ID
                  67 1.R1010
5'-most EST
                  LIB23-008-Q1-E1-B10
                  BLASTX
Method
                  q121902
NCBI GI
BLAST score
                  358
E value
                  2.0e-33
Match length
                  122
% identity
                  65
                  HISTONE H1.1 >gi 1070594 pir HSMU11 histone H1.1 -
NCBI Description
                  Arabidopsis thaliana >gi_16317_emb CAA44314 (X62458)
                  Histone H1 [Arabidopsis thaliana]
                  116503
Seq. No.
Contig ID
                  68 1.R1010
                  jC-atXLIB327421P2d11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g417103
BLAST score
                  679
E value
                  3.0e-71
Match length
                  136
% identity
                  100
                  HISTONE H3.2, MINOR >gi 282871 pir S24346 histone
NCBI Description
                  H3.3-like protein - Arabidopsis thaliana
                  >gi 16324 emb CAA42957 (X60429) histone H3.3 like protein
                  [Arabidopsis thaliana] >gi 404825 emb CAA42958 (X60429)
                  histone H3.3 like protein [Arabidopsis thaliana] >gi 488563
                  (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460)
                  histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone
                  H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2
```

[Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445 (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 116504 Contig ID 68 2.R1010

5'-most EST jC-atXLIB327401P3g04b2

Method BLASTN
NCBI GI 94490734
BLAST score 376
E value 0.0e+00
Match length 429
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA

project)

Seq. No. 116505 Contig ID 68_3.R1010

5'-most EST jC-atXLIB327418P2b03b2

Method BLASTX
NCBI GI g417103
BLAST score 548
E value 5.0e-65
Match length 135
% identity 100

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
(U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460)
histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] $>gi_4885\overline{7}7$ (U09465) histone H3.2

[Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]

>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana
tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi_4490755 emb_CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

 Seq. No.
 116506

 Contig ID
 68_5.R1010

 5'-most EST
 g934728

 Method
 BLASTX

E value

```
g1053045
NCBI GI
BLAST score
                   388
E value
                   2.0e-39
Match length
                   121
% identity
                   79
                   (U38424) histone H3 [Glycine max]
NCBI Description
                   116507
Seq. No.
Contig ID
                   68 6.R1010
                  LIB3177-099-P1-K1-H12
5'-most EST
                   BLASTX
Method
                   g417103
NCBI GI
BLAST score
                   519
                   1.0e-52
E value
Match length
                   121
% identity
                   HISTONE H3.2, MINOR >gi 282871 pir__S24346 histone
NCBI Description
                   H3.3-like protein - Arabidopsis thaliana
                   >gi 16324 emb_CAA42957 (X60429) histone H3.3 like protein
                   [Arabidopsis thaliana] >gi_404825_emb CAA42958_ (X60429)
                   histone H3.3 like protein [Arabidopsis thaliana] >gi 488563
                   (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460)
                   histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone
                   H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2
                   [Medicago sativa] >gi 488577 (U09465) histone H3.2
                   [Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone
                   H3 [Lolium temulentum] >qi 1\overline{435157} emb CAA58445 (X83422)
                   histone H3 variant H3.3 [Lycopersicon esculentum]
                   >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
                   >qi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana
                   tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa]
                   >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
                   coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone
                   H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1
                   (AL035708) Histon H3 [Arabidopsis thaliana]
                   116508
Seq. No.
                   69 1.R1010
Contig ID
                   PLN g166751
5'-most EST
                   BLASTX
Method
NCBI GI
                   q421827
BLAST score
                   1302
E value
                   1.0e-144
Match length
                   284
% identity
                  homeotic protein HAT4 - Arabidopsis thaliana >gi_22759_emb_CAA79670_ (Z19602) HAT4 [Arabidopsis
NCBI Description
                   thaliana] >gi 166752 (M90394) homeobox protein [Arabidopsis
                   thaliana]
                   116509
Seq. No.
                   70 1.R1010
Contig ID
5'-most EST
                   jC-atXP12C99K21T7016a1
Method
                   BLASTX
                   q399298
NCBI GI
                   217
BLAST score
```

3.0e-17

```
66
Match length
% identity
                  70
                  STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6.6 PROTEIN)
NCBI Description
                  >gi_1084343_pir__S22529 cold-regulated protein kin2 -
                  Arabidopsis thaliana >gi 16230 emb CAA38894 (X55053) cold
                  regulated [Arabidopsis thaliana]
                  116510
Seq. No.
                  70_3.R1010
Contig ID
5'-most EST
                  g2413221
                  BLASTX
Method
                  g125408
NCBI GI
BLAST score
                  220
                  6.0e-18
E value
                  66
Match length
                  71
% identity
                  STRESS-INDUCED KIN1 PROTEIN >gi_99734_pir__S11155 kin1
NCBI Description
                  protein - Arabidopsis thaliana >gi_296033_emb_CAA35838_
                  (X51474) kin1 [Arabidopsis thaliana]
                  116511
Seq. No.
                  72 1.R1010
Contig ID
                  g496770
5'-most EST
                  BLASTX
Method
                 g1170839
NCBI GI
                  2514
BLAST score
                  0.0e + 00
E value
                  600
Match length
                  83
% identity
                  LOW-TEMPERATURE-INDUCED 65 KD PROTEIN
NCBI Description
                  >qi 419758 pir S30153 low-temperature-induced protein 65 -
                  Arabidopsis thaliana >gi 16388 emb CAA47902 (X67670) lti65
                   [Arabidopsis thaliana]
                  116512
Seq. No.
                  73 1.R1010
Contig ID
                  LIB25-096-Q1-E1-C5
5'-most EST
                  BLASTX
Method
                  g1170840
NCBI GI
                  3088
BLAST score
E value
                  0.0e + 00
                  710
Match length
% identity
                  LOW-TEMPERATURE-INDUCED 78 KD PROTEIN
NCBI Description
                   (DESSICATION-RESPONSIVE PROTEIN 29B) >gi_419759_pir__S30154
                   low-temperature-induced protein 78 - Arabidopsis thaliana
                  >gi 16390 emb CAA47903 (X67671) lti78 [Arabidopsis
                   thaliana] >gi 348692 (L22567) cor78 [Arabidopsis thaliana]
                   116513
Seq. No.
                  73 2.R1010
Contig ID
5'-most EST
                   g2749030
Method
                  BLASTX
                   q1345516
NCBI GI
                   355
BLAST score
                   2.0e-33
E value
                   92
Match length
```

```
75
% identity
                  (X57600) ltil40 [Arabidopsis thaliana]
NCBI Description
                  116514
Seq. No.
                  74 1.R1010
Contig ID
5'-most EST
                  LIB146-014-Q1-E1-A10
Method
                  BLASTX
                  g266693
NCBI GI
                  785
BLAST score
                  1.0e-83
E value
                  173
Match length
% identity
NCBI Description
                  OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis
                  thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin
                  [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_
                  (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
                  116515
Seq. No.
                  75 1.R1010
Contig ID
                  LIB22-064-Q1-E1-E5
5'-most EST
                  BLASTX
Method
                  g1171991
NCBI GI
BLAST score
                  3629
                  0.0e+00
E value
                  725
Match length
                  98
% identity
                  PHENYLALANINE AMMONIA-LYASE 1 >gi_1076369_pir__S52990
NCBI Description
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis
                  thaliana >gi 497419 (L33677) phenylalanine ammonia lyase
                  [Arabidopsis thaliana]
                  116516
Seq. No.
                  75 2.R1010
Contig ID
                  jC-atXLIB327413P3b12b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1171993
BLAST score
                  3608
                  0.0e+00
E value
                  717
Match length
% identity
                  99
                  PHENYLALANINE AMMONIA-LYASE 2 >gi 1076370 pir__S52991
NCBI Description
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis
                  thaliana >gi 497421 (L33678) phenylalanine ammonia lyase
                   [Arabidopsis thaliana]
                  116517
Seq. No.
Contig ID
                  76 1.R1010
                  LIB3234-057-P1-K1-C3
5'-most EST.
Method
                  BLASTX
                  g1172441
NCBI GI
BLAST score
                  1399
E value
                  1.0e-155
Match length
                  398
                  74
% identity
                  POSSIBLE TRANSCRIPTION FACTOR POSF21 >qi 99685 pir S21883
NCBI Description
                  DNA-binding protein POSF21 - Arabidopsis thaliana
                  >gi 16429 emb CAA43366 (X61031) posF21 [Arabidopsis
```

thaliana] >gi_4589968_gb_AAD26486.1_AC007169_18 (AC007169) DNA-binding protein POSF21 [Arabidopsis thaliana]

116518 Seq. No. 76 2.R1010 Contig ID 5'-most EST LIB3175-002-Q1-K1-H1 BLASTN Method NCBI GI g16428 BLAST score 229 1.0e-126 E value 446 Match length 98 % identity NCBI Description A.thaliana posF21 gene 116519 Seq. No. 77 1.R1010 Contig ID -jC-atXLIB327426P3f06b1 5'-most EST BLASTX Method ,_g131398 NCBI GI 554 BLAST score 1.0e-56 E value 140 Match length % identity 81 PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description >gi 72714 pir F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi 3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb T41858, gb T88021, gb R37531, gb T04679, gb N37520, gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400 come from this gene. [Arabidopsis Seq. No. 116520 77 2.R1010 Contig ID 5'-most EST jC-atXLIB327426P1f04b1 Method BLASTX q131398 NCBI GI BLAST score 543 E value 2.0e-55 Match length 139 % identity PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description >gi 72714 pir F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >qi 16447 emb CAA39441 (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi 3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb X55970. ESTs gb Z17693, gb N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400 come from this gene. [Arabidopsis

Seq. No. 116521 Contig ID 77_3.R1010

5'-most EST jC-atXP13C104G23T7027a1

Method BLASTX NCBI GI g131398

```
BLAST score
                  474
                  2.0e-47
E value
Match length
                  132
                  75
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                  >qi 72714 pir F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi_3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                  gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                  gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400
                  come from this gene. [Arabidopsis
Seq. No.
                  116522
                  77 4.R1010
Contig ID
                  q2446232
5'-most EST
Method
                  BLASTX
                  q131398
NCBI GI
BLAST score
                  479
E value
                  3.0e-48
Match length
                  136
% identity
                  82
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR :
NCBI Description
                  >gi 72714 pir F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi 3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                  gb T41858, gb T88021, gb R37531, gb T04679, gb N37520,
                  gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400
                  come from this gene. [Arabidopsis
Seq. No.
                  116523
Contig ID
                  77 5.R1010
5'-most EST
                  jC-atXLIB327423P4d11b1
                  BLASTX
NCBI GI
                  g131398
BLAST score
                  403
E value
                  5.0e-39
Match length
                  112
% identity
                  79
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                  >qi 72714 pir F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >qi 16447 emb CAA39441 (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi 3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                  gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                  gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                  come from this gene. [Arabidopsis
```

Seq. No. 116524 Contig ID 77 6.R1010

5'-most EST jC-atXP96C248A10T7b1

Method BLASTX NCBI GI g122085 BLAST score 546 E value 1.0e-55 Match length 127 % identity 87

NCBI Description

HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi 20251 emb CAA31969 (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] $>gi_168495$ (M13378) histone H3 [Zea mays] >gi 168497 (M13379) histone H3 [Zea mays] >gi_168506 $(M3\overline{5}388)$ histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] $>gi_1\overline{0}40764$ (M35 $\overline{3}87$) histone H3 [Arabidopsis thaliana] >\(\overline{gi}\)_1314779 (U54827) histone H3 homolog [Brassica napus] $>\overline{g}i_1531754$ emb_CAA57811 (X82414) Histone H3 [Asparagus officinalis] $>\overline{g}i$ $1\overline{6}67592$ (U $\overline{7}7296$) histone 3 [Oryza sativa] >gi 3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs qb H76511 qb H76255, qb AA712452, gb N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >qi 225459 prf 1303352A histone H3 [Helicoverpa zea] >gi 225839 prf 1314298B histone H3 [Arabidopsis thaliana]

116525 Seq. No. Contig ID 77 8.R1010 LIB3177-020-P1-K2-G8 5'-most EST BLASTX Method g131398 NCBI GI BLAST score 227 2.0e-21 E value Match length 126 % identity

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor

- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)

photosystem II 10 kDa polypeptide [Arabidopsis thaliana]

>gi_3152571 (AC002986) Match to photosystem II 10kDa

polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,

qb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

qb_N64965, qb_Z17592 and qb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

 Seq. No.
 116526

 Contig ID
 77_9.R1010

 5'-most EST
 jC-atXP101CE2A3T7013d1

 Method
 BLASTX

 NCBI GI
 g131398

 BLAST score
 116

BLAST score 116 E value 5.0e-44 Match length 133 % identity 76 NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
come from this gene. [Arabidopsis

 Seq. No.
 116527

 Contig ID
 77_10.R1010

 5'-most EST
 jC-atXLIB327421P4f09b1

 Method
 BLASTX

 NCBI GI
 g131398

 BLAST score
 460

 E value
 1.0e-45

 Match length
 124

Match length 124 % identity 79

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 116528 Contig ID 77_11.R1010

5'-most EST jC-atXLIB327437P4d12a2

Method BLASTX
NCBI GI g131398
BLAST score 229
E value 1.0e-18
Match length 123
% identity 36

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 116529 Contig ID 77 12.R1010

5'-most EST jC-atXLIB327421P3h09b1

Method BLASTX
NCBI GI g131398
BLAST score 223
E value 7.0e-18
Match length 145
% identity 31

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi 72714 pir F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi 3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400 come from this gene. [Arabidopsis 116530 Seq. No. 77 13.R1010 Contig ID jC-atXLIB327417P4b04a1 5'-most EST Method BLASTX g131398 NCBI GI BLAST score 182 5.0e-13 E value 124 Match length 42 % identity PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description >gi 72714 pir F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] $>gi_3152571$ (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb T41858, gb T88021, gb R37531, gb T04679, gb N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis 116531 Seq. No. 77 14.R1010 Contig ID jC-atXLIB327422P2a10b2 5'-most EST Method BLASTX g131398 NCBI GI BLAST score 473 3.0e-47 E value 116 Match length % identity PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description >gi 72714 pir F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi 3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb X55970. ESTs gb Z17693, gb N37616, gb T41858, gb T88021, gb R37531, gb T04679, gb N37520, gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400 come from this gene. [Arabidopsis 116532 Seq. No. 77 16.R1010 Contig ID

 Seq. No.
 116532

 Contig ID
 77_16.R1010

 5'-most EST
 LIB35-052-Q1-E1-A8

 Method
 BLASTX

 NCBI GI
 g131398

 BLAST score
 409

 E value
 1.0e-39

 Match length
 143

 % identity
 64

```
NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi_3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb X55970. ESTs gb_Z17693, gb_N37616,
                  gb T41858, gb T88021, gb R37531, gb T04679, gb N37520,
                  gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb T45400
                  come from this gene. [Arabidopsis
                  116533
Seq. No.
                  77 19.R1010
Contig ID
5'-most EST
                  jC-atXLIB327421P3e05b1
Method
                  BLASTX
                  g131398
NCBI GI
BLAST score
                  324
                  1.0e-29
E value
Match length
                  66
                 - 100
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                  >gi 72714 pir F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi_3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb_X55970. ESTs gb Z17693, gb N37616,
                  gb_T41858, gb_T88021, gb R37531, gb T04679, gb N37520,
                  gb_N64965, gb_Z17592 and gb N65338, gb N37466 and gb T45400
                  come from this gene. [Arabidopsis
Seq. No.
                  116534
Contig ID
                  77 22.R1010
5'-most EST
                  LIB35-049-01-E1-G11
Method
                  BLASTX
NCBI GI
                  g131398
BLAST score
                  428
E value
                  6.0e-43
Match length
                  115
% identity
                  85
NCBI Description
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >gi 72714 pir F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi 3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb X55970. ESTs gb Z17693, gb N37616,
                  gb T41858, gb T88021, gb R37531, gb T04679, gb N37520,
                  qb N64965, qb Z17592 and qb N65338, qb N37466 and qb T45400
                  come from this gene. [Arabidopsis
Seq. No.
                  116535
Contig ID
                  77 29.R1010
5'-most EST
                  jC-atXLIB327414P1f04b1
Method
                  BLASTN
NCBI GI
                  g4539290
BLAST score
                  267
                  1.0e-148
E value
Match length
                  404
```

99

% identity

```
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19
                   (ESSA project)
                  116536
Seq. No.
                  78 1.R1010
Contig ID
                  jC-atXLIB327408P2c05b1
5'-most EST
                  BLASTX
Method
                  <sup>-</sup>g231995
NCBI GI
BLAST score
                   320
                   4.0e-29
E value
                   186
Match length
% identity
                   40
                  DEHYDRIN RAB18 >gi 282880 pir S28021 rab18 protein -
NCBI Description
                  Arabidopsis thaliana >gi 16451 emb CAA48178 (X68042) RAB18
                   [Arabidopsis thaliana]
                   116537
Seq. No.
Contig ID
                  78 2.R1010
5'-most EST
                   jC-atXP96C248E6T7b1
Method
                  BLASTN
NCBI GI
                   q3128136
BLAST score
                   284
E value
                   1.0e-158
Match length
                   636
                  84
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K1F13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   116538
Contig ID
                  78 6.R1010
5'-most EST
                  q1327750
Method
                  BLASTX
NCBI GI
                   q231995
BLAST score
                   190
E value
                   3.0e-14
Match length
                   101
% identity
                   43
                  DEHYDRIN RAB18 >gi 282880 pir S28021 rab18 protein -
NCBI Description
                  Arabidopsis thaliana > qi 16451 emb CAA48178 (X68042) RAB18
                   [Arabidopsis thaliana]
Seq. No.
                   116539
Contig ID
                  78 7.R1010
5'-most EST
                  q1053750
Method
                  BLASTX
NCBI GI
                   q166570
BLAST score
                   140
                   2.0e-09
E value
Match length
                  76
% identity
                  (L04173) glycine rich protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  116540
Contig ID
                  83 1.R1010
                  jC-atXLIB327410P2e12b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4098331
```

```
BLAST score
                  800
                  4.0e-85
E value
Match length
                  428
% identity
                  (U76896) beta-tubulin 5 [Triticum aestivum]
NCBI Description
                  116541
Seq. No.
                  83 2.R1010
Contig ID
                  jC-atXLIB327409P4a10b1
5'-most EST
                  BLASTX
Method
                  q4098319
NCBI GI
BLAST score
                  383
                  7.0e-70
E value
Match length
                  142
% identity
                  97
                  (U76744) beta-tubulin 1 [Triticum aestivum]
NCBI Description
                  116542
Seq. No.
Contig ID
                  83 3.R1010
5'-most EST
                  LIB3175-025-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g119350
BLAST score
                  1480
E value
                  1.0e-165
Match length
                  288
% identity
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir_ JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                  thaliana >gi 16271 emb CAA41114 (X58107) enolase
                  [Arabidopsis thaliana]
                  >qi 4581151 qb AAD24635.1 AC006919 13 (AC006919) enolase
                  (2-phospho-D-glycerate hydroylase); identical to P25696
                  [Arabidopsis thaliana]
                 116543
Seq. No.
Contig ID
                  83 4.R1010
5'-most EST
                  jC-atXLIB327423P1h06b1
                  BLASTX
Method
NCBI GI
                  q267083
BLAST score
                  543
E value
                  5.0e-86
Match length
                  181
% identity
                  TUBULIN BETA-9 CHAIN >qi 320190 pir JQ1593 tubulin beta-9
NCBI Description
                  chain - Arabidopsis thaliana >qi 166910 (M84706) beta-9
                  tubulin [Arabidopsis thaliana]
                  116544
Seq. No.
                  83 5.R1010
Contig ID
5'-most EST
                  jC-atXP89C244N2T7090d1
                  BLASTX
Method
NCBI GI
                  q119350
BLAST score
                  1360
                  1.0e-151
E value
                  265
Match length
                  100
% identity
```

% identity

40

```
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                  thaliana >gi_16271_emb_CAA41114 (X58107) enolase
                  [Arabidopsis thaliana]
                  >qi 4581151 qb AAD24635.1 AC006919 13 (AC006919) enolase
                  (2-phospho-D-glycerate hydroylase); identical to P25696
                  [Arabidopsis thaliana]
                  116545
Seq. No.
                  83 6.R1010
Contig ID
                  jC-atXLIB327417P3f02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g135449
BLAST score
                  164
E value
                  6.0e-11
Match length
                  164
% identity
                  TUBULIN BETA-1 CHAIN >gi 100932 pir S14701 tubulin beta-1
NCBI Description
                  chain - maize >gi 295851 emb CAA37060 (X52878) beta 1
                  tubulin [Zea mays]
                  116546
Seq. No.
                  83 7.R1010
Contig ID
5'-most EST
                  LIB22-080-Q1-E2-G1
Method
                  BLASTX
NCBI GI
                  g135467
BLAST score
                  642
E value
                  4.0e-67
Match length
                  118
% identity
                  TUBULIN BETA-4 CHAIN >gi 2129546 pir S68122 beta-tubulin 4
NCBI Description
                  - Arabidopsis thaliana >qi 166640 (M21415) beta-tubulin
                  [Arabidopsis thaliana]
                  116547
Seq. No.
Contig ID
                  83 8.R1010
                  jC-atXP60C198C1T7067d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q135467
BLAST score
                  539
E value
                  5.0e-55
Match length
                  111
% identity
                  TUBULIN BETA-4 CHAIN >gi_2129546_pir S68122 beta-tubulin 4
NCBI Description
                  - Arabidopsis thaliana >qi 166640 (M21415) beta-tubulin
                  [Arabidopsis thaliana]
                  116548
Seq. No.
Contig ID
                  83 9.R1010
5'-most EST
                  LIB35-042-Q1-E1-C8
Method
                  BLASTX
                  g829169
NCBI GI
BLAST score
                  576
                  4.0e-59
E value
Match length
                  241
```

Method

BLASTX

```
NCBI Description (L33263) beta-tubulin [Oryza sativa]
                  116549
Seq. No.
                  83 10.R1010
Contig ID
                  jC-atXLIB327417P4f02b1
5'-most EST
                  BLASTX
Method
                - q267073
NCBI GI
BLAST score
                  512
                  1.0e-51
E value
                  180
Match length
% identity
                  TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi_166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
                  116550
Seq. No.
                  83 11.R1010
Contig ID
                  jC-atXLIB327417P2f01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g135469
BLAST score
                  217
E value
                  4.0e-17
Match length
                  175
% identity
                  TUBULIN BETA-5 CHAIN (CLASS-V) >gi 86470 pir A25401
NCBI Description
                  tubulin beta-5 chain - chicken >gi_459714 (L29435) beta-5
                  tubulin [Gallus gallus]
Seq. No.
                  116551
Contig ID
                  83 13.R1010
5'-most EST
                  jC-atXLIB327410P2e12a1
Method
                  BLASTX
NCBI GI
                  g4415996
BLAST score
                  293
E value
                  3.0e-26
Match length
                  58
% identity
                  (AF059290) beta-tubulin 4 [Eleusine indica]
NCBI Description
Seq. No.
                  116552
                  83 14.R1010
Contig ID
                  LIB3177-042-P1-K2-H9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g267076
BLAST score
                  480
E value
                  3.0e-48
Match length
                  95
% identity
                  TUBULIN BETA-3 CHAIN >gi 81953 pir S20870 tubulin beta-3
NCBI Description
                  chain - garden pea (fragment) >gi 388255 emb CAA38615
                  (X54846) beta-tubulin 3 [Pisum sativum]
                  116553
Seq. No.
                  83 15.R1010
Contig ID
                  jC-atXLIB327418P2b09b2
5'-most EST
```

```
NCBI GI
                  q267081
BLAST score
                  260
E value
                  2.0e-52
                  142
Match length
                  80
% identity
                  TUBULIN BETA-7 CHAIN >gi 320188 pir JQ1591 tubulin beta-7
NCBI Description
                  chain - Arabidopsis thaliana >gi 166906 (M84704) beta-7
                  tubulin [Arabidopsis thaliana] >gi 3980381 (AC004561)
                  tubulin beta-7 chain [Arabidopsis Thaliana]
                  116554
Seq. No.
                  83 17.R1010
Contig ID
                  LIB3177-077-P1-K1-D11
5'-most EST
Method
                  BLASTX
NCBI GI
                  q267083
BLAST score
                  560
                  1.0e-57
E value
Match length
                  107
                  100
% identity
                  TUBULIN BETA-9 CHAIN >gi 320190 pir JQ1593 tubulin beta-9
NCBI Description
                  chain - Arabidopsis thaliana >gi 166910 (M84706) beta-9
                  tubulin [Arabidopsis thaliana]
                  116555
Seq. No.
                  83 23.R1010
Contig ID
5'-most EST
                  jC-atXmonuni26Ce08b1
                  BLASTX
Method
NCBI GI
                  q267077
BLAST score
                  801
                  9.0e-86
E value
Match length
                  166
% identity
                  TUBULIN BETA-5 CHAIN >qi 320186 pir JQ1589 tubulin beta-5
NCBI Description
                  chain - Arabidopsis thaliana >gi 16\overline{69}02 (M84702) beta-5
                  tubulin [Arabidopsis thaliana]
                  116556
Seq. No.
Contig ID
                  83 25.R1010
                  LIB3175-016-P1-K1-C9
5'-most EST
Method .
                  BLASTX
                  g267073
NCBI GI
BLAST score
                  434
                  7.0e-44
E value
Match length
                  99
% identity
NCBI Description
                  TUBULIN BETA-2/BETA-3 CHAIN >qi 320184 pir JQ1587 tubulin
                  beta chain - Arabidopsis thaliana >gi 166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
                  116557
Seq. No.
                  83 26.R1010
Contig ID
5'-most EST
                  LIB23-037-Q1-E1-A11
Method
                  BLASTX
                  g267077
NCBI GI
BLAST score
                  428
                  1.0e-81
E value
```

```
Match length
                  157
% identity
                  93
                  TUBULIN BETA-5 CHAIN >gi_320186_pir__JQ1589 tubulin beta-5
NCBI Description
                  chain - Arabidopsis thaliana >gi 166902 (M84702) beta-5
                  tubulin [Arabidopsis thaliana]
                  116558
Seq. No.
                  83 27.R1010
Contig ID
                  LIB3176-068-P1-K1-D5
5'-most EST
Method
                  BLASTX
                  q135494
NCBI GI
BLAST score
                  249
E value
                  9.0e-33
                  118
Match length
                  72 .
% identity
                  TUBULIN BETA CHAIN >gi_81224_pir__JQ0177 tubulin beta chain
NCBI Description
                  - green alga (Polytomella agilis) >gi 169434 (M33372)
                  beta-1 tubulin (beta-1-tub) [Polytomella agilis] >gi 169438
                  (M33371) beta-3 tubulin (beta-3-tub) [Polytomella agilis]
                  116559
Seq. No.
                  83 29.R1010
Contig ID
5'-most EST
                  LIB23-012-Q1-E1-A10
Method
                  BLASTX
                  g267073
NCBI GI
BLAST score
                  421
                  2.0e-41
E value
                  78
Match length
                  100
% identity
                  TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi_166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
                  116560
Seq. No.
                  84 1.R1010
Contig ID
                  jC-atXLIB327406P3b09b2
5'-most EST
                  BLASTX
Method
                  q282865
NCBI GI
BLAST score
                  1160
                  1.0e-127
E value
                  241
Match length
                  90
% identity
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
NCBI Description
                  >gi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi 4678304 emb CAB41095.1 (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  116561
                  84 2.R1010
Contig ID
                  jC-atXP85C241G11T7b1
5'-most EST
                  BLASTX
Method .
NCBI GI
                  g115764
BLAST score
                  171
E value
                  1.0e-62
```

BLAST score

441

```
Match length
                  238
% identity
                  46
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE I PRECURSOR
NCBI Description
                  (CAB-6A) (LIGHT-HARVESTING COMPLEX I 26 KD PROTEIN)
                  >gi 170494 (J03558) chlorophyll a/b binding protein
                  precursor [Lycopersicon esculentum]
                  116562
Seq. No.
                  84 5.R1010
Contig ID
5'-most EST
                  LIB25-093-Q1-E1-D2
Method
                  BLASTX
                  g282865
NCBI GI
BLAST score
                  819
E value
                  1.0e-87
Match length
                  205
% identity
                  78
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
NCBI Description
                  >qi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi 166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >qi 4678304 emb CAB41095.1 (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
                  116563
Seq. No.
Contig ID
                  86 1.R1010
5'-most EST
                  PLN g166657
Method
                  BLASTX
NCBI GI
                  q544425
BLAST score
                  198
E value
                  1.0e-14
Match length
                  101
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
NCBI Description
                  >qi 419756 pir S30148 glycine-rich protein (clone AtGRP8)
                  - Arabidopsis thaliana >gi 16305 emb CAA78712 (Z14988)
                  glycine rich protein [Arabidopsis thaliana] >gi 166658
                  (L04171) ORF [Arabidopsis thaliana] >gi 166839 (L00649)
                  RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  116564
Contig ID
                  86 2.R1010
5'-most EST
                  LIB25-012-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  q3915847
BLAST score
                  1131
E value
                  1.0e-124
Match length
                  238
% identity
                  92
                  40S RIBOSOMAL PROTEIN S2 >qi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
                  116565 .
Seq. No.
Contig ID
                  86 3.R1010
5'-most EST
                  q2739610
Method ·
                  BLASTX
NCBI GI
                  q544424
```

```
3.0e-43
E value
Match length
                   85
                   100
% identity
                   GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147
NCBI Description
                   glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                   >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                   protein [Arabidopsis thaliana]
                   >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                   glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
                   116566
Seq. No.
Contig ID
                   86 4.R1010
                   jC-atX24037Q1E2A01b1
5'-most EST
                   BLASTX
Method
                   g3915847
NCBI GI
                   339
BLAST score
                   2.0e-60
E value
Match length
                   129
                   91
% identity
                   40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
NCBI Description
                   40S ribosomal protein S2 [Arabidopsis thaliana]
                   116567
Seq. No.
                   86 5.R1010
Contig ID
                   jC-atXP11C98N10T7077d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q544425
BLAST score
                   433
                   1.0e-42
E value
Match length
                   84
                   100
% identity
                   GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
NCBI Description
                   >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8)
                   - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988)
                   glycine rich protein [Arabidopsis thaliana] >gi_166658
                   (L04171) ORF [Arabidopsis thaliana] >gi 166839 (L00649)
                   RNA-binding protein [Arabidopsis thaliana]
                   116568
Seq. No.
                   86 6.R1010
Contig ID
                   jC-atXP73C223F12T7b1
5'-most EST
                   BLASTX
Method
                   q4567236
NCBI GI
BLAST score
                   88
                   2.0e-18
E value
Match length
                   82
% identity
                   (AC007119) glycine-rich RNA binding protein Ccr2
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   116569
Contig ID
                   86 7.R1010
                   jC-atXLIB327416P1d03b1
5'-most EST
                   BLASTX
Method
                   q544424
NCBI GI
```

204

BLAST score

```
E value
                    9.0e-16
                    39
Match length
                    97
% identity
                    GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147
NCBI Description
                    glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                    >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                    protein [Arabidopsis thaliana]
                    >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                    glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
                    116570
Seq. No.
                    86 9.R1010
Contig ID
                    g2759527
5'-most EST
Method
                    BLASTX
                    g544424
NCBI GI
BLAST score
                    462
                    4.0e-46
E value
Match length
                    90
                    99
% identity
                    GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147
NCBI Description
                    glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                    >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
                    [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                    protein [Arabidopsis thaliana]
                    >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
                    116571
Seq. No.
                    86_10.R1010
Contig ID
                    jC-atXLIB327425P1b04b1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g461753
BLAST score
                    221
E value
                    7.0e-18
Match length
                    47
% identity
                    94
                    ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
NCBI Description
                    PRECURSOR >gi_419773_pir__S31164 ATP-dependent ClpB
                    proteinase regulatory chain homolog precursor, chloroplast
                    - garden pea >gi_169128 (L09547) nuclear encoded precursor
                    to chloroplast protein [Pisum sativum]
Seq. No.
                    116572
                    86 11.R1010
Contig ID
                    jC-atXLIB327418P1c03b1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q544425
BLAST score
                    196
E value
                    2.0e-37
Match length
                    84
                    100
% identity
                    GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
NCBI Description
                    >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8)
                    - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988)
                    glycine rich protein [Arabidopsis thaliana] >gi 166658
```

(L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649)

RNA-binding protein [Arabidopsis thaliana]

```
Seq. No.
                  116573
Contig ID
                  86 12.R1010
                  jC-atXLIB327409P2f09b1
5'-most EST
                  BLASTX
Method
                  a544425
NCBI GI
BLAST score
                  198
E value
                  4.0e-15
Match length
                  85
% identity
                  94
                  GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
NCBI Description
                  >gi 419756 pir S30148 glycine-rich protein (clone AtGRP8)
                  - Arabidopsis thaliana >gi 16305 emb CAA78712 (Z14988)
                  glycine rich protein [Arabidopsis thaliana] >gi 166658
                  (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649)
                  RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  116574
Contig ID
                  86 13.R1010
5'-most EST
                  q1054146
Method
                  BLASTX
NCBI GI
                  q544424
BLAST score
                  441
E value
                  7.0e-44
Match length
                  85
                  100
% identity
NCBI Description
                  GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147
                  glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                  >gi 16301 emb CAA78711 (Z14987) glycine rich protein
                  [Arabidopsis thaliana] >qi 166837 (L00648) RNA-binding
                  protein [Arabidopsis thaliana]
                  >qi 4567224 qb AAD23639.1 AC007119 5 (AC007119)
                  glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
                  116575
Seq. No.
Contig ID
                  86 14.R1010
5'-most EST
                  jC-atXLIB327438P4f01a2
Method
                  BLASTX
NCBI GI
                  q4567236
BLAST score
                  188
E value
                  5.0e-14
Match length
                  51
% identity
                  (AC007119) glycine-rich RNA binding protein Ccr2
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  116576
Contig ID
                  86 15.R1010
5'-most EST
                  g2596526
Method
                  BLASTX
NCBI GI
                  g544424
BLAST score
                  306
E value
                  7.0e-28
Match length
                  94
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147
NCBI Description
```

```
protein [Arabidopsis thaliana]
                  >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                  glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
                  116577
Seq. No.
                  86 17.R1010
Contig ID
                  g1159440
5'-most EST
Method
                  BLASTX
                  q544424
NCBI GI
BLAST score
                  204
E value
                  8.0e-16
Match length
                  39
                  97
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir_ S30147
NCBI Description
                  glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                  >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
                  [Arabidopsis thaliana] > gi 166837 (L00648) RNA-binding
                  protein [Arabidopsis thaliana]
                  >qi 4567224 gb AAD23639.1 AC007119 5 (AC007119)
                  glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
                  116578
Seq. No.
Contig ID
                  86 18.R1010
                  jC-atXLIB327422P3h02b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q544425
BLAST score
                  412
E value
                  3.0e-40
Match length
                  83
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
NCBI Description
                  >qi 419756 pir S30148 glycine-rich protein (clone AtGRP8)
                  - Arabidopsis thaliana >gi 16305 emb CAA78712 (Z14988)
                  glycine rich protein [Arabidopsis thaliana] >gi 166658
                  (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649)
                  RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  116579
Contig ID
                  86 30.R1010
5'-most EST
                  q1158912
Method
                  BLASTX
NCBI GI
                  q544425
BLAST score
                  392
E value
                  5.0e-38
Match length
                  75
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
NCBI Description
                  >gi 419756 pir S30148 glycine-rich protein (clone AtGRP8)
                  - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988)
                  glycine rich protein [Arabidopsis thaliana] >gi 166658
```

glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
>gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding

RNA-binding protein [Arabidopsis thaliana]

116580

Seq. No.

(L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649)

```
86 43.R1010
Contig ID
5'-most EST
                  ARABL1-043-Q1-B1-A8
Method
                  BLASTN
                  g166656
NCBI GI
BLAST score
                  129
                  1.0e-66
E value
                  184
Match length
                  94
% identity
                  Arabidopsis thaliana Ccr2 mRNA, partial ORF
NCBI Description
                  116581
Seq. No.
                  87 1.R1010
Contig ID
                  jC-atXP114C240H10T7d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q729102
                  1230
BLAST score
                  1.0e-136
E∷value
                  246
Match length
                  100
% identity
                  CHALCONE--FLAVONONE ISOMERASE >gi 320138 pir__JQ1687
NCBI Description
                  chalcone isomerase (EC 5.5.1.6) - Arabidopsis thaliana
                  >gi 166660 gb_AAA32766.1_ (M86358) chalcone isomerase
                  [Arabidopsis thaliana]
Seq. No.
                  116582
                  88 1.R1010
Contig ID
5'-most EST
                  PLN g166663
Method
                  BLASTX
                  g2342435
NCBI GI
BLAST score
                  1631
E value
                  0.0e + 00
Match length
                  302
% identity
                  100
                  (AB006056) acidic endochitinase [Arabidopsis thaliana]
NCBI Description
                  >gi 2342437 dbj BAA21862_ (AB006057) acidic endochitinase
                   [Arabidopsis thaliana] >gi_2342441_dbj_BAA21864_ (AB006059)
                  acidic endochitinase [Arabidopsis Thalīana]
                  >gi 2342445 dbj BAA21866 (AB006061) acidic endochitinase
                   [Arabidopsis thaliana] >gi 2342449_dbj_BAA21868_ (AB006063)
                  acidic endochitinase [Arabidopsis thaliana]
                  >qi 2342455 dbj BAA21871 (AB006066) acidic endochitinase
                   [Arabidopsis thaliana]
                  116583
Seq. No.
                  89 1.R1010
Contig ID
                  PLN g166665
5'-most EST
Method
                  BLASTX
NCBI GI
                  g320556
BLAST score
                  1719
                  0.0e + 00
E value
Match length
                  335
% identity
                  chitinase (EC 3.2.1.14) precursor, basic - Arabidopsis
NCBI Description
                  thaliana >gi_166666 (M38240) basic chitinase [Arabidopsis
                  thaliana]
```

116584

Seq. No.

```
90 1.R1010
Contig ID
                  jC-atXLIB327406P2g10b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q116392
BLAST score
                  2041
                  0.0e + 00
E value
Match length
                  395
% identity
                  100
NCBI Description
                  CHALCONE SYNTHASE (NARINGENIN-CHALCONE SYNTHASE)
                  >gi 66543 pir SYMUCN naringenin-chalcone synthase (EC
                  2.3.1.74) - Arabidopsis thaliana >gi 166670 (M20308)
                  chalcone synthase [Arabidopsis thaliana]
                  116585
Seq. No.
Contig ID
                  90 2.R1010
5'-most EST
                  q905823
Method
                  BLASTX
                  q3420735
NCBI GI
BLAST score
                  378
                  7.0e-52
E value
Match length
                  153
% identity
                  (AF076336) chalcone synthase B2 [Brassica napus]
NCBI Description
                  116586
Seq. No.
Contig ID
                  91 1.R1010
                  jC-atXP73C223K11T7b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2506443
BLAST score
                  1869
                  0.0e + 00
E value
Match length
                  396
                  93
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi 2117520 pir JQ1285
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  Arabidopsis thaliana >gi 166704 (M64117) glyceraldehyde
                  3-phosphate dehydrogenase [Arabidopsis thaliana]
                  >gi 1402885 emb CAA66816 (X98130)
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) [Arabidopsis thaliana]
                  116587
Seq. No.
                  91 2.R1010
Contig ID
                  LIB24-058-01-E1-C11
5'-most EST
Method
                  BLASTX
NCBI GI
                  q120658
BLAST score
                  515
                  2.0e-64
E value
                  324
Match length
% identity
                  60
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                  CHLOROPLAST >gi 66025 pir DEPMNA
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
```

garden pea >gi 12159 emb CAA36396 (X52148) GAPA [Pisum

sativum] 116588 Seq. No. 91 3.R1010 Contig ID jC-atXLIB327419P4b05b1 5'-most EST BLASTX Method NCBI GI g2506443 BLAST score 600 3.0e-62 E value 159 Match length 75 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, NCBI Description CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >qi 1402885 emb CAA66816 (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana] 116589 Seq. No. 91 4.R1010 Contig ID 5'-most EST. g937651 Method BLASTX g2506443 NCBI GI BLAST score 204 1.0e-15 E value 142 Match length 32 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, NCBI Description CHLOROPLAST >gi 2117520 pir JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -Arabidopsis thaliana >gi 166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) 15.4 (phosphorylating) [Arabidopsis thaliana] 116590 Seq. No. 91 5.R1010 Contig ID 5'-most EST q2748901 Method BLASTX NCBI GI g2506443 BLAST score 83 4.0e-39 E value 112 Match length 82 % identity NCBI Description

(phosphorylating) [Arabidopsis thaliana]

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116591
 Seq. No.
                   91 10.R1010
 Contig ID
                   jC-atXLIB327424P4b06a1
 5'-most EST
 Method
                   BLASTX
                   g2506443
 NCBI GI
                   272
BLAST score
                   2.0e-41
 E value
 Match length
                   134
                   78
 % identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
 NCBI Description
                   CHLOROPLAST >gi_2117520_pir__JQ1285
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                   Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                   3-phosphate dehydrogenase [Arabidopsis thaliana]
                   >gi 1402885 emb CAA66816 (X98130)
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                    (phosphorylating) [Arabidopsis thaliana]
                   116592
 Seq. No.
                   91 11.R1010
 Contig ID
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                   g2708355
 Method
                   BLASTX
                   g120659
 NCBI GI
 BLAST score
                   291
                   3.0e-26
 E value
 Match length
                   75
                   81
 % identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
 NCBI Description
                   >gi 81721 pir B24796 glyceraldehyde-3-phosphate
                   dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13),
                   chloroplast - white mustard (fragment)
                   >gi 829288 emb CAA27845 (X04302) chloroplast GAPDH (233aa)
                   [Sinapis alba]
                   116593
 Seq. No.
 Contig ID
                   92 1.R1010
 5'-most EST
                   PLN g16345
                   BLASTX
 Method
 NCBI GI
                   q399938
 BLAST score
                   780
                    4.0e-83
 E value
                   193
 Match length
                   82
 % identity
                   CHLOROPLAST SMALL HEAT SHOCK PROTEIN PRECURSOR
 NCBI Description
                   >gi 486759 pir S35240 heat shock protein 21 - Arabidopsis
                   thaliana >gi 234873_bbs_55180 heat shock protein
                    [Arabidopsis thaliana, Peptide Chloroplast, 227 aa]
                   >gi 16346_emb_CAA38036_ (X54102) heat shock protein
                    [Arabidopsis thaliana] >gi_166760 (M94455) heat shock
                   protein 21 [Arabidopsis thaliana] >gi_4469018_emb_CAB38279_
                    (AL035602) heat shock protein 21 [Arabidopsis thaliana]
                   116594
 Seq. No.
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93 1.R1010

Contig ID

Contig ID

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5'-most EST
                  jC-atXP110CG7F2T7093a1
Method
                  BLASTX
NCBI GI
                  g113026
BLAST score
                  2679
E value
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Match length
                  576
% identity
                  89
                  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
NCBI Description
                  >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape
                  >gi 255220 bbs 112862 isocitrate lyase, threo-D
                  S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
                  napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
                  isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A
                  isocitrate lyase [Brassica napus]
                  116595
Seq. No.
                  93 3.R1010
Contig ID
5'-most EST
                  jC-atXP95CG11G2T7094d1
                  BLASTX
Method
                  g113026
NCBI GI
BLAST score
                  763
                  2.0e-81
E value
Match length
                  147
% identity
                  97
NCBI Description
                  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
                  >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape
                  >gi_255220_bbs_112862 isocitrate lyase, threo-D
                  S-isocitrate glyoxylate-lyase, IL (EC 4.1.3.1) [Brassica
                  napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
                  isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A
                  isocitrate lyase [Brassica napus]
                  116596
Seq. No.
Contig ID
                  93 5.R1010
5'-most EST
                  LIB3176-040-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g113024
BLAST score
                  268
E value
                  3.0e-23
Match length
                  70
                  77
% identity
                  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
NCBI Description
                  >gi 553043 (M83534) isocitrate lyase [Arabidopsis thaliana]
                  116597
Seq. No.
                  93 6.R1010
Contig ID
5'-most EST
                  g1328300
                  BLASTX
Method
                  g2143227
NCBI GI
BLAST score
                  340
E value
                  1.0e-31
Match length
                  74
                  89
% identity
NCBI Description
                  (Y13356) glyoxysomal isocitrate lyase [Brassica napus]
Seq. No.
                  116598
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95 1.R1010

E value

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5'-most EST
                  jC-alXLIB327435P3d01b1
Method
                  BLASTX
NCBI GI
                  g2129769
BLAST score
                  1458
                  1.0e-162
E value
                  269
Match length
                  100
% identity
                  xyloglucan endo-transglycosylase precursor - Arabidopsis
NCBI Description
                  thaliana >gi 944810 dbj BAA09783 (D63508) endo-xyloglucan
                  transferase [Arabidopsis thaliana]
                  116599
Seq. No.
Contig ID
                  95 4.R1010
                  LIB3175-028-P1-K1-H9
5'-most EST
                  BLASTX
Method
                  q2129769
NCBI GI
                  237
BLAST score
                  1.0e-48
E value
Match length
                  140
                  78
% identity
                  xyloglucan endo-transglycosylase precursor - Arabidopsis
NCBI Description
                  thaliana >gi 944810_dbj_BAA09783_ (D63508) endo-xyloglucan
                  transferase [Arabidopsis thaliana]
Seq. No.
                  116600
                  96 1.R1010
Contig ID
5'-most EST
                  PLN g166779
Method
                  BLASTX
                  q121196
NCBI GI
BLAST score
                  1224
                  1.0e-135
E value
                  228
Match length
                  100
% identity
                  TRICHOME DIFFERENTIATION PROTEIN GL1 >gi_68888_pir__TVMUG1
NCBI Description
                  transforming protein myb homolog GL1 - Arabidopsis thaliana
                  >gi 166780 (M79448) GL1 [Arabidopsis thaliana]
                  116601
Seq. No.
                  97 1.R1010
Contig ID
                  jC-atXLIB327411P2h09b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q129817
                  1754
BLAST score
                  0.0e + 00
E value
                  349
Match length
                  97
% identity
                  BASIC PEROXIDASE E PRECURSOR >gi_81653_pir__JU0458
NCBI Description
                  peroxidase (EC 1.11.1.7) E - Arabidopsis thaliana
                  >gi_166807 (M58381) peroxidase [Arabidopsis thaliana]
                  116602
Seq. No.
Contig ID
                  97 2.R1010
5'-most EST
                  q905920
Method .
                  BLASTX
                  q3395434
NCBI GI
BLAST score
                  158
                  4.0e-10
```

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221
Match length
% identity
                   (AC004683) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >gi 742248_prf__2009327B peroxidase [Arabidopsis thaliana]
                   116603
Seq. No.
                   98 1.R1010
Contig ID
                   LIB23-001-Q1-E1-F9
5'-most EST
                   BLASTX
Method
                   g480907
NCBI GI
                   1782
BLAST score
                   0.0e+00
E value
Match length
                   353
% identity
                   peroxidase (EC 1.11.1.7) - Arabidopsis thaliana
NCBI Description
                   >gi 405611 emb_CAA50677_ (X71794) peroxidase [Arabidopsis
                   thaliana]
                   116604
Seq. No.
                   99 1.R1010
Contig ID
                   jC-atXLIB327429P2b08b1
5'-most EST
                   BLASTX
Method
                   q464444
NCBI GI
BLAST score
                   1254
                   1.0e-138
E value
                   278
Match length
                   89
% identity
                   PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                   COMPLEX 30 KD SUBUNIT) >gi 541889_pir S39900 proteasome -
                   Arabidopsis thaliana >gi_1\overline{6}6830 \ (\overline{M}984\overline{95}) proteasome
                   [Arabidopsis thaliana]
                   116605
Seq. No.
                   99 2.R1010
Contig ID
                   LIB22-021-Q1-E1-F8
5'-most EST
                   BLASTX
Method
                   q3421094
NCBI GI
BLAST score
                   1243
                   1.0e-137
E value
Match length
                   277
% identity
                    (AF043527) 20S proteasome subunit PAF2 [Arabidopsis
NCBI Description
                   thaliana]
                    116606
Seq. No.
                    101 1.R1010
Contig ID
                   LIB\overline{2}3-042-Q1-E1-H6
5'-most EST
                    BLASTX
Method
                    q1174718
NCBI GI
BLAST score
                    4187
E value
                    0.0e + 00
                    942
Match length
                    87
% identity
                   PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR
NCBI Description
                    >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC
                    2.7.1.-) precursor - Arabidopsis thaliana >gi_166888
                    (L00670) protein kinase [Arabidopsis thaliana]
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Contig ID

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Seq. No.
                  116607
                  102_1.R1010 ·
Contig ID
5'-most EST
                  LIB3175-007-P1-K1-G2
                  BLASTX
Method
NCBI GI
                  g1174779
BLAST score
                  2342
                  0.0e + 00
E value
                  475
Match length
                  95
% identity
                  TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi 166894
NCBI Description
                   (M81620) tryptophan synthase beta-subunit [Arabidopsis
                  thaliana] >gi_4490703_emb_CAB38837.1 (AL035680) tryptophan
                  synthase beta-subunit (TSB2) [Arabidopsis thaliana]
                  116608
Seq. No.
                  102 2.R1010
Contig ID
5'-most EST
                  jC-atXP91C247J14T7b1
Method
                  BLASTX
NCBI GI
                  g136251
BLAST score
                  912
                  1.0e-98
E value
                  175
Match length
% identity
                  100
NCBI Description
                  TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR
                  >gi 99767 pir A31393 tryptophan synthase (EC 4.2.1.20)
                  beta chain - Arabidopsis thaliana >gi_166892 (M23872)
                  tryptophan synthase beta subunit [Arabidopsis thaliana]
                  116609
Seq. No.
Contig ID
                  103 1.R1010
                  jC-atXLIB327433P1e12b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g135391
                                                                ٠,
BLAST score
                  2113
E value
                  0.0e + 00
                  432
Match length
% identity
                  93
                  :TUBULIN ALPHA-1 CHAIN >gi_71583_pir__UBMUAM tubulin alpha-1
NCBI Description
                  chain - Arabidopsis thaliana >gi 166896 (M21414)
                  alpha-1-tubulin [Arabidopsis thaliana]
                  116610
Seq. No.
Contig ID
                  109 1.R1010
5'-most EST
                  jC-alX22046Q1E1F04b1
Method
                  BLASTX
NCBI GI
                  g267082
BLAST score
                  2203
E value
                  0.0e + 00
                  430
Match length
% identity
                  97
NCBI Description
                  TUBULIN BETA-8 CHAIN >gi 320189 pir JQ1592 tubulin beta-8
                  chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8
                  tubulin [Arabidopsis thaliana]
                  116611
Seq. No.
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111 1.R1010

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5'-most EST
                    iC-alXLIB327435P4a12b1
                   BLASTX
Method
NCBI GI
                   g135406
BLAST score
                    2113
                    0.0e + 00
E value
Match length
                    432
                    93
% identity
                   TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768 pir_ A32712 tubulin
NCBI Description
                   alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                    alpha-5 tubulin [Arabidopsis thaliana]
                    116612
Seq. No.
                    111 2.R1010
Contig ID
                    iC-alXLIB327434P1a03b1
5'-most EST
                    BLASTX
Method
                    g4689386
NCBI GI
                    765
BLAST score
E value
                    3.0e-81
Match length
                    222
% identity
                    (AF139468) photosystem I reaction center subunit III [Vigna
NCBI Description
                    radiata]
                    116613
Seq. No.
                    111 6.R1010
Contig ID
                    jC-atXLIB327414P2c07a1
5'-most EST
                    BLASTX
Method
                    g135406
NCBI GI
BLAST score
                    633
E value
                    3.0e-66
Match length
                    118
                    100
% identity
                   TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768 pir A32712 tubulin
NCBI Description
                    alpha-5 chain - Arabidopsis thaliana >g\overline{i}_16\overline{69}12 (M17189)
                    alpha-tubulin [Arabidopsis thaliana] >gi 166918 (M84698)
                    alpha-5 tubulin [Arabidopsis thaliana]
                    116614
Seq. No.
                    111_7.R1010
Contig ID
                    q2748136
5'-most EST
Method
                    BLASTX
                    g135406
NCBI GI
BLAST score
                    505
E value
                    3.0e-51
Match length
                    112
% identity
                    TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir_A32712 tubulin
NCBI Description
                    alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                    alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                    alpha-5 tubulin [Arabidopsis thaliana]
                    116615
Seq. No.
Contig ID
                    111 8.R1010
5'-most EST
                    g11\overline{5}9866
                    BLASTX
Method
                    g131187
NCBI GI
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Seq. No.

Contig ID

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BLAST score
                   60
                   9.0e-28
E value
                   74
Match length
                   82
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                    (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                   >gi_72681_pir__F1SP3 photosystem I chain III precursor -
                   spinach >gi_21303_emb_CAA31523_ (X13133) PSI subunit IV
                   preprotein (AA -77 to 154) [Spinacia oleracea] >gi_226166_prf__1413236A photosystem I reaction center IV
                    [Spinacia oleracea]
Seq. No.
                    116616
Contig ID
                    112 1.R1010
                    jC-\overline{a}tXP29C140G21T7040d1
5'-most EST
                   BLASTX
Method
                   q267070
NCBI GI
BLAST score
                    1309
                    0.0e + 00
E value
                    430
Match length
                    96
% identity
                   TUBULIN ALPHA-6 CHAIN >gi_282852_pir__JQ1597 tubulin alpha-6 chain - Arabidopsis thaliana >gi_166920 (M84699)
NCBI Description
                    TUA6 [Arabidopsis thaliana] >gi_2244853_emb_CAB10275_
                    (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis
                    thaliana]
                    116617
Seq. No.
Contig ID
                    112 3.R1010
                    jC-atXLIB327422P3c07b2
5'-most EST
                    BLASTX
Method
                    g267069
NCBI GI
                    696
BLAST score
                    2.0e-73
E value
Match length
                    130
% identity
                    TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                    tubulin alpha chain - Arabidopsis thaliana >gi_166914
                    (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                    (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                    116618
Seq. No.
                    112 4.R1010
Contig ID
                    jC-atXP109C91P17T7s1
5'-most EST
                    BLASTX
Method
NCBI GI
                    g464840
                    308
BLAST score
                    4.0e-28
E value
                    60
Match length
                    100
% identity
                    TUBULIN ALPHA-1 CHAIN >gi_421781_pir__S32666 tubulin
NCBI Description
                    alpha-1 chain - fern (Anemia phyllitidis)
                    >gi 296494 emb CAA48927_ (X69183) alpha tubulin [Anemia
                  . phyllitidis]
                    116619
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112 5.R1010

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5'-most EST
                  g3449678
                  BLASTX
Method
                  g2098753
NCBI GI
BLAST score
                  167
                  1.0e-11
E value
                  37
Match length
                  84
% identity
                  (U92646) alpha-2-tubulin [Gecarcinus lateralis]
NCBI Description
                  116620
Seq. No.
                  115 1.R1010
Contig ID
                  jC-atXLIB327406P2c08b1
5'-most EST
                  BLASTX
Method
                  g280386
NCBI GI
BLAST score
                  662
                  2.0e-69
E value
                  128
Match length
                  100
% identity
                  ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana
NCBI Description
                  >gi 166930 (J05507) ubiquitin extension protein (UBQ1)
                  [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin
                  extension protein (UBQ2) [Arabidopsis thaliana]
                  >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135)
                  ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]
Seq. No.
                  116621
Contig ID
                  115 2.R1010
5'-most EST
                  g2722578
Method
                  BLASTX
                  q280386
NCBI GI
BLAST score
                  662
                  2.0e-69
E value
                  128
Match length
                  100
% identity
                  ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana
NCBI Description
                  >gi 166930 (J05507) ubiquitin extension protein (UBQ1)
                   [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin
                  extension protein (UBQ2) [Arabidopsis thaliana]
                  >qi 4678227 gb AAD26972.1 AC007135 8 (AC007135)
                  ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]
Seq. No.
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                  115 3.R1010
Contig ID
                  jC-atXP102CE5A10T7b1
5'-most EST
Method
                  BLASTX
                  g280386
NCBI GI
BLAST score
                  604
                  1.0e-62
E value
                  119
Match length
                  98
% identity
                  ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana
NCBI Description
                  >gi 166930 (J05507) ubiquitin extension protein (UBQ1)
                  [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin
                  extension protein (UBQ2) [Arabidopsis thaliana]
                  >gi 4678227 gb AAD26972.1 AC007135 8 (AC007135)
                  ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]
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Seq. No.
                  116623
                  115 5.R1010
Contig ID
                  jC-atXLIB327418P2a02b2
5'-most EST
                  BLASTX
Method
                  g280386
NCBI GI
                  274
BLAST score
                  4.0e-24
E value
Match length
                  63
                  86
% identity
                  ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana
NCBI Description
                  >gi 166930 (J05507) ubiquitin extension protein (UBQ1)
                  [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin
                  extension protein (UBQ2) [Arabidopsis thaliana]
                  >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135)
                  ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]
                  116624
Seq. No.
                  115 6.R1010
Contig ID
5'-most EST
                  g2414041
Method
                  BLASTX
                  g280386
NCBI GI
                  455
BLAST score
                  3.0e-45
E value
                  104
Match length
% identity
                  86
                  ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana
NCBI Description
                  >qi 166930 (J05507) ubiquitin extension protein (UBQ1)
                  [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin
                  extension protein (UBQ2) [Arabidopsis thaliana]
                  >qi 4678227 qb AAD26972.1 AC007135 8 (AC007135)
                  ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]
                  116625
Seq. No.
                  120 1.R1010
Contig ID
5'-most EST
                  jC-atXP31C146M15T7d2
Method
                  BLASTX
                  q3024666
NCBI GI
BLAST score
                  1679
                  0.0e + 00
E value
Match length
                  335
                  97
% identity
                  STRICTOSIDINE SYNTHASE 1/2 PRECURSOR >gi 1754983 (U43713)
NCBI Description
                  strictosidine synthase [Arabidopsis thaliana] >gi_1754985
                  (U43945) strictosidine synthase [Arabidopsis thaliana]
                  116626
Seq. No.
                  120 2.R1010
Contig ID
                  jC-atXLIB327417P1b12b1
5'-most EST
                  BLASTX
Method
                  g3024666
NCBI GI
BLAST score
                  880
                  8.0e-95
E value
                  203
Match length
                  83
% identity
                  STRICTOSIDINE SYNTHASE 1/2 PRECURSOR >gi_1754983 (U43713)
NCBI Description
                  strictosidine synthase [Arabidopsis thaliana] >gi_1754985
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(U43945) strictosidine synthase [Arabidopsis thaliana]

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121 1.R1010
      Contig ID
                         g1053655
      5'-most EST
                         BLASTX
     Method
     NCBI GI
                         g72319
                         190
      BLAST score
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      E value
                         125 ...
     Match length
      % identity
                         dehydrin-like protein - Arabidopsis thaliana
>gi_17684_emb_CAA45524_ (X64199) dehydrin [Arabidopsis
     NCBI Description
                         thaliana]
                                       *--
                          116628
     Seq. No.
                          122 · 1.R1010
      Contig ID
                          jC-atXLIB327420P3g05b1
      5'-most EST
                          116629
      Seq. No.
                          122 2.R1010
      Contig ID
                          jC-atXP73C223G22T7b1
      5'-most EST
      Method
                          BLASTX
      NCBI GI
                          q1769905
1159
      BLAST score
111
                          1.0e-127
      E value
Match length
                          263
                         86
      % identity
                          (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
      NCBI Description
                          [Arabidopsis thaliana]
j*E
ij1
                          116630
      Seq. No.
                          122 4.R1010
à.
      Contig ID
      5'-most EST
                          jC-alXLIB327436P4c01b1
àŁ
                          116631
      Seq. No.
                          122 6.R1010
      Contig ID
131
                          jC-atXP73C223G22T7d2
      5'-most EST
                          BLASTX
      Method
      NCBI GI
                          q1769905
                          426
      BLAST score
      E value
                          1.0e-41
                          169
      Match length
                          57
      % identity
                          (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
      NCBI Description
                          [Arabidopsis thaliana]
                          116632
      Seq. No.
                          122 9.R1010
      Contig ID
                          q398305
      5'-most EST
      Method
                          BLASTX
                          q1769905
      NCBI GI
                          586
      BLAST score
                          3.0e-60
      E value
                          274
      Match length
      % identity
                          51
                          (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
      NCBI Description
                          [Arabidopsis thaliana]
```

Seq. No.

116627

```
Seq. No.
                  116633
                  122 10.R1010
Contig ID
5'-most EST
                  q2747402
                  BLASTX
Method
                  q1769905
NCBI GI
BLAST score
                  103
                  8.0e-33
E value
Match length
                  86
                  77
% identity
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  116634
Contig ID
                  122 12.R1010
5'-most EST
                  jC-atX35040Q1E1D02b1
Method
                  BLASTX
                  q1769905
NCBI GI
BLAST score
                  496
E value
                  9.0e-50
Match length
                  216
% identity
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                  [Arabidopsis thaliana]
                  116635
Seq. No.
Contig ID
                  122 14.R1010
5'-most EST
                  jC-atX35042Q1E1G02b1
Method
                  BLASTX
NCBI GI
                  q1769905
BLAST score
                  192
E value
                  2.0e-14
Match length
                  115
% identity
                  41
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  116636
Contig ID
                  122 16.R1010
5'-most EST
                  g2763904
Method
                  BLASTX
NCBI GI
                  g1769905
BLAST score
                  246
E value
                  6.0e-21
Match length
                  89
% identity
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC).
                  [Arabidopsis thaliana]
Seq. No.
                  116637
Contig ID
                  123 1.R1010
5'-most EST
                  LIB23-051-Q1-E1-F7
Method
                  BLASTX
NCBI GI
                  g3915085
BLAST score
                  2362
E value
                  0.0e + 00
Match length
                  505
```

```
% identity
                   92
                  TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
NCBI Description
                   4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)
                   >gi 1773289 (U71081) cinnamate-4-hydroxylase [Arabidopsis
                   thaliana] >gi 1946370 (U93215) cinnamate-4-hydroxylase
                   [Arabidopsis thaliana]
                   116638
Seq. No.
Contig ID
                   124 1.R1010
5'-most EST
                   jC-atXLIB327408P3d08b1
Method
                   BLASTX
                   q4249409
NCBI GI
BLAST score
                   676
E value
                   6.0e-71
Match length
                   160
                   88
% identity
NCBI Description
                   (AC006072) putative sugar transporter [Arabidopsis
                   thaliana]
Seq. No.
                   116639
                   124 3.R1010
Contig ID
5'-most EST
                   LIB22-070-Q1-E1-B3
Method
                   BLASTX
                   g1785622
NCBI GI
BLAST score
                   330
                   8.0e-31
E value
Match length
                  71
% identity
                   92
                   (Z84202) ORFc [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   116640
Contig ID
                   125 1.R1010
                   jC-atXLIB327407P4a03b1
5'-most EST
Method
                   BLASTX
                   q2507421
NCBI GI
BLAST score
                   579
                   2.0e-59
E value
Match length
                  113
                   100
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277
NCBI Description
                   (U81042) translation initiation factor [Arabidopsis
                   thaliana] >gi 4490709 emb CAB38843.1 (AL035680)
                   translation initiation factor [Arabidopsis thaliana]
                   116641
Seq. No.
                   125 2.R1010
Contig ID
5'-most EST
                   g2750073 🚁
Method
                  BLASTX
                   q2507421
NCBI GI
BLAST score
                   451
                  7.0e-45
E value
Match length
                  90
% identity
                  98
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277
NCBI Description
                   (U81042) translation initiation factor [Arabidopsis
```

thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.

Contig 'ID

```
Seq. No.
                  116642
                  127_1.R1010
Contig ID
5'-most EST
                  PLN_g1592673
Method
                  BLASTX
NCBI GI
                  g1429211 ·
                  555
BLAST score
E value
                  1.0e-56
Match length
                  184
                  66
% identity
NCBI Description
                  (X99116) HMG-I/Y protein [Arabidopsis thaliana] >gi 2809402
                   (AF041253) high mobility group protein a [Arabidopsis
                  thaliana]
                  116643
Seq. No.
                  128 1.R1010
Contig ID
.5'-most EST
                  jC-atXP79C230O2T7b1
Method
                  BLASTX
NCBI GI
                  q1809305
BLAST score
                  456
E value
                  4.0e-45
Match length
                  135
% identity
                  75
NCBI Description
                  (U72241) histone H1-3 [Arabidopsis thaliana] >gi 1809315
                  (U73781) histone H1-3 [Arabidopsis thaliana]
                  >gi 4406813 gb AAD20121 (AC006201) Histone H1 [Arabidopsis
                  thaliana]
                  116644
Seq. No.
                  128 3.R1010
Contig ID
5'-most EST
                  PLN_g1809314
Method
                  BLASTX
NCBI GI
                  g1809305
BLAST score
                  456
E value
                  4.0e-45
Match length
                  135
% identity
                  75
NCBI Description
                  (U72241) histone H1-3 [Arabidopsis thaliana] >gi_1809315
                  (U73781) histone H1-3 [Arabidopsis thaliana]
                  >gi_4406813_gb_AAD20121_ (AC006201) Histone H1 [Arabidopsis
                  thaliana]
                  116645
Seq. No.
Contig ID
                  129 1.R1010
5'-most EST
                  jC-atXP65C206N21T7042d1
Method
                  BLASTX
NCBI GI
                  g2506496
BLAST score
                  1008
E value
                  1.0e-110
Match length
                  208
% identity
                  GLUTATHIONE S-TRANSFERASE ERD11 (CLASS PHI)
NCBI Description
                  >gi_1890156_emb_CAA72413_ (Y11727) gluthatione
                  S-transferase [Arabidopsis thaliana]
                  116646
```

129_2.R1010

```
5'-most EST
                   g1053688
                   BLASTX
Method
NCBI GI
                   a2266412
BLAST score
                   558
                   3.0e-57
E value
Match length
                   156
                  78
% identity
NCBI Description
                  (Y14251) glutathione S-transferase [Arabidopsis thaliana]
                   116647
Seq. No.
Contig ID
                   129_3.R1010
                   jC-atXP92C249B20T7021d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2266412
BLAST score
                   553
E value
                   1.0e-56
Match length
                   124
% identity
                   89
NCBI Description
                  (Y14251) glutathione S-transferase [Arabidopsis thaliana]
                   116648
Seq. No.
Contig ID
                   130_1.R1010
5'-most EST
                   jC-atXP54C186G1T7055d1
Method
                   BLASTX
NCBI GI
                   g3341698
BLAST score
                   642
E value
                   7.0e-67
Match length
                   202
% identity
                   65
                   (AC003672) blue copper-binding protein II [Arabidopsis
NCBI Description
                   thaliana]
                   116649
Seq. No.
                   130_3.R1010
Contig ID
                                                                     . X.
5'-most EST
                   g957469
                  BLASTX
Method
NCBI GI
                   q1848237
BLAST score
                   485
E value
                  1.0e-48
Match length
                  167
% identity
                   63
                   (U57320) blue copper-binding protein II [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   116650
                   131_1.R1010
Contig ID
5'-most EST
                   jC-alXLIB327434P4f12b1
Method
                  BLASTX
                   g2495365
NCBI GI
BLAST score
                   3008
E value
                   0.0e + 00
Match length
                  699
% identity
                  86
NCBI Description
                  HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf 1908431B
                  heat shock protein HSP81-2 [Arabidopsis thaliana]
                  116651
Seq. No.
```

```
Contig ID
                  131 3.R1010
                  jC-atXP89C245B9T7052d1
5'-most EST
Method
                  BLASTX
                  q2495365
NCBI GI
                  686
BLAST score
                  4.0e-72
E value
                  161 .
Match length
% identity
                  85
                  HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf 1908431B
NCBI Description
                  heat shock protein HSP81-2 [Arabidopsis thaliana]
                  116652
Seq. No.
Contig ID
                  131 4.R1010
5'-most EST
                  LIB3175-077-P1-K1-H6
Method
                  BLASTX
                  g4585980
NCBI GI
BLAST score
                  625
                  2.0e-65
E value
                  137
Match length
                  88
% identity
                  (AC005287) Very similar to TATA binding protein-associated
NCBI Description
                  factor [Arabidopsis thaliana]
                  116653
Seq. No.
                131 7.R1010
Contig ID
5'-most EST
                  g2759112
                  BLASTX
Method
                  q2495365
NCBI GI
BLAST score
                  462
E value
                  3.0e-46
                  90
Match length
% identity
                  99
                  HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf 1908431B
NCBI Description
                  heat shock protein HSP81-2 [Arabidopsis thaliana]
                  116654
Seq. No.
Contig ID
                  131 8.R1010
                  jC-atXLIB327407P3f11b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2495365
BLAST score
                  544
E value
                  1.0e-67
Match length
                  170
                  84
%-identity
                  HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf 1908431B
NCBI Description
                  heat shock protein HSP81-2 [Arabidopsis thaliana]
Seq. No.
                  116655
Contig ID
                  131 10.R1010
5'-most EST
                  jC-atXLIB327411P1d07b1
                  BLASTX
Method
                  q2495365
NCBI GI
BLAST score
                  825
E value
                  1.0e-88
Match length
                  161
                  99
% identity
NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B
```

Method '

NCBI GI BLAST score

E value

BLASTX q3914239

2128 0.0e+00

heat shock protein HSP81-2 [Arabidopsis thaliana] 116656 Seq. No. 131 12.R1010 Contig ID jC-atXLIB327419P3h07b2 5'-most EST BLASTX Method q2495365 NCBI GI 299 BLAST score 2.0e-45 E value 144 Match length 75 % identity HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127_prf__1908431B NCBI Description heat shock protein HSP81-2 [Arabidopsis thaliana] Seq. No. 116657 133 1.R1010 Contig ID PLN g1773294 5'-most EST BLASTX Method q1773295 NCBI GI BLAST score 2738 0.0e + 00E value 593 Match length % identity 92 (U76707) regulatory protein NPR1 [Arabidopsis thaliana] NCBI Description >gi_1916912 (U87794) transcription factor inhibitor I kappa B homolog [Arabidopsis thaliana] Seq. No. 116658 134 1.R1010 Contig ID 5'-most EST q587062 Method BLASTX q3122659 NCBI GI BLAST score 1142 1.0e-125 E value Match length 216 % identity 99 PEROXIREDOXIN (REHYDRIN HOMOLOG) >gi 1926269 emb_CAA72804_ NCBI Description (Y12089) peroxiredoxin [Arabidopsis thaliana] Seq. No. 116659 135 1.R1010 Contig ID PLN_g1944131 5'-most EST BLASTX Method q1944132 NCBI GI 1651 BLAST score 0.0e+00E value Match length 375 % identity (AB002560) CUC2 [Arabidopsis thaliana] NCBI Description 116660 Seq. No. Contig ID 136 1.R1010 $jC-\overline{a}lXLIB327436P3e05b1$ 5'-most EST

73.

E value

5.0e-20

```
Match length
                     423
                     97
% identity
                    PROTEIN PHOSPHATASE 2C ABI2 (PP2C)
NCBI Description
                    >gi_1945140_emb_CAA70163_ (Y08966) ABI2 protein phosphatase
2C [Arabidopsis thaliana] >gi_1945142_emb_CAA70162_
(Y08965) ABI2 protein phosphatase 2C [Arabidopsis thaliana]
                    >gi 2564213 emb CAA72538 (Y11840) ABI2 [Arabidopsis
                     thaliana]
Seq. No.
                    116661
Contig ID
                     138_1.R1010
5'-most EST
                     PLN_g2160755
Method
                     BLASTX
NCBI GI
                     q2160756
BLAST score
                     4988
E value
                     0.0e + 00
Match length
                     980
                     98
% identity
NCBI Description
                     (U96879) CLV1 receptor kinase [Arabidopsis thaliana]
                     116662
Seq. No.
Contig ID
                     141 1.R1010
5'-most EST
                     jC-atXLIB327414P3a05a1
Method
                     BLASTX
                     a2507587
NCBI GI
BLAST score
                     284
                     5.0e-25
E value
Match length
                     57
                    88
% identity
                    METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)
NCBI Description
                    >gi 1361998 pir S57861 metallothionein 2a - Arabidopsis
                    thaliana >g\bar{i}_55\bar{59}76 (U15108) metallothionein-like protein
                     [Arabidopsis thaliana] >gi_1580892_prf__2116236A
                    metallothionein 1 [Arabidopsis thaliana]
Seq. No.
                     116663
Contig ID
                     141 2.R1010
5'-most EST
                     jC-atXP44C171F15T7d1
Method
                    BLASTX
NCBI GI
                    a2507587
BLAST score
                     113
E value
                     1.0e-18
Match length
                     51
% identity
NCBI Description
                    METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)
                    >gi 1361998 pir__S57861 metallothionein 2a - Arabidopsis
                    thaliana >g\bar{i}_55\bar{5}976 (U15108) metallothionein-like protein
                     [Arabidopsis thaliana] >gi_1580892_prf__2116236A
                    metallothionein 1 [Arabidopsis thaliana]
                    116664
Seq. No.
                    141_4.R1010
g2723219
Contia ID
5'-most EST
Method
                    BLASTX
NCBI GI
                    g2507587
BLAST score
                    239
```

```
51
Match length
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)
NCBI Description
                   >gi 1361998 pir__S57861 metallothionein 2a - Arabidopsis
                   tha\overline{l}iana >g\overline{l}_55\overline{59}76 (U15108) metallothionein-like protein
                   [Arabidopsis thaliana] >gi_1580892_prf__2116236A
                   metallothionein 1 [Arabidopsis thaliana]
Seq. No.
                   116665
                   141 7.R1010
Contig ID
                   g2762272
5'-most EST
Method
                   BLASTX
                   q2507587
NCBI GI
BLAST score
                   259
E value
                   2.0e-22
                   55
Match length
% identity
                   85
                   METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G)
NCBI Description
                   >gi 1361998 pir__S57861 metallothionein 2a - Arabidopsis
                   thaliana >g\bar{i} 555976 (U15108) metallothionein-like protein
                   [Arabidopsis thaliana] >gi 1580892 prf 2116236A
                   metallothionein 1 [Arabidopsis thaliana]
                   116666
Seq. No.
Contig ID
                  . 144 1.R1010
5'-most EST
                   PLN g2204098 ...
                   BLASTX
Method
                   g2204089
NCBI GI
BLAST score
                   773
                   2.0e-81
E value
                   748
Match length
% identity
                   (Z82989) FCA gamma [Arabidopsis thaliana]
NCBI Description
                   116667
Seq. No.
                   145 1.R1010
Contig ID
5'-most EST
                   g2759454
                   BLASTX
Method
NCBI GI
                   g1809127
BLAST score
                   928
E value
                   1.0e-100
Match length
                   177
% identity
                   (U77674) terminal flower 1 [Arabidopsis thaliana]
NCBI Description
                   >qi 2208929 dbj BAA20483 (D86932) terminal flower1
                   [Arabidopsis thaliana] >gi 2208931 dbj BAA20484 (D87130)
                   terminal flower1 [Arabidopsis thaliana]
                   >gi 2208933 dbj BAA20485 (D87519) terminal flower1
                   [Arabidopsis thaliana]
                   116668
Seq. No.
                   146 1.R1010
Contig ID
5'-most EST
                   LIB25-020-Q1-E1-E11
Method
                   BLASTX
NCBI GI
                   g2181186
BLAST score
                   1755
```

0.0e + 00

E value

```
Match length
                  363
                  95
% identity
                   (X97323) outward rectifying potassium channel KCO1
NCBI Description
                   [Arabidopsis thaliana] >gi 2230761 emb CAA69158 (Y07825)
                  kcol [Arabidopsis thaliana]
                  116669
Seq. No.
                  146 4.R1010
Contig ID
                  jC-atXP102CE4F1T7069d1
5'-most EST
Method
                  BLASTX
                  g2181186
NCBI GI
BLAST score
                  413
                  4.0e-56
E value
                  135
Match length
% identity
NCBI Description
                   (X97323) outward rectifying potassium channel KCO1
                   [Arabidopsis thaliana] >qi 2230761 emb CAA69158 (Y07825)
                  kcol [Arabidopsis thaliana]
                  116670
Seq. No.
Contig ID
                  148 1.R1010
                  jC-atXLIB327413P4g01b1
5'-most EST
Method
                  BLASTX
                  q1702988
NCBI GI
                  1208
BLAST score
E value
                  1.0e-133
Match length
                  260
% identity
                  14-3-3-LIKE PROTEIN GF14 UPSILON >qi 1508785 (L09109) GF14
NCBI Description
                  upsilon chain [Arabidopsis thaliana]
                  >gi 2232148 gb AAB62225 (AF001415) 14-3-3-like protein
                  GF14 upsilon [Arabidopsis thaliana]
                  116671
Seq. No.
                  148 2.R1010
Contiq ID
                  LIB3234-003-P1-K1-G7
5'-most EST
Method
                  BLASTX
                  q3023217
NCBI GI
BLAST score
                   1318
                   1.0e-146
E value
Match length
                   261
% identity
                   14-3-3-LIKE PROTEIN GF14 NU >gi 1531631 (U60445) GF14 nu
NCBI Description
                   [Arabidopsis thaliana]
                   116672
Seq. No.
                   151 1.R1010
Contig ID
5'-most EST
                   PLN q22676
                   BLASTX
Method
                   g1169451
NCBI GI
BLAST score
                   2556
                   0.0e + 00
E value
Match length
                   478
% identity
                  PROBABLE GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE A6 PRECURSOR
NCBI Description
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1,3-ENDOGLUCANASE) >gi_322510 pir S31906
```

```
116673
Seq. No.
Contig ID
                   152 1.R1010
                   LIB3176-120-P2-K1-B11
5'-most EST
Method
                   BLASTX
NCBI GI
                   q548355
BLAST score
                   2493
                   0.0e + 00
E value
                   498
Match length
% identity
NCBI Description
                   NITRATE REDUCTASE 1 (NR1) >gi 486751 pir__S35228 nitrate
                   reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana
                   >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase
                   [Arabidopsis thaliana] >gi 448286 prf 1916406A nitrate
                   reductase [Arabidopsis thaliana]
                   116674
Seq. No.
                   154 1.R1010
Contig ID
                   LIB25-011-Q1-E1-B9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2281334
BLAST score
                   2469
E value
                   0.0e+00
                   459
Match length
`% identity
                   100
                   (U83619) putative pectate lyase [Arabidopsis thaliana]
NCBI Description
                   116675
Seq. No.
                   155 1.R1010
Contig ID
                   PLN g1669865
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3122232
BLAST score
                   811
                   9.0e-87
E value
Match length
                   194
% identity
                   MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR
NCBI Description
                   >qi 1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana]
                   >qi 4454008 emb CAA23061 (AL035396) Arabidopsis
                   mitochondrion-localized small heat shock protein
                   (AtHSP23.6-mito) [Arabidopsis thaliana]
                   116676
Seq. No.
Contig ID
                   156 1.R1010
                   jC-atXLIB327427P2e11b1
5'-most EST
                   BLASTX
Method
                   q2338712
NCBI GI
BLAST score
                   262
E value
                   2.0e-22
Match length
                   69
 % identity
                   (AF013959) metallothionein-like protein [Arabidopsis
NCBI Description
```

beta-1,3-glucanase homolog - Arabidopsis thaliana

[Arabidopsis thaliana]

>gi_22677_emb_CAA49853_ (X70409) A6 [Arabidopsis thaliana]
>gi_2244764_emb_CAB10187_ (Z97335) AMP-binding protein

thalianal

E value

```
116677
Seq. No.
Contig ID '
                   156 2.R1010
5'-most EST
                   jC-atXLIB327414P1a11a1
Method
                   BLASTX
                   g2338712
NCBI GI
                   211
BLAST score
                   1.0e-16
E value
                   40
Match length
% identity
                   (AF013959) metallothionein-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   116678
Seq. No.
                   156 5.R1010
Contig ID
5'-most EST
                   jC-atXLIB327401P4e03b2
                   BLASTN
Method.
                   g16472
NCBI GI
                   389
BLAST score
                   0.0e+00
E value
                   397
Match length
                   100
% identity
NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type
                   116679
Seq. No.
                   156 6.R1010
Contig ID
5'-most EST
                   g2581626
                   BLASTN
Method
                   g16472
NCBI GI
BLAST score
                   469
                   0.0e+00
E value
Match length
                   537
                   98
% identity
                   A.thaliana rRNA repeat unit, most frequent IGR type
NCBI Description
Seq. No.
                   116680
                   156 7.R1010
Contig ID
                   ARABL1-046-Q1-B1-G9
5'-most EST
Seq. No.
                   116681
                   156 8.R1010
Contig ID
5'-most EST
                   g2747696
Method
                   BLASTN
NCBI GI
                   q16472
                   330
BLAST score
                   0.0e + 00
E value
Match length
                   346
                   99
% identity
NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type
                   116682
Seq. No.
                   156 9.R1010
Contig ID
5'-most EST
                   g2580717
Method
                   BLASTN
                   q2618603
NCBI GI
                   269
BLAST score
                   1.0e-150
```

```
273
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSL3, complete sequence [Arabidopsis thaliana]
                  116683
Seq. No.
                  170 1.R1010 ·
Contig ID
                  jC-atXLIB327411P3c02b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2352492
BLAST score
                  3105
E value
                  0.0e + 00
                  594
Match length
% identity
NCBI Description
                  (AF005047) transport inhibitor response 1 [Arabidopsis
                  thaliana] >gi 2352494 (AF005048) transport inhibitor
                  response 1 [Arabidopsis thaliana]
                  116684
Seq. No.
                  171 1.R1010
Contig ID
5'-most EST
                  jC-atXP94CH4G8T7012d1
                  BLASTX
Method
                  g2654088
NCBI GI
BLAST score
                  3490
                  0.0e + 00
E value
Match length
                  712
% identity
                   (AF033118) potassium transporter [Arabidopsis thaliana]
NCBI Description
                  >gi 2688979 (AF029876) high-affinity potassium transporter;
                  AtKUP1p [Arabidopsis thaliana] >gi_3150413 (AC004165)
                  high-affinity potassium transporter (AtKUP1) [Arabidopsis
                  thaliana] >qi 3420045 (AC004680) high-affinity potassium
                  transporter (AtKUP1) [Arabidopsis thaliana]
                  116685
Seq. No.
                  172 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327422P1g10b1
                  BLASTX
Method
NCBI GI
                  g2459425
BLAST score
                   965
E value
                  1.0e-104
Match length
                  181
% identity
                   (AC002332) plastid protein [Arabidopsis thaliana]
NCBI Description
                   116686
Seq. No.
Contig ID
                  173 1.R1010
5'-most EST
                   jC-atXLIB327427P4a06b2
                  BLASTX
Method
NCBI GI
                  g2454176
BLAST score
                   2509
E value
                   0.0e + 00
Match length
                   501
% identity
                   (U69134) cytochrome P450 monooxygenase [Arabidopsis
NCBI Description
                  thaliana] >gi 3164128 dbj BAA28532 (D78599) cytochrome
```

P450 monooxygenase [Arabidopsis thaliana]

5'-most EST

```
monooxygenase (CYP83A1) [Arabidopsis thaliana]
                  116687
Seq. No.
Contig ID
                 · 173 2.R1010
                  jC-atXLIB327426P1h08b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1352188
BLAST score
                   427
                  1.0e-41
E value
Match length
                  193
                  66
% identity
                  CYTOCHROME P450 83 (CYPLXXXIII) >gi 619745 (U18929)
NCBI Description
                  cytochrome p450 dependent monooxygenase [Arabidopsis
                  thaliana]
                  116688
Seq. No.
                  177 1.R1010
Contig ID
5'-most EST
                  g394835
Method
                  BLASTX
                  q3915639
NCBI GI
BLAST score
                  1801
                  0.0e + 00
E value
                  354
Match length
                  96
% identity
                  ALTERNATIVE OXIDASE 1A PRECURSOR >gi_2506083_dbj_BAA22625_
NCBI Description
                   (D89875) alternative oxidase [Arabidopsis thaliana]
                  116689
Seq. No.
                  179 1.R1010
Contig ID
5'-most EST
                  LIB23-067-Q1-E1-H9
                  BLASTX
Method
                  g166708
NCBI GI
BLAST score
                  2153
                  0.0e+00
E value
                   439
Match length
% identity
                   (M64118) glyceraldehyde-3-phosphate dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
                  116690
Seq. No.
                  180 1.R1010
Contig ID
                  LIB3177-086-P1-K1-A11
5'-most EST
Method
                  BLASTX
                  g2581783
NCBI GI
BLAST score
                  810
                   6.0e-87
E value
                  160
Match length
% identity
                   (U94998) class 1 non-symbiotic hemoglobin [Arabidopsis
NCBI Description
                  thaliana] >gi_4678203_gb_AAD26949.1_AC007134_7 (AC007134)
                  class 1 non-symbiotic hemoglobin (AHB1) [Arabidopsis
                  thaliana]
Seq. No.
                  116691
Contig ID
                  181 1.R1010
```

>gi 4455306 emb_CAB36841 (AL035528) cytochrome P450

jC-atXLIB327421P3e09b1

Seq. No.

116696

```
Method
                   BLASTX
 NCBI GI
                   g2581785
BLAST score
                   808
 E value
                   3.0e-86
 Match length
                   158
 % identity
                   100
                   (U94999) class 2 non-symbiotic hemoglobin [Arabidopsis
 NCBI Description
                   thaliana]
                   116692
 Seq. No.
                   182 1.R1010
 Contig ID
                   LIB35-027-Q1-E1-C5
 5'-most EST
 Method
                   BLASTX
 NCBI GI.
                   g2597826
 BLAST score
                   1488
 E value
                   1.0e-166
 Match length
                   274
 % identity
                   100
 NCBI Description (Y14590) class IV chitinase [Arabidopsis thaliana]
 Seq. No.
                   116693
 Contig ID
                   183 1.R1010
 5'-most EST
                   LIB3177-056-P1-K1-D11
 Method
                   BLASTX
 NCBI GI
                   g3882356 .
 BLAST score
                   503
 E value
                   9.0e-95
 Match length
                   265
 % identity
                   66
 NCBI Description
                   (U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis
                   thaliana]
 Seq. No.
                   116694
 Contig ID
                   183 2.R1010
 5'-most EST
                   jC-atXP25C125A2T7d1
 Method
                   BLASTX
 NCBI GI
                   g2598932
 BLAST score
                   776
 E value
                   8.0e-83
 Match length
                   165
 % identity
 NCBI Description
                   (AF027157) auxin-responsive protein IAA2 [Arabidopsis
                   thaliana]
                   116695
 Seq. No.
 Contig ID
                   183 3.R1010
 5'-most EST
                   g623630
 Method
                   BLASTX
 NCBI GI
                   q1352056
 BLAST score
                   520
 E value
                   1.0e-52
 Match length
                   114
 % identity
 NCBI Description
                   AUXIN-RESPONSIVE PROTEIN IAA2 >qi 454283 (L15449)
                   auxin-responsive protein [Arabidopsis thaliana]
```

```
Contig ID
                   183 4.R1010
                   q27\overline{5}9893
5'-most EST
Method
                   BLASTX
                   q2598932
NCBI GI
BLAST score
                   390 ·
                   8.0e-41
E value
                   112
Match length
% identity
                   (AF027157) auxin-responsive protein IAA2 [Arabidopsis
NCBI Description
                   thaliana]
                   116697
Seq. No.
                   183 7.R1010
Contig ID
5'-most EST
                   LIB23-004-Q1-E1-F2
Method
                   BLASTX
                   g1352056
NCBI GI
BLAST score
                   301
                   2.0e-28
E value
Match length
                   67
% identity
                   99
                   AUXIN-RESPONSIVE PROTEIN IAA2 >gi 454283 (L15449)
NCBI Description
                   auxin-responsive protein [Arabidopsis thaliana]
                   116698
Seq. No.
Contig ID
                   184 1.R1010
5'-most EST
                   LIB35-049-Q1-E1-E10
Method
                   BLASTX
NCBI GI
                  g2129570
BLAST score
                   559
                   2.0e-57
E value
Match length
                   115
% identity
                   99
                   DAD-1 homolog - Arabidopsis thaliana
NCBI Description
                   >gi 1184193 emb CAA64837 (X95585) DAD-1 homologue
                   [Arabidopsis thaliana]
                   116699
Seq. No.
                   185 1.R1010
Contig ID
                   LIB24-039-Q1-E1-F7
5'-most EST
Method
                   BLASTX
                   g99681
NCBI GI
BLAST score
                   1009
                   1.0e-110
E value
                   294
Match length
% identity
                   70
                   cold-regulated protein cor47 - Arabidopsis thaliana
NCBI Description
                   (fragment) >gi 388259 emb CAA42483 (X59814) Cold and ABA
                   regulated gene [Arabidopsis thaliana]
                   116700
Seq. No.
                   185 2.R1010
Contig ID
5'-most EST
                   jC-atXP65C206O21T7074d1
Method
                   BLASTX
                   g2062167
NCBI GI
                   803
BLAST score
                   7.0e-86
E value
                   155
Match length
```

```
% identity
                   99
NCBI Description
                   (ACO01645) Proline-rich protein APG isolog [Arabidopsis
                   thaliana]
Seq. No.
                   116701
Contig ID
                   185 3.R1010
5'-most'EST
                   q4714033
Method
                   BLASTX
NCBI GI
                   q3319344
BLAST score
                   936
E value
                   1.0e-101
                   305
Match length
                   50
% identity
                   (AF077407) contains similarity to UDP-glucoronosyl and
NCBI Description
                   UDP-glucosyl transferases (Pfam: UDPGT.hmm, score: 85.94)
                   [Arabidopsis thaliana]
Seq. No.
                   116702
                   185 4.R1010
Contig ID
                   q47\overline{1}4010
5'-most EST
Method
                  BLASTX
                   q3319344
NCBI GI
BLAST score
                   338
                  3.0e-31
E value
Match length
                   66
% identity
                   100
                   (AF077407) contains similarity to UDP-glucoronosyl and
NCBI Description
                   UDP-glucosyl transferases (Pfam: UDPGT.hmm, score: 85.94)
                   [Arabidopsis thaliana]
                   116703
Seq. No.
Contig ID
                   185 5.R1010
                   jC-atXP102CE2G2T7057d1
5'-most EST
Method
                   BLASTX
                   q99681
NCBI GI
BLAST score
                   380
E value
                   4.0e-42
                   92
Match length
                   100
% identity
                  cold-regulated protein cor47 - Arabidopsis thaliana
NCBI Description
                   (fragment) >gi_388259_emb_CAA42483_ (X59814) Cold and ABA
                   regulated gene [Arabidopsis thaliana]
                   116704
Seq. No.
Contia ID
                   185 10.R1010
5'-most EST
                   LIB25-102-Q1-E1-C6
                   BLASTX
Method
NCBI GI
                   g2129637
BLAST score
                   207
                   2.0e-16
E value
                   58
Match length
                   74
% identity
NCBI Description
                  low temperature-induced protein cor47 - Arabidopsis
                   thaliana >gi_975646_emb_CAA62449_ (X90959) dehydrin
                   [Arabidopsis thaliana]
```

116705

Seq. No.

\$4. . - . · ·

Contig ID

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Contig ID
                  186 1.R1010
5'-most EST
                  LIB3176-071-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q2500190
BLAST score
                  902
                  3.0e-97
E value
Match length
                  191
                  92
% identity
                  RAC-LIKE GTP BINDING PROTEIN ARAC1 >gi_1292908 (U41295) GTP
NCBI Description
                  binding protein [Arabidopsis thaliana] >gi_2435520
                  (AF024504) Arabidopsis thaliana GTP-binding protein (ARAC1)
                  (NID:g1292907) [Arabidopsis thaliana] >gi 4097563 (U64919)
                  ATGP2 [Arabidopsis thaliana]
                  116706
Seq. No.
                  186 2.R1010
Contig ID
                  LIB25-100-Q1-E1-E5
5'-most EST
Method
                  BLASTX
                  q3036799
NCBI GI
BLAST score
                  926
                  1.0e-100
E value
Match length
                  197
                  92
% identity
NCBI Description
                  (AL022373) ras-related small GTP-binding protein
                  [Arabidopsis thaliana] >gi 3406757 (AF079487) rac-like GTP
                  binding protein Arac6 [Arabidopsis thaliana]
                  >gi 3805861 emb CAA21481 (AL031986) ras-related small
                  GTP-binding protein [Arabidopsis thaliana]
                  >gi_4336891_gb_AAD17999_ (AF107663) rac homolog
                  [Arabidopsis thaliana]
                  116707
Seq. No.
                  186 3.R1010
Contig ID
5'-most EST
                  g315273
Method
                  BLASTN
NCBI GI
                  g3212846
BLAST score
                  49
                  3.0e-18
E value
Match length
                  81
% identity
                  90
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  116708
Seq. No.
                  186 4.R1010
Contig ID
5'-most EST
                  jC-atXLIB327421P2e06b1
Method
                  BLASTX
NCBI GI
                  g3212871
BLAST score
                  884
E value
                  2.0e-95
Match length
                  182
% identity
                  90
NCBI Description
                  (AC004005) putative translation initiation factor
                  [Arabidopsis thaliana]
                  116709
Seq. No.
```

188 1.R1010

```
5'-most EST
                   jC-atXLIB327423P4f07b1
 Method
                   BLASTX
 NCBI GI
                   q1076302
 BLAST score
                   501
                   2.0e-50
 E value
                   102
 Match length
                   100
 % identity
                   cold-regulated protein cor15a precursor - Arabidopsis
 NCBI Description
                   thaliana >gi_413922_emb_CAA45499_ (X64138) cor15
                   [Arabidopsis thaliana] >gi_507149 (U01377) cor15a
                   [Arabidopsis thaliana]
                   >gi 4559337 gb AAD22999.1_AC007087 18 (AC007087)
                   cold-regulated protein cor15a precursor [Arabidopsis
                   thaliana] >gi 444330_prf __1906379A cor15 gene [Arabidopsis
                   thaliana]
                   116710
 Seq. No.
                   189 1.R1010
 Contig ID
                   jC-atXLIB327402P4d01b1
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   g2664198
 BLAST score
                   1724
                   0.0e + 00
 E value
Match length
                   594
 % identity
                   (AJ003215) GTL1 [Arabidopsis thaliana]
 NCBI Description
                   116711
 Seq. No.
                   191 1.R1010
 Contig ID
 5'-most EST
                   PLN g416489
 Method
                   BLASTX
 NCBI GI
                   g481812
 BLAST score
                   2268
 E value
                   0.0e + 00
 Match length
                   552
 % identity
                   81
                   DNA-binding protein GT-2 - Arabidopsis thaliana
 NCBI Description
                   >gi 416490 emb CAA51289 (X72780) GT-2 factor [Arabidopsis
                   thaliana]
                   116712
 Seq. No.
 Contig ID
                   191 2.R1010
                   iC-atXLIB327439P1e06b2
 5'-most EST
                   BLASTX
 Method
                   g481812
 NCBI GI
                    596
 BLAST score
 E value
                   8.0e-62
                   129
 Match length
 % identity
                   53
                   DNA-binding protein GT-2 - Arabidopsis thaliana
 NCBI Description
                   >gi 416490 emb CAA51289 (X72780) GT-2 factor [Arabidopsis
                    thaliana]
                   116713
 Seq. No.
                   192 1.R1010
 Contig ID
                   LIB35-022-Q1-E1-G8
 5'-most EST
```

BLASTX

Method

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                               ja L
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                               ΗŁ
                               is L
```

Method

```
NCBI GI
                   g2687686
BLAST score
                   516
E value
                   2.0e-52
Match length
                   101
% identity
                   100
                  (AJ000110) cystatin [Arabidopsis thaliana]
NCBI Description
                   116714
Seq. No.
                   192 2.R1010
Contig ID
5'-most EST
                   g315745
                   BLASTX
Method
                   q2687686
NCBI GI
BLAST score
                   516
                   2.0e-52
E value
Match length
                   101
% identity
                   (AJ000110) cystatin [Arabidopsis thaliana]
NCBI Description
                   116715
Seq. No.
                   192 3.R1010
Contig ID
5'-most EST
                   LIB3176-046-P1-K1-H12
                   BLASTX
Method
            16 37
                   q2687686
NCBI GI
BLAST score
                   114
                   2.0e-35
E value
Match length
                   86
% identity
                   (AJ000110) cystatin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   116716
                   193 1.R1010
Contig ID
5'-most EST
                   PLN g2695702
                   BLASTX
Method
                   g2695703
NCBI GI
BLAST score
                   1655
                   0.0e + 00
E value
Match length
                   355
% identity
NCBI Description
                   (Y10555) CONSTANS [Arabidopsis thaliana]
                   >gi 2695705 emb CAA71588 (Y10556) CONSTANS [Arabidopsis
                   thaliana]
Seq. No.
                   116717
                   194 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327416P3f12b1
                   BLASTX
Method
                   q1354510
NCBI GI
BLAST score
                   1794
                   0.0e + 00
E value
                   366
Match length
% identity
                   (U55205) HAL2-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   116718
Contig ID
                   195 1.R1010
5'-most EST
                   LIB22-005-Q1-E1-C2
                   BLASTX
```

% identity

```
NCBI GI
                  g2738756
                  2233
BLAST score
                  0.0e + 00
E value
                   465
Match length
                  93
% identity
                  (AF016282) 5'-adenylylsulfate reductase [Arabidopsis-
NCBI Description
                  thaliana] >gi 4773905 gb AAD29775.1 AF074021 7 (AF074021)
                  5'-adenylylsulfate reductase [Arabidopsis thaliana]
                  116719
Seq. No.
                  195 2.R1010
Contig ID
                  jC-atXLIB327427P3c10b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2738756
BLAST score
                  515
                  3.0e-77
E value
                  175
Match length
% identity
                  85
                   (AF016282) 5'-adenylylsulfate reductase [Arabidopsis
NCBI Description
                   thaliana] >gi 4773905 gb AAD29775.1 AF074021 7 (AF074021)
                   5'-adenylylsulfate reductase [Arabidopsis thaliana]
                   116720
Seq. No.
Contig ID
                   196 1.R1010
5'-most EST
                   jC-atXLIB327430P4f08b1
Method
                  BLASTX
NCBI GI
                   g2160142
BLAST score
                   2253
E value
                   0.0e + 00
Match length
                   454
% identity
                   (ACO00375) Strong similarity to Arabidopsis APR2
NCBI Description
                   (qb U56921). [Arabidopsis thaliana] >gi 2738758 (AF016283)
                   5'-adenylylsulfate reductase [Arabidopsis thaliana]
                   116721
Seq. No.
Contig ID
                   197 1.R1010
5'-most EST
                   PLN g1710113
Method
                   BLASTX
NCBI GI
                   g2738760
BLAST score
                   2105
E value
                   0.0e + 00
Match length
                   458
                   90
% identity
                   (AF016284) 5'-adenylylsulfate reductase [Arabidopsis
NCBI Description
                   thaliana] >gi 2961344 emb CAA18102.1 (AL022140) PRH26
                  protein [Arabidopsis thaliana]
                   116722
Seq. No.
Contig ID
                   198 1.R1010
5'-most EST
                   jC-atXLIB327413P1d03b1
Method
                   BLASTX
NCBI GI
                   g3914234
BLAST score
                   1789
E value
                   0.0e + 00
Match length
                   369
                   95
```

```
NCBI Description ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE)
                   (ORNITHINE TRANSCARBAMYLASE) >gi 2764518 emb CAA04115
                   (AJ000476) Ornithine carbamoyltransferase [Arabidopsis
                  thaliana] >gi 2764737 emb CAA05510 (AJ002524) ornithine
                  carbamoyltransferase [Arabidopsis thaliana]
Seq. No.
                  116723
                  199 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327406P2b03b1
Method
                  BLASTX
                  g2764941
NCBI GI
BLAST score
                  607
E value
                  7.0e-63
Match length
                  106
% identity
                  100
NCBI Description
                  (X98255) transcriptionally stimulated by gibberellins;
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  116724
Seq. No.
Contig ID
                  199 2.R1010
                  LIB3176-018-P1-K1-F4
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2764941
BLAST score
                  603
E value
                  2.0e-62
Match length
                  106
% identity
                  99
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  116725
Seq. No.
                  199_3.R1010
Contig ID
5'-most EST
                  g2413796
Method
                  BLASTX
                  g2764941
NCBI GI
BLAST score
                  106
E value
                  4.0e-49
                  107
Match length
% identity
                  88
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
Seq. No.
                  116726
                  199 7.R1010
Contig ID
5'-most EST
                  g2413803
Method
                  BLASTX
NCBI GI
                  g2764941
BLAST score
                  397
E value
                  2.0e-38
Match length
                  92
                  79
% identity
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
```

thaliana]

Method

BLASTX

```
11.6727
Seq. No.
                199_11.R1010
Contig ID
                  jC-atXP104CE10E12T7b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2160156
BLAST score
                   615
E value
                  1.0e-63
Match length
                   123
% identity
                   98
                   (AC000132) Strong similarity to S. pombe leucyl-tRNA
NCBI Description
                  synthetase (gb Z73100). [Arabidopsis thaliana]
Seq. No.
                  116728
                  200 1.R1010
Contig ID
                  jC-alXLIB327436P1g11b1
5'-most EST
                  BLASTX
Method
                   g2780192
NCBI GI
BLAST score
                   1371
                  1.0e-152
E value
                  268
Match length
                   95
% identity
                   (AJ222713) unnamed protein product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  116729
                  201 1.R1010
Contig ID
                  LIB3234-004-P1-K1-A10
5'-most EST
Method
                  BLASTX
                   q2702279
NCBI GI
BLAST score
                  2558
E value
                  0.0e + 00
                   542
Match length
                   92
% identity
                   (AC003033) putative phosphate transporter [Arabidopsis
NCBI Description
                   thaliana] >gi_2780345_dbj_BAA24280_ (AB000093) inorganic
                  phosphate transporter [Arabidopsis thaliana] >gi_2914691
                   (AC003974) putative phosphate transporter [Arabidopsis
                   thaliana]
Seq. No.
                  116730
                  202 1.R1010
Contig ID
5'-most EST
                  LIB23-012-Q1-E1-A1
Method
                  BLASTX
NCBI GI
                  q3914666
BLAST score
                  1042
                  1.0e-113
E value
Match length
                  262
% identity
                  81
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR
NCBI Description
                  >gi_2791998_emb_CAA74895_ (Y14566) ribosomal protein L4
                   [Arabidopsis thaliana] >\overline{gi}2792000_emb_CAA74894_ (Y14565)
                  ribosomal protein L4 [Arabidopsis thaliana]
                  116731
Seq. No.
                  203 1.R1010
Contig ID
5'-most EST
                  LIB23-046-Q1-E1-F3
```

```
q3122858
NCBI GI
                  2791
BLAST score
                  0.0e+00
E value
Match length
                  624
% identity
                  91
                  D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR
NCBI Description
                  >gi 2189964 dbj BAA20405 (AB003280) Phosphoglycerate
                  dehydrogenase [Arabidopsis thaliana]
                  >qi 2804258 dbj BAA24440 (AB010407) phosphoglycerate
                  dehydrogenase [Arabidopsis thaliana]
                  116732
Seq. No.
                  205 1.R1010
Contig ID
                  LIB25-050-Q1-E1-G12
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3668173
BLAST score
                  1370
                  1.0e-152
E value
                  270
Match length
% identity
                  97
NCBI Description
                  (AB006777) vegetative storage protein [Arabidopsis
                  thaliana]
                  116733
Seq. No.
                  205 2.R1010
Contig ID
5'-most EST
                  jC-alXLIB327434P1e02b1
Method
                  BLASTX
NCBI GI
                  q3668175
BLAST score
                  1347
E value
                  1.0e-149
Match length
                  265
% identity
NCBI Description
                  (AB006778) vegetative storage protein [Arabidopsis
                  thaliana]
Seq. No.
                  116734
                  205 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327413P4e11a1
Method
                  BLASTX
NCBI GI
                  q1448937
BLAST score
                  283
                  1.0e-24
E value
Match length
                  89
% identity
                  58
NCBI Description
                  (L48180) the BAN237 cDNA clone was shown to be expressed
                  only in anthers not in leaves or other floral organs;
                  anther-specific gene product; putative [Brassica
                  campestris]
Seq. No.
                  116735
                  207 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327405P4g10b1
Method
                  BLASTX
NCBI GI
                  q2865462
BLAST score
                  1765
                  0.0e + 00
E value
Match length
                  352
```

```
% identity
NCBI Description
                   (AF043130) lactate dehydrogenase [Arabidopsis thaliana]
                    116736
Seq. No.
                    208 1.R1010
Contig ID
                    LIB3168-048-P1-K1-G2
5'-most EST
                    BLASTX
Method
NCBI GI
                    g1169515
BLAST score
                    790
E value
                    1.0e-84
Match length
                    152
% identity
                    99
                   EM-LIKE PROTEIN GEA1 >gi 2119768 pir S34819 embryonic
NCBI Description
                    abundant protein Em1 - Arabidopsis thaliana
                   >gi_298070_emb_CAA77509_ (Z11158) Em protein [Arabidopsis
thaliana] >gi_298072_emb_CAA77979_ (Z11921) Em protein
                    homologue [Arabidopsis thaliana] >gi 3068708 (AF049236) Em1
                    protein [Arabidopsis thaliana]
                    116737
Seq. No.
                    209 1.R1010
Contig ID
5'-most EST
                    jC-atXLIB327420P3g08b1
Method
                    BLASTX
                    g2895510
NCBI GI
                    2865
BLAST score
                    0.0e + 00
E value
                    592
Match length
% identity
                    (AF033204) putative pectin methylesterase [Arabidopsis
NCBI Description
                    thaliana]
                    116738
Seq. No.
Contig ID
                    210 1.R1010
5'-most EST
                    LIB22-059-Q1-E1-E1
Method
                    BLASTX
                   g2618723
NCBI GI
BLAST score
                    1120
E value
                    1.0e-123
Match length
                    229
% identity
                    93
                    (U49073) IAA17 [Arabidopsis thaliana] >gi 2921756
NCBI Description
                    (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana]
                   >gi_4389514_gb_AAB70451_ (AC000104) Identical to
Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs
                    gb_H36782 and gb_F14074 come from this gene. [Arabidopsis
                    thaliana]
Seq. No.
                    116739
Contig ID
                    212_1.R1010
5'-most EST
                    PLN_g902788
                   BLASTX
Method
NCBI GI
                   q1708461
BLAST score
                    2106
E value
                   0.0e + 00
Match length
                    422
                    97
% identity
NCBI Description IAA-AMINO ACID HYDROLASE HOMOLOG 1 PRECURSOR >gi 902789
```

```
>qi 2921829 gb AAC04865.1 (AF047031) IAA-amino acid
                  hydrolase [Arabidopsis thaliana]
                   116740
Seq. No.
                   213 1.R1010
Contig ID
                  jC-atXP10C97B8T7d1
5'-most EST
                  BLASTX ·
Method
                  q464985
NCBI GI
BLAST score
                   550
E value
                  1.0e-78
Match length
                  147
% identity
                   99
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A)
                  >gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana]
                  116741
Seq. No.
                  213 2.R1010
Contig ID
5'-most EST
                  jC-atXP85CG7F10T7b1
                  BLASTX
Method
                  g464985
NCBI GI
BLAST score
                  791
E value
                  2.0e-84
Match length
                  148
                  99
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 8) (UBIQUITÎN CARRIER PROTEIN 8) (UBCAT4A)
                  >gi 398699_emb_CAA78713_ (Z14989) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana]
                  116742
Seq. No.
                  213 3.R1010
·Contig ID
5'-most EST
                  LIB25-007-Q1-E1-B10
Method
                  BLASTX
                  q441457
NCBI GI
BLAST score
                  578
E value
                  1.0e-59
                  150
Match length
% identity
                  76
NCBI Description
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
                  esculentum]
                  116743
Seq. No.
                  213 4.R1010
Contig ID
5'-most EST
                  ARABL1-043-Q1-B1-H10
                  BLASTX
Method
NCBI GI
                  q464985
BLAST score
                  737
E value
                  4.0e-78
Match length
                  148
% identity
                  93
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A)
                  >gi 398699 emb CAA78713 (Z14989) ubiquitin conjugating
```

(U23795) ILL1 [Arabidopsis thaliana]

enzyme homolog [Arabidopsis thaliana]

```
Seq. No.
                  116744
                  213 6.R1010
Contig ID
                  jC-atXP95CG12H1T7008b1
5'-most ÉST
Method
                  BLASTX
NCBI GI
                  g4490332
BLAST score
                  1326
E value
                  1.0e-147
Match length
                  263
% identity
                  100
NCBI Description
                  (AL035656) putative protein [Arabidopsis thaliana]
                  116745
Seq. No.
                  213 7.R1010
Contig ID
5'-most EST
                  g1159415
                  BLASTX
Method
NCBI GI
                  q464985
BLAST score
                  468
                  9.0e-47
E value
                  123
Match length
% identity
                  77
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN
                  LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A)
                  >gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana]
                  116746
Seq. No.
Contig ID
                  213 12.R1010
5'-most EST
                  jC-atXP62C204A8T7d2
Method
                  BLASTX
NCBI GI
                  g3790593
BLAST score
                  560
E value
                  1.0e-57
Match length
                  101
% identity
                  100
NCBI Description
                  (AF079185) RING-H2 finger protein RHY1a [Arabidopsis
                  thaliana]
                 116747
Seq. No.
Contig ID
                  213 14.R1010
5'-most EST
                  LIB3177-099-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q4490332
BLAST score
                  1319
E value
                  1.0e-146
Match length
                  263
                  100
% identity >>
NCBI Description (AL035656) putative protein [Arabidopsis thaliana]
Seq. No.
                  116748
Contig ID
                  213 18.R1010
5'-most EST
                  g905580
Method
                  BLASTX
NCBI GI
                  q464985
BLAST score
                  308
E value
                  5.0e-28
Match length
```

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ori and and and the first of th
```

Contig ID

5'-most EST

```
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A)
                  >gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana]
Seq. No.
                  116749
                  213 19.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P1c06b1
Method
                  BLASTN
NCBI GI
                  q4490324
BLAST score
                  241
E value
                  1.0e-133
Match length
                  675
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
NCBI Description
                  (ESSA project)
                  116750
Seq. No.
                  213 20.R1010
Contig ID
5'-most EST
                  ARABL1-035-Q1-B1-F10
Method
                  BLASTX
NCBI GI
                  g1142614
BLAST score
                  74
E value
                  5.0e-24
Match length
                  65
% identity
                  91
NCBI Description
                  (U17250) ubiquitin conjugating enzyme, E2 [Brassica
                  oleracea]
                  116751
Seq. No.
                  213 23.R1010
Contig ID
5'-most EST
                  jC-atX22062Q1E1A05b1
Method
                  BLASTX
                  g4490332
NCBI GI
BLAST score
                  321
E value
                  2.0e-29
                  96
Match: length
% identity
                  68
NCBI Description
                  (AL035656) putative protein [Arabidopsis thaliana]
                  116752
Seq. No.
                  214 1.R1010
Contig ID
5'-most EST
                  LIB23-072-Q1-E1-G11
Method
                  BLASTX
                  g421826
NCBI GI
BLAST score
                  1347
E value
                  1.0e-149
Match length
                  280
% identity
                  91
NCBI Description
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                  >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana]
                  116753
Seq. No.
```

214 2.R1010

g1158560

```
Method
                  BLASTX
NCBI GI
                  q421826
BLAST score
                  494
E value
                  9.0e-50
Match length
                  149
% identity
NCBI Description
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                  >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana]
                  116754
Seq. No.
Contig ID
                  214 4.R1010
                  jC-atXLIB327413P4h08a1
5'-most EST
                  BLASTX
Method
                  g421826
NCBI GI
BLAST score
                  328
                  5.0e-30
E value
Match length
                  65
                  100
% identity
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                  >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana]
Seq. No.
                  116755
Contig ID -.
                  214 5.R1010
5'-most EST
                  ARABL1-036-Q1-E1-A8
Method
                  BLASTX
NCBI GI
                  q421826
BLAST score
                  491
                  2.0e-49
E value
Match length
                  96
                  100
% identity
NCBI Description
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                  >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana]
                  116756
Seq. No.
                  217_1.R1010
Contig ID
5'-most EST
                  LIB3176-007-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2924779
BLAST score
                  2141
                  0.0e + 00
E value
Match length
                  462
                  92
% identity
NCBI Description
                  (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
                 thaliana] >gi_2981616_dbj_BAA25248_ (AB008854)
                  3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                  >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA
                  thiolase [Arabidopsis thaliana]
                  116757
Seq. No.
Contig ID
                  217: 2.R1010
5'-most EST
                  jC-atXLIB327431P4f06a1
Method
                  BLASTX
NCBI GI
                  g2494125
BLAST score
```

593

Match length

118

```
E value
                  2.0e-61
Match length
                  152
                  80
% identity
                  (AC002376) Strong similarity to Cucumis acetyl-CoA
NCBI Description
                  acyltransferase (gb D70895). [Arabidopsis thaliana]
                  116758
Seq. No.
                  217 3.R1010
Contig ID
5'-most EST
                  LIB3177-066-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2924779
BLAST score
                  334
E value
                  7.0e-31
Match length
                  65
                  100
% identity
                  (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
NCBI Description
                  thaliana] >gi 2981616_dbj_BAA25248_ (AB008854)
                  3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                  >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA
                  thiolase [Arabidopsis thaliana]
                  116759
Seq. No.
Contig ID
                  217 4.R1010
5'-most EST
                  jC-alXLIB327434P1b03b1
Method
                  BLASTX
                  g2924779
NCBI GI
                  732
BLAST score
                  1.0e-77
E value
Match length
                  145
                  100
% identity
                  (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
NCBI Description
                  thaliana] >gi 2981616 dbj BAA25248 (AB008854)
                  3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                  >gi 2981618 dbj BAA25249 (AB008855) 3-ketoacyl-CoA
                  thiolase [Arabidopsis thaliana]
                  116760
Seq. No.
                  218: 1, R1010
Contig ID
5'-most EST
                  jC-atXLIB327430P1e02b1
Method
                  BLASTX
                  q2982583
NCBI GI
BLAST score
                  2066
                  0.0e + 00
E value
                  391
Match length
                  100
% identity
                  (AJ003135) polygalacturonase [Arabidopsis thaliana]
NCBI Description
                  >gi 3152948 emb CAA06610_ (AJ005584) polygalacturonase
                  [Arabidopsis thaliana]
                  116761
Seq. No.
Contig ID
                  219 1.R1010
5'-most EST
                  g2413187
Method
                  BLASTX
NCBI GI
                  g2995990°
BLAST score
                  270
E value
                  3.0e-52
```

Contig ID

```
% identity
                  (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
                  116762
Seq. No.
Contig ID
                  219 2.R1010
                  LIB3177-041-P1-K2-C9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2995990
BLAST score
                  316
E value
                  7.0e-30
Match length
                  101
% identity
                  72
                  (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
                  116763
Seq. No.
                  219 6.R1010
Contig ID
                  LIB25-004-Q1-E1-D9
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2995990
BLAST score
                  488
                  4.0e-49
E value
Match length
                  114
% identity
                  82
                  (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
                  116764
Seq. No.
                  219_7.R1010
Contig ID
5'-most EST
                  jC-atXP37C157H6T7d2
Method
                  BLASTN
                  g2995991
NCBI GI
BLAST score
                  192
                  1.0e-103
E value
                  581
Match length
% identity
                  Arabidopsis thaliana dormancy-associated protein (DRM1)
NCBI Description
                  gene, complete cds
                  116765
Seq. No.
                  219 8.R1010
Contig ID
5'-most EST
                  g2747454
Method
                  BLASTN
NCBI GI
                  g2995991
BLAST score
                  338
                  0.0e + 00
E value
Match length
                  473
% identity
                  96
                  Arabidopsis thaliana dormancy-associated protein (DRM1)
NCBI Description
                  gene, complete cds
                  116766
Seq. No.
```

220 1.R1010 -

```
5'-most EST
                  PLN_g313681
                  BLASTX
Method
NCBI GI
                  q1346701
BLAST score
                  2128
                  0.0e + 00
E value
Match length
                  422
% identity
                  EXOPOLYGALACTURONASE CLONE GBGE184 PRECURSOR (EXOPG)
NCBI Description
                   (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_421831_pir__S34199 exopolygalacturonase (clone GBGe184)
                  - Arabidopsis thaliana >gi_313682_emb_CAA51032_ (X72291)
                  exopolygalacturonase [Arabidopsis thaliana]
                  >gi 3004440_emb_CAA76127_ (Y16230) polygalacturonase
                   [Arabidopsis thaliana]
                  116767
Seq. No.
                  221 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327408P4e07b1
Method
                  BLASTX
                  g1346702
NCBI GI
BLAST score
                  1980
E value
                  0.0e + 00
Match length
                  444
% identity
                  85
                  EXOPOLYGALACTURONASE CLONE GBGA483 PRECURSOR (EXOPG)
NCBI Description
                  (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_421832_pir__S34200 exopolygalacturonase (clone GBGa483)
                  - Arabidopsis thaliana >gi_313684_emb_CAA51033_ (X72292)
                  exopolygalacturonase [Arabidopsis thaliana]
                  116768
Seq. No.
                  222 1.R1010
Contig ID
                  LIB146-005-Q1-E1-A7
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3021336
BLAST score
                  3284
                  0.0e + 00
E value
Match length
                  650
% identity
                  98
                  (AJ224957) RGA-like [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  116769
                  222 3.R1010
Contig ID
                  jC-atXLIB327406P1h05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3021336
BLAST score
                  518
                  1.0e-52
E value
Match length
                  114
                  89
% identity
NCBI Description
                  (AJ224957) RGA-like [Arabidopsis thaliana]
Seq. No.
                  116770
                  223 1.R1010
Contig ID
                  PLN_g303499
5'-most EST
Method
                  BLASTX
```

g729905

NCBI GI

```
BLAST score
                  2558
E value
                  0.0e + 00
Match length
                  554
% identity
                  90
                  PUTATIVE SERINE/THREONINE-PROTEIN KINASE PK7
NCBI Description
                  >gi_320562_pir__JC1385 protein kinase (EC 2.7.1.37) -
                  Arabidopsis thaliana >gi_303500_dbj_BAA01716_ (D10910)
                  serine/threonine protein kinase [Arabidopsis thaliana]
                  116771
Seq. No.
                  224_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327426P1a02b1
Method
                  BLASTX
NCBI GI
                  q730645
BLAST score
                  714
                  2.0e-75
E value
Match length
                  152
% identity
                  93
                  40S RIBOSOMAL PROTEIN S15 >gi 629556 pir S43412 ribosomal
NCBI Description
                  protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_
                  (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                  >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15
                  [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104)
                  Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                  gb R29788, gb ATTS0365 come from this gene. [Arabidopsis
                  thaliana]
                  116772
Seq. No.
                  224 2.R1010
Contig ID
5'-most EST
                  LIB25-061-Q1-E1-G1
Method
                  BLASTX
NCBI GI
                  g730645
BLAST score
                  708
E value
                  9.0e-75
                  152
Match length
% identity
                  92
NCBI Description
                  40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal
                  protein S15 - Arabidopsis thaliana >gi 313152 emb CAA80679
                  (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                  >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15
                  [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104)
                  Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                  gb R29788, gb ATTS0365 come from this gene. [Arabidopsis
                  thaliana]
                  116773
Seq. No.
                  224_3.R1010
Contig ID
5'-most EST
                  LIB3177-013-P1-K2-G12
Method
                  BLASTX
NCBI GI
                  g730645
BLAST score
                  282
E value
                  4.0e-25
Match length
                  76
                  .08
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S15 >gi 629556 pir _S43412 ribosomal
                  protein S15 - Arabidopsis thaliana >gi 313152 emb CAA80679_
                  (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
```

>gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15
[Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104)
Strong similarity to Oryza 40S ribosomal protein S15. ESTs
gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

```
116774
Seq. No.
Contig ID
                   225 1.R1010
                   LIB3176-037-P1-K1-A1
5'-most EST
                   BLASTX
Method
                   g3150037
NCBI GI
BLAST score
                   1489
E value
                   1.0e-166
Match length
                   295
                   97
% identity
                  (U66462) ATR1 [Arabidopsis thaliana]
NCBI Description
                   116775
Seq. No.
                   226_1.R1010
Contig ID
5'-most EST
                   PLN g3242076
Method
                   BLASTX
                   g3242077
NCBI GI
BLAST score
                   2605
                   0.0e+00
E value
Match length
                   508
% identity
                   100
NCBI Description
                   (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
                   116776
Seq. No.
                   226 2.R1010
Contig ID
5'-most EST
                   jC-atXP33C148J19T7d2
```

Method BLASTX
NCBI GI g3242077
BLAST score 367
E value 7.0e-35
Match length 73
% identity 99

NCBI Description (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 116777 Contig ID 227_1.R1010

5'-most EST jC-atXP104CE10C3T7b1

Method BLASTX
NCBI GI g3273743
BLAST score 483
E value 3.0e-48
Match length 115
% identity 84

NCBI Description (AF057357) lipid transfer protein 2 precursor [Arabidopsis

thaliana] >gi_3786019 (AC005499) unknown protein

[Arabidopsis thaliana]

Seq. No. 116778 Contig ID 227 2.R1010

5'-most EST jC-atXP102CE5E8T7b1

Method BLASTX NCBI GI g3273743

```
BLAST score
                   620
E value.
                   2.0e-64
Match length
                  118
                  100
% identity
                   (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                  thaliana] >gi 3786019 (AC005499) unknown protein
                   [Arabidopsis thaliana]
                  116779
Seq. No.
                  227 3.R1010
Contig ID
5'-most EST
                  g2414093
Method
                  BLASTX
                  g3273743
NCBI GI
                  208
BLAST score
                  4.0e-16
E value
                  109
Match length
                  39
% identity
                  (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                  thaliana] >gi 3786019 (AC005499) unknown protein
                   [Arabidopsis thaliana]
                  116780 .
Seq. No.
                  227 5.R1010
Contig ID
5'-most EST
                  g25\overline{8}1615
Method
                  BLASTX
NCBI GI
                  g3273743
BLAST score
                  190
                  1.0e-40
E value
Match length
                  111
% identity
                  83
                  (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                  thaliana] >gi 3786019 (AC005499) unknown protein
                   [Arabidopsis thaliana]
Seq. No.
                  116781
                  227 7.R1010
Contig ID
5'-most EST
                  g2413841
Method
                  BLASTN
                  g3785992 ·
NCBI GI
BLAST score
                  150
                  2.0e-78
E value
                  398
Match length
                  62
% identity
                  Arabidopsis thaliana chromosome II BAC T6A23 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  116782
Seq. No.
                  227 9.R1010
Contig ID
5'-most EST
                  g1520303
Method
                  BLASTX
NCBI GI
                  g2497737
BLAST score
                  177
                  3.0e-25
E value
Match length
                  92
                  68
% identity
NCBI Description
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
                  >qi 732524 (U22175) germination-specific lipid transfer
```

BLAST score

1039

protein 3 [Brassica napus]

```
116783
Seq. No.
                 -227 13.R1010
Contig ID
                  LIB3234-039-P1-K1-G12
5'-most EST
                  BLASTX
Method.
                  g3273743
NCBI GI
BLAST score
                  169
                  1.0e-36
E value
                  84
Match length
                  96
% identity
                  (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                  thaliana] >gi_3786019 (AC005499) unknown protein
                   [Arabidopsis thaliana]
                  116784
Seq. No.
                  228 1.R1010
Contig ID
5'-most EST
                  LIB25-088-Q1-E1-E9
Method
                  BLASTX
                  g3286693
NCBI GI
BLAST score
                  1695
                  0.0e+00
E value
                  332
Match length
                  100
% identity
                  (Y15433) 33 kDa polypeptide of oxygen-evolving complex
NCBI Description
                   (OEC) in photosystem II [Arabidopsis thaliana]
                  116785
Seq. No.
                  228 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327420P1d11b1
Method
                  BLASTX
                   q4835233
NCBI GI
BLAST score
                   1210
                   1.0e-133
E value
                   258
Match length
% identity
                   93
                   (AL049862) putative protein 1 photosystem II
NCBI Description
                  oxygen-evolving complex [Arabidopsis thaliana]
Seq. No.
                  116786
                  228 3.R1010
Contig ID
                   jC-atXLIB327418P1c10b1
5'-most EST
Method
                  BLASTX
                   q4835233
NCBI GI
BLAST score
                   671
                   2.0e-70
E value
                  168
Match length
                  85
% identity
                   (AL049862) putative protein 1 photosystem II
NCBI Description
                  oxygen-evolving complex [Arabidopsis thaliana]
Seq. No.
                  116787
Contig ID
                  228 4.R1010
5'-most EST
                  q931390
Method
                  BLASTX
NCBI GI
                  q4835233
```

```
E value
                  1.0e-113
Match length
                  249
% identity
                  76
NCBI Description
                  (AL049862) putative protein 1 photosystem II
                  oxygen-evolving complex [Arabidopsis thaliana]
                  116788
Seq. No.
                  228 5.R1010
Contig ID
                  g937373
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3286693
BLAST score
                  534
E value
                  2.0e-54
Match length
                  132
                  87
% identity
                  (Y15433) 33 kDa polypeptide of oxygen-evolving complex
NCBI Description
               (OEC) in photosystem II [Arabidopsis thaliana]
                  116789
Seq. No.
                  229 1.R1010
Contig ID
5'-most EST
                  PLN g2285791
Method
                  BLASTX
NCBI GI
                  g2285792
BLAST score
                  851
E value
                  2.0e-91
Match length
                  168
% identity
                  100
NCBI Description
                  (AB004568) cyanase [Arabidopsis thaliana]
                  >gi 3287503 dbj BAA31224 (AB015748) cyanase [Arabidopsis
                  thaliana]
                  116790
Seq. No.
Contig ID
                  229 2.R1010
5'-most EST
                  jC-atXP102CE4E2T7005d1
Method
                  BLASTX
                  g2285792
NCBI GI
BLAST score
                  608
                  8.0e-67
E value
Match length
                  156
                  90
% identity
NCBI Description
                  (AB004568) cyanase [Arabidopsis thaliana]
                  >gi 3287503 dbj BAA31224 (AB015748) cyanase [Arabidopsis
                  thaliana]
                  116791
Seq. No.
                  230 1.R1010
Contig ID
5'-most EST
                  LIB3234-043-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g3335171
BLAST score
                  725
                  1.0e-76
E value
Match length
                  211
% identity
                  69
                  (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  116792
Contig ID
                  230 4.R1010
```

```
5'-most EST
                  LIB3234-003-P1-K1-H4
Method
                  BLASTN
                  g3335170
NCBI GI
BLAST score
                  228
                  1.0e-125
E value
Match length
                  367
% identity
                  91
                  Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene,
NCBI Description
                  complete cds
                  116793
Seq. No.
                  231_1.R1010
Contig ID
5'-most EST
                  g2747777
Method
                  BLASTX
                  g3342550
NCBI GI
                  291
BLAST score
                  5.0e-26
E value
Match length
                  . 107
% identity
                  56
                  (AF076979) late-embryogenesis abundant M10 protein
NCBI Description
                  [Arabidopsis thaliana] >gi_3894195 (AC005662)
                  late-embryogenesis abundant M10 protein [Arabidopsis
                  thaliana]
                  116794
Seq. No.
                  232 1.R1010
Contig ID
                  jC-alXLIB327436P1f11b1
5'-most EST
Method
                  BLASTX
                  g3342904
NCBI GI
BLAST score
                  2687
                  0.0e + 00
E value
                  560
Match length
% identity
                  91
                  (AF077855) flower-specific pectin methylesterase precursor
NCBI Description
                  [Arabidopsis thaliana]
                  116795
Seq. No.
Contig ID
                  232 2.R1010
                  jC-alXLIB327436P3c06b1
5'-most EST
                  BLASTX
Method
                  g3522958
NCBI GI
BLAST score
                  902
                  2.0e-97
E value
Match length
                  242
                  76
% identity
NCBI Description
                  (AC004411) putative pectinesterase [Arabidopsis thaliana]
                  116796
Seq. No.
Contig ID
                  232 3.R1010
5'-most EST
                  g2048421
Method
                  BLASTX
NCBI GI
                  g3522959
BLAST score
                  306
E value
                  7.0e-41
Match length
                  126
% identity
                  71
                  (AC004411) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
```

```
116797
Seq. No.
                . 232 4.R1010
Contig ID
                  jC-atXLIB327418P2e12b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3522959
BLAST score
                  211
E value
                  3.0e-33
Match length
                  105
                  76
% identity
                  (AC004411) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  116798
                  232 5.R1010
Contig ID
5'-most EST
                  jC-atXP121C118B2T7030d1
                  BLASTX
Method
                  q3522958
NCBI GI
BLAST score
                  789
                  1.0e-94
E value
                  260
Match length
                  72
% identity
                  (AC004411) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  116799
                  232 6.R1010
Contig ID
                  jC-alxLIB327435P4c03b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3522958
BLAST score
                  77
                  1.0e-90
E value
                  192
Match length
                  92
% identity
                  (AC004411) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  116800
                  232 7.R1010
Contig ID
5'-most EST
                  jC-atXLIB327416P1f04a1
Method
                  BLASTX
NCBĮ GI
                  g3522959
BLAST score
                  956
E value
                  1.0e-105
                  210
Match length
                  94
% identity
                  (AC004411) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                  116801
Seq. No.
                  233_1.R1010
Contig ID
5'-most EST
                  PLN_g3549625
Method
                  BLASTX
                  g423988
NCBI GI
BLAST score
                  3064
E value
                  0.0e + 00
                  598
Match length
                  98
% identity
                  serine/threonine kinase homolog PRO25 - Arabidopsis
NCBI Description
                  thaliana >gi 166813 (L04999) serine threonine kinase
                  [Arabidopsis thaliana]
```

```
Seq. No.
                  116802
                   233_2.R1010
Contig ID
5'-most EST
                  PLN g3355307
Method
                  BLASTX
NCBI GI
                   g3355308 ·
BLAST score
                   3837
E value
                   0.0e + 00
Match length
                   738
                   98
% identity
NCBI Description
                   (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]
Seq. No.
                  116803
Contig ID
                   234 1.R1010
5'-most EST
                   jC-atXP96C249I24T7b1
                  BLASTX
Method
NCBI GI
                   g320558
BLAST score
                   731
                   3.0e-77
E value
                   190
Match length
                  79
% identity
                  DNA-binding protein - Arabidopsis thaliana >gi_601843
NCBI Description
                   (M25268) DNA-binding protein [Arabidopsis thaliana]
                   116804
Seq. No.
Contig ID
                   235 1.R1010
5'-most EST
                   g2393406
                  BLASTN
Method
                   g3413422
NCBI GI
BLAST score
                   343
                   0.0e+00
E value
                   402
Match length
                   98
% identity
                  Arabidopsis thaliana gene encoding protein tyrosine
NCBI Description
                  phosphatase, ORF1 and ORF2 genes
                   116805
Seq. No.
Contig ID
                  235 2.R1010
5'-most EST
                  LIB3177-065-P1-K1-A11
Method
                  BLASTX
                   q4557229
NCBI GI
BLAST score
                   173
                   2.0e-12
E value
                  69
Match length
                   43
% identity
NCBI Description
                  angio-associated, migratory cell protein
                  >gi 3121739_sp_Q13685_AAMP_HUMAN ANGIO-ASSOCIATED MIGRATORY
                  CELL PROTEIN >gi_2134759_pir___139383 angio-associated
                  migratory cell protein - human >gi 870803 (M95627)
                   angio-associated migratory cell protein [Homo sapiens]
                  116806
Seq. No.
Contig ID
                   236 1.R1010
5'-most EST
                  LIB23-041-Q1-E1-D8
                  BLASTX
Method
NCBI GI
                  g114085
BLAST score
                   946
```

```
1.0e-102
E value
Match length
                  203
                  94
% identity
NCBI Description RAS-RELATED PROTEIN ARA-1 >gi 81597 pir JS0163 Ara protein
                  - Arabidopsis thaliana >gi 538283 (M25471) ras-related
                  protein [Arabidopsis thaliana]
                  116807
Seq. No.
                  237 1.R1010
Contig ID
5'-most EST
                  PLN_g3420800
                  BLASTX
Method
                  g3420801
NCBI GI
BLAST score
                  2192
E value
                  0.0e + 00
                  428
Match length
                  100
% identity
                  (AF081066) IAA-amino acid hydrolase homolog ILL3
NCBI Description
                  [Arabidopsis thaliana]
                  116808
Seq. No.
Contig ID
                  238 1.R1010
5'-most EST
                  LIB22-084-Q1-E1-B7
Method
                  BLASTX
NCBI GI
                  g3461884
BLAST score
                  1437
                  1.0e-160
E value
Match length
                  281
% identity
                  100
                  (AB006082) phosphoribosyl-ATP pyrophosphohydrolase
NCBI Description
                  [Arabidopsis thaliana] >gi_3461886_dbj BAA32529 (AB006083)
                  phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis
                  thaliana]
                  116809
Seq. No.
Contig ID
                  240 1.R1010
5'-most EST
                  LIB3168-072-P1-K1-E11
                  BLASTX
Method
NCBI GI
                  g3242706
BLAST score
                  495
                  1.0e-49
E value
Match length
                  191
                  57
% identity
                  (AC003040) cyclin-dependent kinase inhibitor protein
NCBI Description
                  [Arabidopsis thaliana] >gi 3550262 (AF079587)
                  cyclin-dependent kinase inhibitor; ICK1 [Arabidopsis
                  thaliana]
                  116810
Seq. No.
                  240 2.R1010
Contig ID
5'-most EST
                  jC-atXP10C96D15T7d2
Method
                  BLASTX
                  g2052502
NCBI GI
BLAST score
                  261
                  1.0e-22
E value
Match length
                  81
% identity
NCBI Description (U94772) cyclin-dependent kinase inhibitor protein
```

[Arabidopsis thaliana]

```
116811
Seq. No.
                   241 1.R1010
Contig ID
                  g40<del>6</del>835
5'-most EST
Method
                  BLASTX
                  g3075394
NCBI GI
BLAST score
                   2679
                   0.0e + 00
E value
                   549
Match length
                   94
% identity
                  (ACO04484) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana] >gi 3559809 emb_CAA09311_ (AJ010713) fiddlehead
                  protein [Arabidopsis thaliana]
                   116812
Seq. No.
                   241 3.R1010
Contig ID
5'-most EST
                  g2749275
                  BLASTX
Method
                  g3075394
NCBI GI
BLAST score
                   61
                   1.0e-35
E value
                   81
Match length
% identity
                   93
                  (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead
                  protein [Arabidopsis thaliana]
                   116813
Seq. No.
                  244 1.R1010
Contig ID
5'-most EST
                   PLN g3687653
Method
                   BLASTX
                   g3687654
NCBI GI
BLAST score
                   3595
E value
                  0.0e + 00
                   761
Match length
                   93
% identity
                   (AF047975) putative ethylene receptor; ETR2 [Arabidopsis
NCBI Description
                   thaliana]
                   116814
Seq. No.
                   245 1.R1010
Contig ID
5'-most EST
                   PLN g3687655
                   BLASTX
Method
NCBI GI
                   g2341041
BLAST score
                   2911
                   0.0e+00
E value
                   619
Match length
                  93
% identity
                   (AC000104) Arabidopsis thaliana putative ethylene receptor
NCBI Description
                   (ERS2) gene (gb AF047976). EST gb_W43451 comes from this
                   gene. [Arabidopsis thaliana] >gi_3687656 (AF047976)
                   putative ethylene receptor; ERS2 [Arabidopsis thaliana]
```

116815

Method

BLASTX

```
Method
                   BLASTX
NCBI GI
                   q2341041
BLAST score
                   55
E value
                   2.0e-61
Match length
                   150
% identity
                   (AC000104) Arabidopsis thaliana putative ethylene receptor
NCBI Description
                   (ERS2) gene (gb_AF047976). EST gb_W43451 comes from this
                   gene. [Arabidopsis thaliana] >gi_3687656 (AF047976)
putative ethylene receptor; ERS2 [Arabidopsis thaliana]
Seq. No.
                   116816
                   246 1.R1010
Contig ID
                   LIB24-038-01-E1-A4
5'-most EST
Method ·
                   BLASTX
                   q3334223
NCBI GI
BLAST score
                   2244
                   0.0e + 00
E value
                   445
Match length
% identity
                   4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)
NCBI Description
                   >gi_2145039 (AF000228) p-hydroxyphenylpyruvate dioxygenase
                   [Arabidopsis thaliana] >gi_2392518 (U89267)
                   p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]
                   >gi_3098559_gb_AAC15697.1_ (AF047834)
                   4-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]
Seq. No.
                   116817
                   247 1.R1010
Contig ID
                   jC-atXP65C207L24T7075d1
5'-most EST
Method
                   BLASTX
                   g1174162
NCBI GI
BLAST score
                   895
                   1.0e-96
E value
Match length
                   160
% identity
                   100
                   (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                   thaliana] >gi_3746915 (AF091106) E2
                   ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
                   116818
Seq. No.
                   250 1.R1010
Contig ID
                   g11\overline{5}9551
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1408471
BLAST score
                   643
                   5.0e-67
E value
Match length
                   139
% identity
NCBI Description
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
                   thaliana] >gi_3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                   116819
Seq. No.
                   251_1.R1010
PLN_g3860162
Contig ID
5'-most EST
```

```
NCBI GI
                   q3860163
                   5908
BLAST score
                   0.0e + 00
E value
Match length
                   1189
                   96
% identity
                   (AF098962) disease resistance protein RPP1-WsA [Arabidopsis
NCBI Description
                   thaliana]
                   116820
Seq. No.
                   251 3.R1010
Contig ID
                  LIB\overline{2}2-016-Q1-E1-D5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3860167
BLAST score
                   761
                  6.0e-81
E value
                   230
Match length
                   77
% identity
                   (AF098964) disease resistance protein RPP1-WsC [Arabidopsis
NCBI Description
                   thaliana]
                   116821
Seq. No.
                   251 4.R1010
Contig ID
5'-most EST
                   jC-atXP55C186L2T7d2
Method ...
                   BLASTX
                   g3860167
NCBI GI
BLAST score
                   219
                   1.0e-17
E value
                   95
Match length
                   58
% identity
                   (AF098964) disease resistance protein RPP1-WsC [Arabidopsis
NCBI Description
                   thaliana]
                   116822
Seq. No.
                   251 5.R1010
Contig ID
                   jC-atXLIB327432P4d12b1
5'-most EST
                   BLASTX
Method
                   g3860165
NCBI GI
BLAST score
                   640
                   6.0e-67
E value
Match length
                   145
% identity
                   88
                   (AF098963) disease resistance protein RPP1-WsB [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   116823
                   251_6.R1010
Contig ID
5'-most EST
                  LIB24-096-Q1-E1-D8
Method
                   BLASTX
NCBI GI
                   g3860167
BLAST score
                   618
E value
                   2.0e-64
Match length
                   155
                   22
% identity
                   (AF098964) disease resistance protein RPP1-WsC [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No.

Match length

908 .

```
252 1.R1010
Contig ID
5'-most EST
                    LIB22-035-Q1-E1-D9
Method
                    BLASTX
NCBI GI
                    g3882355
BLAST score
                    1994
E value
                    0.0e + 00
Match length
                    372
% identity
                    100
NCBI Description
                    (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis
                    thaliana]
Seq. No.
                    116825
Contig ID
                    253 1.R1010
5'-most EST
                    PLN g166749
Method
                    BLASTX
NCBI GI
                    g123340
BLAST score
                    2837
                    0.0e + 00
E value
Match length
                    584
% identity .
NCBI Description
                    3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 1 (HMG-COA
                    REDUCTASE 1) (HMGR1) >gi_99714_pir__A32107
                    hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) -
                    Arabidopsis thaliana >gi_16336_emb_CAA33139_ (X15032)
                    hydroxy methylglutaryl CoA reductase (AA 1-\overline{5}92)
                    [Arabidopsis thaliana] >gi_166750 (J04537) 3-hydroxy-3-methylglutaryl CoA reductase [Arabidopsis
                    thaliana] >gi 388556 (L19261) hydroxymethylglutaryl CoA
                    reductase [Arabidopsis thaliana]
                    116826
Seq. No.
                    253 2.R1010
Contig ID
                    jC-atxP53C185D15T7047d1
5'-most EST
                    BLASTX
Method
                    q123340
NCBI GI
BLAST score
                    558
                    3.0e-57
E value
Match length
                    151
% identity
                    66
                    3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 1 (HMG-COA
NCBI Description
                    REDUCTASE 1) (HMGR1) >gi_99714_pir__A32107 hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) -
                    Arabidopsis thaliana >gi_16336_emb_CAA33139_ (X15032)
                    hydroxy methylglutaryl \overline{CoA} reductase (AA 1-\overline{5}92)
                    [Arabidopsis thaliana] >gi_166750 (J04537) 3-hydroxy-3-methylglutaryl CoA reductase [Arabidopsis
                    thaliana] >gi_388556 (L19261) hydroxymethylglutaryl CoA
                    reductase [Arabidopsis thaliana]
Seq. No.
                    116827
Contig ID
                    254_1.R1010
5'-most EST
                    PLN g3901293
Method
                    BLASTX
NCBI GI
                    g3901294
BLAST score
                    4225
E value
                    0.0e + 00
```

```
90
% identity
NCBI Description
                  (AF089711) rpp8 [Arabidopsis thaliana]
                  116828
Seq. No.
                  254 2.R1010
Contig ID
5'-most EST
                  jC-atXmonuni26Dd03a1
Method
                  BLASTN
NCBI GI
                  g3241916
BLAST score
                  413
                  0.0e + 00
E value
                  450
Match length
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K15N18, complete sequence [Arabidopsis thaliana]
                  116829
Seq. No.
                  255 1.R1010
Contig ID
5'-most EST
                  LIB35-016-Q1-E1-C11
Method
                  BLASTX
                  g1488255
NCBI GI
BLAST score
                  2441
                  0.0e + 00
E value
Match length
                  520
% identity
                  92
                  (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
NCBI Description
                  >gi_2961381_emb_CAA18128_ (AL022141) ferulate-5-hydroxylase
                   (FAH1) [Arabidopsis thaliana] >gi 3925365 (AF068574)
                  ferulate-5-hydroxylase [Arabidopsis thaliana]
Seq. No.
                  116830
                  256 1.R1010
Contig ID
5'-most EST
                  LIB22-002-Q1-E1-A8
                  BLASTX
Method
NCBI GI
                  g3953601
BLAST score
                  927
E value
                  1.0e-100
Match length
                  186
% identity
                  100
NCBI Description
                  (AB008489) response regulator 6 [Arabidopsis thaliana]
Seq. No.
                  116831
                  257_1.R1010
Contig ID
5'-most EST
                  jC-atXP86CG10B3T7b1
Method
                  BLASTX
NCBI GI
                  g1352347
BLAST score
                  954
                  1.0e-103
E value
Match length
                  231
% identity
NCBI Description
                  ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)
                  >gi_480620_pir_s37103 translation elongation factor eEF-1
                  beta-Al chain - Arabidopsis thaliana (cv. Colombia)
                  >gi 398608 emb CAA52751 (X74733) elongation factor-1 beta
                  Al [Arabidopsis thaliana]
Seq. No.
                  116832
```

257 2.R1010

Contig ID

NCBI GI

```
5'-most EST
                    jC-alXLIB327436P4d03b1
 Method
                    BLASTX
 NCBI GI
                    g1352347
 BLAST score
                    492
                    2.0e-49
 E value

    Match length

                    98
 % identity
                    99
                    ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)
 NCBI Description
                    >gi_480620_pir__S37103 translation elongation factor eEF-1
                    beta-Al chain - Arabidopsis thaliana (cv. Colombia)
                    >gi 398608 emb CAA52751 (X74733) elongation factor-1 beta
                    Al [Arabidopsis thaliana]
 Seq. No.
                    116833
                    257 3.R1010
 Contig ID
 5'-most EST
                    LIB3168-060-P1-K1-H7
 Method
                    BLASTX
                    g1352347
 NCBI GI
                    93
 BLAST score
                    4.0e-35
 E value
 Match length
                    152
 % identity
                    56
                    ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)
 NCBI Description
                    >gi_480620_pir__S37103 translation elongation factor eEF-1
                    beta-A1 chain - Arabidopsis thaliana (cv. Colombia)
                    >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta
                    Al [Arabidopsis thaliana]
                    116834
 Seq. No.
 Contig ID
                    257 5.R1010
 5'-most EST
                    jC-atXP89C245E8T7064d1
 Method
                    BLASTX
                    g4406807
 NCBI GI
 BLAST score
                    499
 E value
                    2.0e-50
                    97
 Match length
                    100
 % identity
 NCBI Description
                    (AC006201) putative elongation factor beta-1 [Arabidopsis
                    thaliana]
                    116835
 Seq. No.
                    258 1.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327432P4f06b1
 Method
                    BLASTX
                    g4008006
 NCBI GI
                    2990
 BLAST score
                    0.0e+00
 E value
                    645
 Match length
 % identity
                    92
                    (AF084034) receptor-like protein kinase [Arabidopsis
 NCBI Description
                    thaliana]
                    116836
 Seq. No.
                    259 1.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327427P3c02b2
 Method
                    BLASTX
```

g4039153.

```
279
BLAST score
E value
                  2.0e-24
Match length
                  54
% identity
                  100
NCBI Description
                  (AF104221) low temperature and salt responsive protein
                  LTI6A [Arabidopsis thaliana] >gi_4325217_gb_AAD17302
                - (AF122005) hydrophobic protein [Arabidopsis thaliana]
                  116837
Seq. No.
                  259 2.R1010
Contig ID
5'-most EST
                  LIB35-034-Q1-E1-E6
Method
                  BLASTX
NCBI GI
                  q4039153
BLAST score
                  279
E value
                  1.0e-24
Match length
                  54
% identity
                  100
                  (AF104221) low temperature and salt responsive protein
NCBI Description
                  LTI6A [Arabidopsis thaliana] >gi 4325217 gb AAD17302
                   (AF122005) hydrophobic protein [Arabidopsis thaliana]
Seq. No.
                  116838
Contig ID
                  259_3.R1010
5'-most EST
                  jC-atXP100C251K2T7b1
Method
                  BLASTX
                  a4512684
NCBI GI
BLAST score
                  603
E value
                  2.0e-62
                  131
Match length
% identity
                  (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4559324 gb AAD22986.1 AC007087 5 (AC007087) unknown
                  protein [Arabidopsis thaliana]
                  116839
Seq. No.
Contig ID
                  259 5.R1010
                  jC-atXmonuni26Ae01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  a4512684
BLAST score
                  373
                  9.0e-36
E value
Match length
                  81
% identity
NCBI Description
                  (AC006931) unknown protein [Arabidopsis thaliana]
                  >gi_4559324_gb_AAD22986.1_AC007087_5 (AC007087) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  116840
                  261 1.R1010
Contig ID
5'-most EST
                  LIB25-038-Q1-E1-C2
Method
                  BLASTX
                  q464707
NCBI GI
BLAST score
                  709
E value
                  7.0e-75
                                                                  ٠, ٠,
Match length
                  152
% identity
                  91
                  40S RIBOSOMAL PROTEIN S18 >gi 480908 pir_ S37496 ribosomal
NCBI Description
```

protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana]
>gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

116841 Seq. No. Contig ID 261_2.R1010 5'-most EST jC-atXLIB327416P3c07b1 BLASTX Method g464707 NCBI GI BLAST score 709 9.0e-75 E value Match length 152 % identity 91 NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A

[Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

261 3.R1010 Contig ID jC-atXLIB327419P2d06b2 5'-most EST Method BLASTX NCBI GI g464707 BLAST score 709 E value 8.0e-75 Match length 152 % identity 91 NCBI Description

Seq. No.

116842

40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962) S18 ribosomal protein [Arabidopsis thaliana]

>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
[Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
gb_R30430 come from this gene. [Arabidopsis thaliana]
>gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
protein [Arabidopsis thaliana]

gb_R30430 come from this gene. [Arabidopsis thaliana]

>gi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal

Seq. No. 116843 Contig ID 261_7.R1010 5'-most EST jC-atXLIB327407P1h09a2 Method BLASTX NCBI GI q464707 BLAST score 194 E value 1.0e-26 Match length 78 % identity 81 NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and

 Seq. No.
 116844

 Contig ID
 262_1.R1010

 5'-most EST
 PLN_g4105632

 Method
 BLASTX

Method BLASTX
NCBI GI g4105633
BLAST score 3701
E value 0.0e+00
Match length 766
% identity 95

NCBI Description (AF048982) putative ethylene receptor [Arabidopsis

protein [Arabidopsis thaliana]

thaliana]

Seq. No. 116845 Contig ID 264_1.R1010

5'-most EST jC-alX24100Q1E1C02b1

Method BLASTX
NCBI GI g4185513
BLAST score 711
E value 5.0e-75
Match length 135
% identity 100

NCBI Description (AF102823) actin depolymerizing factor 5 [Arabidopsis thaliana] >gi 4185517 (AF102825) actin depolymerizing

factor 5 [Arabidopsis thaliana]

```
Seq. No.
                  116846
                  265 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327420P3d10b1
Method
                  BLASTX
NCBI GI
                  g4193382
BLAST score
                  391
                  9.0e-38
E value
Match length
                  86
% identity
                  86
                  (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
NCBI Description
                  >gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                  thaliana]
                  116847
Seq. No.
Contig ID
                  266 1.R1010
                  PLN g4210448
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4210449
BLAST score
                  2436
                  0.0e+00
E value
Match length
                  664
                  86
% identity
                  (AB016471) ARR1 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  116848
                  267 1.R1010
Contig ID
5'-most EST
                  ARABL1-019-Q1-B1-H9
                  BLASTX
Method
NCBI GI
                  g4234768
                  1562
BLAST score
E value
                  1.0e-174
Match length
                  281
                  100
% identity
NCBI Description
                  (AF069468) sterol-C5-desaturase [Arabidopsis thaliana]
                  116849
Seq. No.
                  268_1.R1010 ..
Contig ID
5'-most EST
                  PLN_g429154
                  BLASTX
Method
                  g729773
NCBI GI
BLAST score
                  2245
                  0.0e + 00
E value
Match length
                  483
                  90
% identity
                  HEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK
NCBI Description
                  TRANSCRIPTION FACTOR 1) (HSTF 1) >gi_429155_emb_CAA53761_
                   (X76167) heat shock factor [Arabidopsis thaliana]
                  116850
Seq. No.
Contig ID
                  269 1.R1010
5'-most EST
                  jC-atXP78C229K23T7b1
Method
                  BLASTX
NCBI GI
                  g136636
                                             1 Big 14
BLAST score
                  817
E value
                  2.0e-87
Match length
                  152
```

E value Match length

```
% identity
                   100
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                   >gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -
                   Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_
                   Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                   >qi 166924 (M62721) ubiquitin carrier protein [Arabidopsis
                   thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme
                    [Arabidopsis thaliana]
Seq. No.
                   116851
                   269 2.R1010
Contig ID
                   jC-atXLIB327425P3c04b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g136636
BLAST score
                   657
E value
                   9.0e-69
Match length
                   145
% identity
NCBI Description
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                   LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                   >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -
                   Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin
                   Conjugating Enzyme (E.C.\overline{6}.3.2.\overline{19}) >\overline{gi} 29\overline{8}1894 pdb 2AAK
                   Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                   >gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis
                   thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme
                    [Arabidopsis thaliana]
                   116852
Seq. No.
Contig ID
                   269_3.R1010
5'-most EST
                   q1217090
                   BLASTX
Method
                   q136636
NCBI GI
BLAST score
                   232
                    4.0e-19
E value
Match length
                   80
% identity
                   70
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                   >qi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -
                   Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin
                   Conjugating Enzyme (E.C.\overline{6}.3.2.\overline{19}) >\overline{g}i 29\overline{8}1894 pdb 2AAK
                   Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                   >gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis
                   thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme
                    [Arabidopsis thaliana]
Seq. No.
                   116853
                   270 1.R1010
Contig ID
5'-most EST
                   LIB25-014-Q1-E1-B1
Method
                   BLASTX
NCBI GI · ·
                   g1174844
BLAST score
                   743
```

1.0e-78

152

```
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 2) (UBIQUITIN CARRIER PROTEIN 2)
                  >qi 1076426 pir S43783 ubiquitin-conjugating enzyme UBC2 -
                  Arabidopsis thaliana >gi_431264 (L19353) ubiquitin
                  conjugating enzyme [Arabidopsis thaliana]
                  >gi_2689243_emb_CAA73476_ (Y13031) ubiquitin conjugating
                  enzyme [Arabidopsis thaliana] >gi_2947065 (AC002521)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  116854
Seq. No.
Contig ID
                  271 1.R1010
5'-most EST
                  g1159674
Method
                  BLASTX
                  g1076429
NCBI GI
BLAST score
                  580
E value
                  7.0e-60
Match length
                  132.
                  86
% identity
                  ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis
NCBI Description
                  thaliana >gi_807095_bbs_158369 UBC6=E2-related
                  ubiquitin-conjugating protein [Arabidopsis thaliana,
                  Peptide, 183 aa] >gi_3702350 (AC005397) ubiquitin-protein
                  ligase [Arabidopsis thaliana]
                  116855
Seq. No.
Contig ID
                  271 2.R1010
5'-most EST
                  LIB24-026-Q1-E1-B7
Method
                  BLASTX
NCBI GI
                  q1174851
BLAST score
                  618
                  3.0e-64
E value
Match length
                  141
% identity
                  84
                  UBIQUITIN-CONJUGATING ENZYME E2-21 KD 3 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 6) (UBIQUITIN CARRIER PROTEIN 6)
                  116856
Seq. No.
                  272 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327408P4c08b1
Method
                  BLASTX
NCBI GI
                  q1076427
BLAST score
                  634
E value
                  9.0e-68
Match length
                  133
% identity
                  ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis
NCBI Description
                  thaliana
Seq. No.
                  116857
Contig ID
                  272 2.R1010
5'-most EST
                  g2722570
Method
                  BLASTX
                  g1174850
NCBI GI
BLAST score
                  594
E value
                  2.0e-61
Match length
                  151
```

```
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)
                  116858
Seq. No.
Contig ID
                  273 1.R1010
                  LIB3168-044-P1-K1-E11
5'-most EST
Method
                  BLASTX
                  q4325282
NCBI GI
BLAST score
                  1265
                  1.0e-139
E value
Match length
                  320
% identity
                  76
                  (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                  >gi 4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                  [Arabidopsis thaliana]
                  116859
Seq. No.
Contig ID
                  273 2.R1010
                  jC-atXLIB327427P2h07a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q729470
BLAST score
                  1552
E value
                  1.0e-173
Match length
                  359
% identity
                  82
                  MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
NCBI Description
                  (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi 542089 pir JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
                   (Z21493) mitochondrial formate dehydrogenase precursor
                  [Solanum tuberosum]
                  116860
Seq. No.
Contig ID
                  273 4.R1010
5'-most EST
                  g906442
Method
                  BLASTX
NCBI GI
                  g729470
BLAST score
                  231
                  5.0e-19
E value
Match length
                  70
% identity
                  70
                  MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
NCBI Description
                  (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
                   (Z21493) mitochondrial formate dehydrogenase precursor
                  [Solanum tuberosum]
Seq. No.
                  116861
                  276 1.R1010
Contig ID
                  LIB3177-046-P1-K2-H9
5'-most EST
                  BLASTX .
Method
                  q1173218 ···
NCBI GI
BLAST score
                  667
                  6.0e-70
E value
```

Match length

```
% identity
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  116862
Seq. No.
                  276 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327421P1d11b1
                  BLASTX
Method
NCBI GI
                  g1173218
BLAST score
                  667
E value
                  7.0e-70
                  130
Match length
                  100
% identity
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  116863
Seq. No.
                  276 3.R1010
Contig ID
                  jC-atXLIB327437P4d04a2
5'-most EST
                  BLASTX
Method.
                  g1173218
NCBI GI
BLAST score
                  153
                  2.0e-39
E value
Match length
                  105
                  71
% identity
                  40S RIBOSOMAL PROTEIN S15A >qi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  116864
Seq. No.
                  276 5.R1010
Contig ID
                  LIB3176-025-P1-K1-H2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1173218
                  92
BLAST score
E value
                  1.0e-16
Match length
                  100
% identity
                  61
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  116865
Seq. No.
                  277_1.R1010
Contig ID
                  PLN_g16420
5'-most EST
Method
                  BLASTX
                  q404670
NCBI GI
BLAST score
                   5601
E value
                  0.0e + 00
                  1120
Match length
% identity
                  (L21154) phytochrome A [Arabidopsis thaliana] >gi_3482934
NCBI Description
                   (AC003970) phytochrome A [Arabidopsis thaliana]
```

Seq. No.

```
Contig ID
                  277 5.R1010
                   jC-atXP102CE2H12T7027d1
5'-most EST
                   BLASTX
Method
                   q404670
NCBI GI
                   497
BLAST score
E value
                   4.0e-50
Match length
                   101
% identity
                  100
NCBI Description
                   (L21154) phytochrome A [Arabidopsis thaliana] >gi_3482934
                   (AC003970) phytochrome A [Arabidopsis thaliana]
                  116867
Seq. No.
                   278 1.R1010
Contig ID
                  LIB3176-086-P1-K1-H9
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4454567
BLAST score
                   3253
E value
                  0.0e + 00
                   623
Match length
                  100
% identity
                   (AF128407) EDS1 [Arabidopsis thaliana]
NCBI Description
                  116868
Seq. No.
Contig ID
                   279 1.R1010
5'-most EST
                   jC-atXLIB327428P1a06b2
Method
                  BLASTX
                  g1170373
NCBI GI
BLAST score
                   3175
E value
                  0.0e + 00
                  651
Match length
                  96
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__$46302
NCBI Description
                  heat shock cognate protein 70-1 - Arabidopsis thaliana
                  >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70
                  cognate [Arabidopsis thaliana]
                  116869
Seq. No.
                   279 2.R1010
Contig ID
5'-most EST
                   jC-atXP89CG6B8T7029d1
Method
                  BLASTX
                  g1703723
NCBI GI
BLAST score
                  2379
                  0.0e + 00
E value
                  498
Match length
                  95
% identity
                  ATP SYNTHASE BETA CHAIN >gi 733448 (U23082) CF1 ATP
NCBI Description
                  synthase 'beta subunit [Spinacia oleracea]
                  116870
Seq. No.
                  279 3.R1010
Contig ID
5'-most EST
                  LIB3176-065-P1-K1-F3
                  BLASTX
Method
                  g1170373
NCBI GI
BLAST score
                  390
E value
                  1.0e-121
Match length
                  264
                  88
% identity
```

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NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No. 116871 Contig ID 279 6.R1010

5'-most EST jC-atXP74C225C23T7093d1

Method BLASTN
NCBI GI g4589414
BLAST score 668
E value 0.0e+00
Match length 707
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14B15, complete sequence

Seq. No. 116872 Contig ID 279_9.R1010

5'-most EST jC-atXP100C269G2T7b1

Method BLASTX
NCBI GI 9450880
BLAST score 555
E value 8.0e-57
Match length 123
% identity 89

NCBI Description (X77199) heat shock cognate 70-1 [Arabidopsis thaliana]

 Seq. No.
 116873

 Contig ID
 279_10.R1010

 5'-most EST
 g931290

 Method
 BLASTX

 NCBI GI
 g1170373

 BLAST score
 550

 E value
 2.0e-56

 Match length
 159

Match length 159 % identity 77

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302

heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70

cognate [Arabidopsis thaliana]

116874 Seq. No. 279 11.R1010 Contig ID 5'-most EST g2748784 Method BLASTX q1170373 NCBI GI BLAST score 122 E value 9.0e-32 Match length 92

84

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir __S46302

heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70

cognate [Arabidopsis thaliana]

Seq. No. 116875

% identity

```
279 12.R1010
Contig ID
                  jC-atXLIB327431P4c06a1
5'-most EST
Method
                  BLASTN
                  g2114077
NCBI GI
BLAST score
                  191
E value
                  1.0e-103
Match length
                  451
% identity
                  95
NCBI Description
                  Arabidopsis thaliana DNA for larger subunit of Rubisco,
                  beta subunit of coupling factor one, partial cds
Seq. No.
                  116876
                  279 15.R1010
Contig ID
5'-most EST
                  q2748794
Method
                  BLASTX
NCBI GI
                  g450880
BLAST score
                  75
                  1.3e+00
E value
Match length
                  81
                  47
% identity
NCBI Description
                  (X77199) heat shock cognate 70-1 [Arabidopsis thaliana]
                  116877
Seq. No.
                  279 16.R1010
Contig ID
                  LIB3234-041-P1-K1-G2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3850914
BLAST score
                  773
                  3.0e-82
E value
Match length
                  200
                  79
% identity
NCBI Description
                  (AF060397) ATP synthase beta subunit [Stirlingia latifolia]
                  116878
Seq. No.
Contig ID
                  279 19.R1010
5'-most EST
                  LIB25-104-Q1-E1-B3
Method
                  BLASTX
NCBI GI
                  q2655420
BLAST score
                  556
E value
                  3.0e-57
Match length
                  114
% identity
                  92
NCBI Description
                  (AF035414) heat shock cognate protein HSC70 [Brassica
                  napus]
Seq. No.
                  116879
Contig ID
                  279 20.R1010
                  LIB23-071-Q1-E1-F9
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2114077
BLAST score
                  228
E value
                  1.0e-125
Match length
                  414
% identity
                  90
                  Arabidopsis thaliana DNA for larger subunit of Rubisco,
NCBI Description
                  beta subunit of coupling factor one, partial cds
```

```
116880
Seq. No.
                  279 22.R1010
Contig ID
                  jC-atXP101CE2D1T7031d1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g114591
BLAST score
                   437
                   4.0e-43
E value
Match length
                  114
                  81
% identity
                  ATP SYNTHASE EPSILON CHAIN >gi_81663_pir__S01903
NCBI Description
                  H+-transporting ATP synthase (\overline{EC} 3.6.1.34) epsilon chain -
                  Arabidopsis thaliana chloroplast >gi_11334_emb_CAA31381
                   (X12889) Cfl ATPase epsilon subunit (AA 1 - 132)
                   [Arabidopsis thaliana]
                  116881
Seq. No.
                  279 24.R1010
Contig ID
5'-most EST
                  jC-atXLIB327426P2g08a1
Method ·
                  BLASTN
NCBI GI
                  g4063545
BLAST score
                  45
                  5.0e-16
E value
                  94
Match length
                  85
% identity
NCBI Description
                  Francoa appendiculata ATP synthase beta subunit (atpB)
                  gene, chloroplast gene encoding chloroplast protein,
                  partial cds
                  116882
Seq. No.
                  279 29.R1010
Contig ID
5'-most EST
                  jC-atXLIB327401P2a12a1
Method
                  BLASTX
NCBI GI
                  g2347208
BLAST score
                  280
                  8.0e-25
E value
                  108
Match length
                  45
% identity
                  (AC002338) APG protein isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  116883
Contig ID
                  280 1.R1010
5'-most EST
                  PLN g4521162
Method
                  BLASTX
NCBI GI
                  g3860275
BLAST score
                  930
E value
                  1.0e-101
Match length
                  175
% identity
NCBI Description
                   (AC005824) putative GTP-binding protein [Arabidopsis
                  thaliana] >gi_4314395_gb_AAD15605_ (AC006232) putative
                  terminal flower 1 (TFL1) [Arabidopsis thaliana]
                  >gi 4521159 dbj BAA75933.1 (AB024712) ATC [Arabidopsis
                  thaliana] >gi 4521161 dbj BAA75931.1 (AB024714) ATC
                  [Arabidopsis thaliana] >gi 4521163 dbj BAA75932.1
                   (AB024715) ATC [Arabidopsis thaliana]
```

Seq. No. 116884

E value

```
281 1.R1010
Contig ID
5'-most EST
                  LIB3175-004-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g2760833
BLAST score
                  1416
E value
                  1.0e-164
Match length
                  298
                  99
% identity
                  (AC003105) unknown protein [Arabidopsis thaliana]
NCBI Description
                  116885
Seq. No.
Contig ID
                  284 1.R1010
                  jC-atXLIB327438P1b05a1
5'-most EST
                  BLASTX
Method
                  a1170028
NCBI GI
                  2291
BLAST score
E value
                  0.0e + 00
                  474
Match length
% identity .
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA
NCBI Description
                  1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1)
                  >gi 454357 (U03773)
                  glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis
                  thaliana]
                  116886
Seq. No.
                  287 1.R1010
Contig ID
5'-most EST
                  jC-alX25049Q1E1C09b1
Method
                  BLASTX
NCBI GI
                  g629511
BLAST score
                  322
                  6.0e-50
E value
Match length
                  130
% identity
NCBI Description
                  cold-regulated protein corl5b precursor - Arabidopsis
                  thaliana >gi_4559338_gb_AAD23000.1_AC007087_19 (AC007087)
                  cold-regulated protein cor15b precursor [Arabidopsis
                  thaliana]
                  116887
Seq. No.
                  288 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327431P4g02a1
Method
                  BLASTN
                  q457715
NCBI GI
BLAST score
                  418
                  0.0e + 00
E value
Match length
                  496
% identity
                  100
NCBI Description A.thaliana CXc750 gene
Seq. No.
                  116888
                  289 1.R1010
Contig ID
                  LIB3176-037-P1-K1-G11
5'-most EST
Method
                  BLASTX
                  q730688
NCBI GI
                  1056
BLAST score
```

1.0e-115

```
Match length
                   203
% identity
                   100
NCBI Description
                   MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S19 PRECURSOR
                   >gi_2129722_pir__S71114 ribosomal protein S19 precursor, mitochondrial - Arabidopsis thaliana
                   >gi_457760_emb_CAA54951_ (X77989) ribosomal protein S19
                   [Arabidopsis thaliana] >gi_459422 emb_CAA54965 (X78035)
                   mitochondrial ribosomal protein S19, nuclear encoded
                    [Arabidopsis thaliana]
Seq. No.
                   116889
Contig ID
                   290 1.R1010
                   jC-atXLIB327409P1d11b1
5'-most EST
Method
                   BLASTX
                   a464662
NCBI GI
                   1158
BLAST score
E value
                   1.0e-127
Match length
                   325
% identity
                   74
                   CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING
NCBI Description
                   PROTEIN RNP-T) (RNA-BINDING PROTEIN 1)
>gi_282884_pir__S28057 RNA-binding protein RNP-T -
                   Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255)
                   RNA-binding protein [Arabidopsis thaliana] >gi_387569
                    (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana]
                   >gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis
                   thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding
                   protein RNP-T precursor [Arabidopsis thaliana]
                   >gi 737169 prf 1921382A RNA-binding protein [Arabidopsis
                   thaliana]
                   116890
Seq. No.
Contig ID
                   290_3.R1010
                   jC-\overline{a}tXLIB327414P2e07a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q464662
BLAST score
                   299
                   9.0e-27
E value
Match length
                   194
                   42
% identity
                   CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING
NCBI Description
                   PROTEIN RNP-T) (RNA-BINDING PROTEIN 1) >gi_282884_pir__S28057 RNA-binding protein RNP-T -
                   Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255)
                   RNA-binding protein [Arabidopsis thaliana] >gi 387569
                    (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana]
                   >gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis
                   thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding
                   protein RNP-T precursor [Arabidopsis thaliana]
```

116891 Seq. No. 290 5.R1010 Contig ID: 5'-most EST jC-atXLIB327410P3a07b1

thalianal

Method BLASTX

NCBI GI q464662

>gi_737169_prf__1921382A RNA-binding protein [Arabidopsis

```
BLAST score
                  468
E value
                  1.0e-46
Match length
                  193
% identity
                  44
                  CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING
NCBI Description
                  PROTEIN RNP-T) (RNA-BINDING PROTEIN 1)
                  >gi 282884 pir S28057 RNA-binding protein RNP-T -
                  Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255)
                  RNA-binding protein [Arabidopsis thaliana] >gi_387569
                   (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana]
                  >gi 475718 (U08467) RNA-binding protein 1 [Arabidopsis
                  thaliana] >gi_4220513emb_CAA22986_ (AL035356) RNA-binding
                  protein RNP-T precursor [Arabidopsis thaliana]
                  >gi 737169 prf 1921382A RNA-binding protein [Arabidopsis
                  thaliana]
                  116892
Seq. No.
                  291 1.R1010
Contig ID
5'-most EST
                  PLN_g166716
Method
                  BLASTX
NCBI GI
                  g1076393
BLAST score
                  1276
                  1.0e-141
E value
Match length
                  255
                  100
% identity
NCBI Description
                  RCI14A protein - Arabidopsis thaliana
                  >gi 540559 emb CAA52237 (X74140) RCI14A [Arabidopsis
                  thaliana]
                  116893
Seq. No.
                  295 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327408P4g07b1
Method
                  BLASTX
NCBI GI
                  g2492860
BLAST score
                  2233
                  0.0e + 00
E value
Match length
                  472
% identity
                  93
NCBI Description
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 2 PRECURSOR (GSA
                  2) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 2) (GSA-AT 2)
                  >gi 498914 (U10278) glutamate-1-semialdehyde
                  aminotransferase [Arabidopsis thaliana]
                  116894
Seq. No.
Contig ID
                  298 1.R1010
                  jC-\overline{a}tXLIB327410P3c08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g499301
BLAST score
                  1960
E value
                  0.0e+00
Match length
                  421
                  91
% identity
NCBI Description
                  (X77116) ABI1 [Arabidopsis thaliana] >gi 549981 (U12856)
                  abscisic acid insensitive protein [Arabidopsis thaliana]
```

ABII [Arabidopsis thaliana]

>gi 4538937 emb CAB39673.1 (AL049483) protein phosphatase

```
Seq. No.
                  116895
                  299 1.R1010
Contig ID
                  PLN g2289779
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1208408
BLAST score
                  2968
E value
                  0.0e + 00
Match length
                  568
% identity
                  100
NCBI Description
                   (D14824) nitrite reductase [Arabidopsis thaliana]
                  >gi_2289780_dbj_BAA21672_ (AB006032) nitrite reductase
                   [Arabidopsis thaliana] >gi_4335728_gb_AAD17406_ (AC006248)
                  nitrate reductase [Arabidopsis thaliana]
                  116896
Seq. No.
                  300 1.R1010
Contig ID
5'-most EST
                  PLN g514317
                  BLASTX
Method
NCBI GI
                  g2129726
BLAST score
                  336
                  1.0e-165
E value
Match length
                  320
% identity
                  RNA polymerase II third largest chain RPB35.5A -
NCBI Description
                  Arabidopsis thaliana >gi_514318 (L34770) RNA polymerase II
                  third largest subunit [Arabidopsis thaliana]
                  >gi_4544370_gb_AAD22281.1_AC006920_5 (AC006920) RNA
                  polymerase II, third largest subunit [Arabidopsis thaliana]
Seq. No.
                  116897
                  302_1.R1010
Contig ID
5'-most EST
                  PLN_g474889
Method
                  BLASTX
                  q1174740
NCBI GI
BLAST score
                  6377
E value
                  0.0e + 00
Match length
                  1450
% identity
                  88
NCBI Description
                  DNA TOPOISOMERASE II >gi_2129576_pir__S53599 DNA
                  topoisomerase II - Arabidopsis thaliana >gi 474890 (L21015)
                  topoisomerase II [Arabidopsis thaliana]
                  116898
Seq. No.
Contig ID
                  304_1.R1010
                  PLN_g527620
5'-most EST
                  BLASTX
Method
                  g1170168
NCBI GI
BLAST score
                  1294
E value
                  1.0e-143
Match length
                  282
% identity
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT1 (HD-ZIP PROTEIN 1)
NCBI Description
                  >gi_549883 (U09332) homeobox protein [Arabidopsis thaliana]
                  >gi_549884 (U09333) homeobox protein [Arabidopsis thaliana]
```

[Arabidopsis thaliana]

>gi_2245105_emb_CAB10527_ (Z97343) unnamed protein product

NCBI GI

```
Seq. No.
                  116899
Contig ID
                  305 1.R1010
                  jC-atXLIB327411P1h02b1
5'-most EST
Method
                  BLASTX
                  g1170409
NCBI GI
BLAST score
                  1293
E value
                  1.0e-143
Match length
                  278
% identity
                  90
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22)
NCBI Description
                  >gi_549887 (U09336) homeobox protein [Arabidopsis thaliana]
                  >gi_549888 (U09337) homeobox protein [Arabidopsis thaliana]
                  >gi 4490724 emb CAB38927.1 (AL035709) homeobox protein
                  HAT22 [Arabidopsis thaliana]
                  116900
Seq. No.
                  306 1.R1010
Contig ID
5'-most EST
                  g1216827
                  BLASTX
Method
NCBI GI
                  g1170170
BLAST score
                  1009
                  1.0e-109
E value
Match length .
                  315
% identity
                  66
NCBI Description
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT3 (HD-ZIP PROTEIN 3)
                  >gi 549889 (U09338) homeobox protein [Arabidopsis thaliana]
                  >gi 549890 (U09339) homeobox protein [Arabidopsis thaliana]
                  116901
Seq. No.
                  307 1.R1010
Contig ID
                  LIB22-027-Q1-E1-G7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1170172
BLAST score
                  1160
E value
                  1.0e-127
                  274
Match length
                  84
% identity
                  HOMEOBOX-LEUCINE ZIPPER -PROTEIN HAT9 (HD-ZIP PROTEIN 9)
NCBI Description
                  >gi 549892 (U09341) homeobox protein [Arabidopsis thaliana]
                  116902
Seq. No.
                  308 1.R1010
Contig ID
                  jC-\overline{a}tXP31C144I9T7d2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1172816
                  865
BLAST score
                  4.0e-93
E value
                  182
Match length
% identity
                  93
NCBI Description
                  60S RIBOSOMAL PROTEIN L11A (L16A) >gi 624938 emb CAA57395
                  (X81799) ribosomal protein L16 [Arabidopsis thaliana]
                  116903
Seq. No.
                  308 2.R1010
Contig ID
                  jC-atXP122C117K4T7075a1
5'-most EST
Method
                  BLASTX
```

g1172817

NCBI Description

```
BLAST score
                  444
E value
                  9.0e-44
Match length
                  96
                  88
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L11B (L16B) >gi 550547 emb CAA57396
                  (X81800) ribosomal protein L16 [Arabidopsis thaliana]
                  >gi 4539392_emb_CAB37458.1_ (AL035526) ribosomal protein
                  L11, cytosolic [Arabidopsis thaliana]
                  116904
Seq. No.
                  308 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327426P1d08b1
Method
                  BLASTX
NCBI GI
                  q1172816
BLAST score
                  649
                  6.0e-68
E value
                  129
Match length
                  98
% identity
                  60S RIBOSOMAL PROTEIN L11A (L16A) >gi 624938 emb CAA57395 (m)
NCBI Description
                  (X81799) ribosomal protein L16 [Arabidopsis thaliana]
                  116905
Seq. No.
                  308 6.R1010
Contig ID
5'-most EST
                  LIB24-078-Q1-E1-G3
                  BLASTX
Method
NCBI GI
                  g1172817
                  242
BLAST score
                  7.0e-45
E value
                  107
Match length
% identity
                  86
                  60S RIBOSOMAL PROTEIN L11B (L16B) >qi 550547 emb CAA57396
NCBI Description
                  (X81800) ribosomal protein L16 [Arabidopsis thaliana]
                  >gi 4539392 emb_CAB37458.1_ (AL035526) ribosomal protein
                  L11, cytosolic [Arabidopsis thaliana]
                  116906
Seq. No.
                  308 7.R1010
Contig ID
5'-most EST
                  LIB3234-086-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g1172816
BLAST score
                  175
                  1.0e-12
E value
                  96
Match length
                  50
% identity
                  60S RIBOSOMAL PROTEIN L11A (L16A) >gi 624938 emb CAA57395_
NCBI Description
                  (X81799) ribosomal protein L16 [Arabidopsis thaliana]
                  116907
Seq. No.
                  309 1.R1010
Contig ID
5'-most EST
                  LIB24-133-Q1-E1-C7
Method
                  BLASTX
NCBI GI
                  g1172874
BLAST score
                  1732
                  0.0e + 00
E value
                  392
Match length
                  86
% identity
```

DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

```
>gi_479589_pir__S34823 dehydration-induced protein RD22 -
Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
[Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene
[Arabidopsis thaliana]
116908
309 2 R1010
```

Seq.- No. 116908 Contig ID 309_2.R1010

5'-most EST LIB3175-003-P1-K1-B4

Method BLASTN
NCBI GI g560770
BLAST score 274
E value 1.0e-152
Match length 469
% identity 96

NCBI Description Arabidopsis thaliana rd22 gene, complete cds

116909 Seq. No. 311 1.R1010 Contig ID 5'-most EST PLN_g16424 BLASTX Method NCBI GI g130192 BLAST score 5559 E value 0.0e + 00Match length 1086 100

% identity 100
NCBI Description PHYTOCHROME C >gi_65880_pir__FKMUC phytochrome C -

Arabidopsis thaliana >gi 16425 emb CAA35223 (X17343) phyC

photoreceptor [Arabidopsis thaliana]

Seq. No. 116910 Contig ID 312_1.R1010

5'-most EST LIB35-052-Q1-E1-E4

Method BLASTX
NCBI GI g1183004
BLAST score 696
E value 4.0e-73
Match length 333
% identity 54

NCBI Description (D45848) calmodulin-related protein [Arabidopsis thaliana]

>gi 3402707 (AC004261) calmodulin-related protein

[Arabidopsis thaliana]

Seq. No. 116911 Contig ID 313_1.R1010

5'-most EST jC-alXLIB327435P2d03b1

Method BLASTX
NCBI GI g1168728
BLAST score 1773
E value 0.0e+00
Match length 360
% identity 94

NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883)

cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 116912
Contig ID 316_1.R1010

5'-most EST jC-atXLIB327424P1a01b2

BLAST score

```
Method
                    BLASTX
NCBI GI
                    q1172816
                    865
BLAST score
                    5.0e-93
E value
                    182
Match length
% identity
                    60S RIBOSOMAL PROTEIN L11A (L16A) >gi_624938_emb_CAA57395
NCBI Description
                     (X81799) ribosomal protein L16 [Arabidopsis thaliana]
                    116913
Seq. No.
Contig ID
                    318 1.R1010
                    LIB22-027-Q1-E1-A5
5'-most EST
Method
                    BLASTX
                    a2129531
NCBI GI
                    1451
BLAST score
                    1.0e-161
E value
Match length
                    486
% identity
                    acyl-(acyl carrier protein) thioesterase (clone TE 3-2) -
NCBI Description
                    Arabidopsis thaliana
                    116914
Seq. No.
Contig ID
                     318_2.R1010
                    PLN_g804947
5'-most EST
Method
                    BLASTX
                    g1076360
NCBI GI
BLAST score
                     2102
                     0.0e + 00
E value
Match length
                     412
% identity
                    oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) -
NCBI Description
                    Arabidopsis thaliana >gi_2129530_pir__S69195 acyl-(acyl carrier protein) thioesterase (clone TE 1-1) - Arabidopsis
                     thaliana >gi 634003_emb CAA85387_ (Z36910) acyl-(acyl
                    carrier protein) thioesterase [Arabidopsis thaliana]
                     116915
Seq. No.
                     318 3.R1010
Contig ID
                     jC-atXP86CG4H5T7d2
 5'-most EST
Method
                     BLASTX
                     g1076360
NCBI GI
                     698
BLAST score
                     2.0e-73
E value
                     212
Match length
 % identity
                     oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) -
NCBI Description
                     Arabidopsis thaliana >gi_2129530_pir__S69195 acyl-(acyl carrier protein) thioesterase (clone TE 1-1) - Arabidopsis
                     thaliana >gi_634003_emb_CAA85387_ (Z36910) acyl-(acyl
                     carrier protein) thioesterase [Arabidopsis thaliana]
                     116916
 Seq. No.
                     320 1.R1010
 Contig ID
                     iC-atXP94CG11D5T7b1
 5'-most EST
Method
                     BLASTX
                     q681904
 NCBI GI
                     1199
```

```
E value
                   1.0e-132
                   324 -
Match length
                   76
% identity
                   (D31711) cp29 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   116917
                   320 2.R1010
Contig ID
5'-most EST
                   g27\overline{4}9501
Method
                   BLASTN
                   g681901
NCBI GI
BLAST score
                   392
E value
                   0.0e + 00
Match length
                   587
                   97
% identity
                  Arabidopsis thaliana gene for chloroplast RNA-binding
NCBI Description
                   protein cp29, complete cds (exon1, exon2, exon3, exon4)
                   116918
Seq. No.
                   320 5.R1010
Contig ID
5'-most EST
                   jC-atXLIB327414P4d05a2
Method
                   BLASTX
NCBI GI
                   g107.6303
BLAST score
                   240
E value
                  8.0e-30
Match length
                   112
% identity
                   71
                   RNA-binding protein cp29 precursor - Arabidopsis thaliana
NCBI Description
                   >gi 681902 dbj BAA06518 (D31710) cp29 [Arabidopsis
                   thaliana]
                   116919
Seq. No.
                   320 6.R1010
Contig ID
5'-most EST
                   g937356
Method
                   BLASTX
NCBI GI
                   g1076303
BLAST score
                   200
E value
                   3.0e-15
                  146
Match length
% identity
                   42
NCBI Description
                  RNA-binding protein cp29 precursor - Arabidopsis thaliana
                   >gi 681902 dbj BAA06518 (D31710) cp29 [Arabidopsis
                   thaliana]
                   116920
Seq. No.
                   320_7.R1010
Contig ID
                   jC-\overline{a}tXLIB327415P4d10b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1076303
BLAST score
                   414
E value
                   2.0e-40
Match length
                   106
% identity
                   57
NCBI Description
                  RNA-binding protein cp29 precursor - Arabidopsis thaliana
                   >gi 681902 dbj BAA06518 (D31710) cp29 [Arabidopsis
                   thaliana]
```

Seq. No.

Method

BLASTX

```
320 8.R1010
Contig ID
                  LIB23-035-Q1-E112-F3
5'-most EST.
                  BLASTX
Method
                  q1076303
NCBI GI
BLAST score
                  148
                  2.0e-31
E value
                  76
Match length
                  50
% identity
NCBI Description
                  RNA-binding protein cp29 precursor - Arabidopsis thaliana
                  >gi 681902 dbj BAA06518 (D31710) cp29 [Arabidopsis
                  thalianal
                  116922
Seq. No.
                   320 9.R1010
Contig ID
5'-most EST
                  LIB3176-060-P1-K1-G1
Method
                  BLASTX
                  g1076303
NCBI GI
BLAST score
                  283
E value
                   4.0e-53
Match length
                   133
                  59
% identity
NCBI Description
                  RNA-binding protein cp29 precursor - Arabidopsis thaliana
                  >gi_681902_dbj_BAA06518_ (D31710) cp29 [Arabidopsis
                  thaliana] ...
                   116923
Seq. No.
                   322 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327408P2b01b1
                  BLASTX
Method
NCBI GI
                   q1076308
BLAST score
                   1283
                   1.0e-142
E value
Match length
                   306
% identity
NCBI Description
                  RNA-binding protein cp33 precursor - Arabidopsis thaliana
                  >qi 681910 dbj BAA06522 (D31714) cp33 [Arabidopsis
                   thaliana]
Seq. No.
                   116924
                   323 1.R1010
Contig ID
5'-most EST
                  LIB3176-005-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   q132677
BLAST score
                   1166
E value
                   1.0e-128
Match length
                   258
                   90
% identity
NCBI Description
                  50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15)
                  >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor,
                  chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_
                   (Z11508) Plastid ribosomal protein CL15 [Arabidopsis
                   thalianal
                   116925
Seq. No.
Contig ID
                   324 1.R1010
5'-most EST
                  PLN_g735917
```

NCBI GI

BLAST score

q1703446

1568

```
1.0e-175
E value
Match length
                  315
                  97
% identity
NCBI Description
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
                  >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana
                      735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis
Seq. No.
                  116926
                  325 1.R1010
Contig ID
                  LIB3168-051-P1-K1-B12
5'-most EST
                  BLASTX
Method
                  q1170317
NCBI GI
                  2870
BLAST score
E value
                  0.0e + 00
                  562
Match length
% identity
                  3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 2 (HMG-COA
NCBI Description
                  REDUCTASE 2) (HMGR2) >gi_388558 (L19262)
                  3-hydroxy-3-methylglutaryl-CoA reductase [Arabidopsis
                  thaliana] >gi_2262168 (AC002329)
                  3-hydroxy-3-methylglutaryl-CoA reductase (HMG2 protein)
                  [Arabidopsis thaliana]
                  116927
Seq. No.
                  326 1.R1010
Contig ID
                  jC-atXLIB327420P4g05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q121075
                  696
BLAST score
E value
                  3.0e-73
Match length
                  166
% identity
                  83
NCBI Description
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi 166725
                  (M82921) H-Protein precursor [Arabidopsis thaliana]
                  >gi 861215 (U27144) glycine decarboxylase complex H-protein
                  precursor [Arabidopsis thaliana] >gi_3608151 (AC005314)
                  glycine decarboxylase complex H-protein [Arabidopsis
                  thaliana] >gi_445119_prf__1908425A Gly
                  decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
                  116928
Seq. No.
                  326 2.R1010
Contig ID
                  LIB24-062-Q1-E1-A1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g121075
BLAST score
                  445
E value
                  5.0e-44
Match length
                  149
% identity
                  72
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >qi 166725
NCBI Description
                  (M82921) H-Protein precursor [Arabidopsis thaliana]
                  >gi 861215 (U27144) glycine decarboxylase complex H-protein
                  precursor [Arabidopsis thaliana] >gi_3608151 (AC005314)
                  glycine decarboxylase complex H-protein [Arabidopsis
```

5.

```
thaliana] >gi_445119_prf__1908425A Gly decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
```

```
Seq. No.
                  116929
                  326 3.R1010 °
Contig ID
5'-most EST
                  LIB25-041-Q1-E1-C4
Method
                  BLASTX
NCBI GI
                  q121075
BLAST score
                  747
E value
                  2.0e-79
Match length
                  165
% identity
                  89
NCBI Description
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi 166725
                  (M82921) H-Protein precursor [Arabidopsis thaliana]
                  >gi 861215 (U27144) glycine decarboxylase complex H-protein
                  precursor [Arabidopsis thaliana] >gi_3608151 (AC005314)
                  glycine decarboxylase complex H-protein [Arabidopsis
                  thaliana] >gi 445119 prf 1908425A Gly
                  decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
                  116930
Seq. No.
                  326 5.R1010
Contig ID
5'-most EST
                  LIB3177-087-P1-K1-C2
                  BLASTX
Method
                  g121075
NCBI GI
BLAST score
                  458
E value
                  1.0e-45
Match length
                  141
% identity
                  73
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi 166725
NCBI Description
                  (M82921) H-Protein precursor [Arabidopsis thaliana]
                  >gi 861215 (U27144) glycine decarboxylase complex H-protein
                  precursor [Arabidopsis thaliana] >gi_3608151 (AC005314)
                  glycine decarboxylase complex H-protein [Arabidopsis
                  thaliana] >gi_445119_prf__1908425A Gly
                  decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
                  116931
Seq. No.
Contig ID
                  328 1.R1010
                  LIB25-081-Q1-E1-B10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g886116
BLAST score
                  1531
E value
                  1.0e-171
Match length
                  284
                  100
% identity
NCBI Description
                  (U27609) TCH4 protein [Arabidopsis thaliana] >gi 2952473
                  (AF051338) xyloglucan endotransglycosylase related protein
                  [Arabidopsis thaliana]
Seq. No.
                  116932
                  329_1.R1010
Contig ID
5'-most EST
                  LIB25-059-Q1-E1-F10
Method
                  BLASTN
NCBI GI
                  q3702731
BLAST score
                  423
```

0.0e + 00

E value

```
Match length
                  846
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFC19, complete sequence [Arabidopsis thaliana]
                  116933
Seq. No.
Contig ID
                  330 1.R1010
5'-most EST
                  LIB23-067-Q1-E1-E1
Method
                  BLASTX
                  g1708463
NCBI GI
BLAST score
                  2017
                  0.0e + 00
E value
Match length
                  431
% identity
                  91
                  IAA-AMINO ACID HYDROLASE >gi 887785 (U23794) ILR1
NCBI Description
                  [Arabidopsis thaliana]
                  116934
Seq. No.
Contig ID
                  331 1.R1010
5'-most EST
                  LIB24-101-Q1-E1-C1
                  BLASTX
Method
                  g1170121
NCBI GI
                  1165
BLAST score
                  1.0e-128
E value
Match length
                  224
                  100
% identity
                  GLUTATHIONE S-TRANSFERASE 103-1A >gi 2129602 pir S66354
NCBI Description
                  glutathione transferase (EC 2.5.1.18), auxin-inducible -
                  Arabidopsis thaliana >gi_895700_emb_CAA61504_ (X89216)
                  glutathione transferase [Arabidopsis thaliana] >gi 929957
                  (U30489) glutathione S-transferase [Arabidopsis thaliana]
                  >gi 940381 dbj BAA07917 (D44465) Glutathione S-Transferase
                  [Arabidopsis thaliana] >gi 3980390 (AC004561) glutathione
                  S-transferase [Arabidopsis thaliana]
Seq. No.
                  116935
                  332 1.R1010
Contig ID
5'-most EST
                  LIB3234-047-P1-K1-F4
                  BLASTX
Method
NCBI GI
                  q625977
BLAST score
                  1313
                  1.0e-145
E value
Match length
                  262
                  95
% identity
                  p40 protein homolog - Arabidopsis thaliana >gi 402904.
NCBI Description
                  (U01955) laminin receptor-like protein [Arabidopsis
                  thaliana]
                  116936
Seq. No.
                  332_2.R1010
Contig ID
5'-most EST
                  g2747735
Method
                  BLASTX
                  g585382
NCBI GI
BLAST score
                  334
                  3.0e-31
E value
                  79
Match length
```

% identity

```
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) (LAMININ RECEPTOR HOMOLOG)
                   >qi 322536 pir S30570 laminin receptor homolog -
                   Arabidopsis thaliana >gi 16380 emb CAA48794 (X69056)
                   laminin receptor homologue [Arabidopsis thaliana]
Seq. No.
                   116937
                   333 1.R1010
Contig ID
                   jC-atXP89CG6C7T7077d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1076365
BLAST score
                   2668
E value
                   0.0e + 00
Match length
                   586
% identity
NCBI Description
                  pectinesterase (EC 3.1.1.11) PME1 precursor - Arabidopsis
                   thaliana >gi_2129666_pir__JC4778 pectinesterase (EC
                   3.1.1.11) 1 - Arabidopsis thaliana >gi_550306_emb_CAA57275 (X81585) ATPME1 [Arabidopsis thaliana] >gi_903895 (U25649)
                   ATPME1 precursor [Arabidopsis thaliana]
                   116938
Seq. No.
Contig ID
                   334_1.R1010
5'-most EST
                   q2747663
Method
                   BLASTX
                   g2118220 :
NCBI GI
BLAST score
                   576
                   4.0e-59
E value
Match length
                   164
                   74
% identity
                  H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
NCBI Description
                   (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581)
                   vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                   thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16
                   kDa proteolipid [Arabidopsis thaliana]
                   >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar
                   H+-transporting ATPase 16K chain [Arabidopsis thaliana]
                   >gi 4539311 emb CAB38812.1_ (AL035679) H+-transporting
                   ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
                   >gi 4589976 gb AAD26493.1_AC007195_7 (AC007195) vacuolar
                   H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
                   116939
Seq. No.
Contig ID
                   334 2.R1010
5'-most EST
                   jC-atXLIB327420P4h09b1
Method
                   BLASTX
NCBI GI
                   g2118220
BLAST score
                   576
E value
                   4.0e-59
Match length
                   164
% identity
NCBI Description
                   H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                   (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581)
                   vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                   thaliana] >gi 926933 (L44583) vacuolar H+-pumping ATPase 16
                   kDa proteolipid [Arabidopsis thaliana]
                   >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar
```

H+-transporting ATPase 16K chain [Arabidopsis thaliana]

Contig ID

Method

NCBI GI

5'-most EST

```
>gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar
                  H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
                  116940
Seq. No.
                  334 5.R1010'
Contig ID
                  LIB24-075-Q1-E1-E7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2118220
BLAST score
                  410
E value
                  4.0e-40
Match length
                  117
                  74
% identity
                  H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
NCBI Description
                  (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581)
                  vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                  thaliana] >gi 926933 (L44583) vacuolar H+-pumping ATPase 16
                  kDa proteolipid [Arabidopsis thaliana]
                  >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar
                  H+-transporting ATPase 16K chain [Arabidopsis thaliana]
                  >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting
                  ATPase 16K-chain P2, vacuolar [Arabidopsis thaliana]
                  >gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar
                  H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
                  116941
Seq. No.
                  335 1.R1010
Contig ID
5'-most EST
                  PLN_g928941
                  BLASTX
Method
                  g2129592
NCBI GI
BLAST score
                  1561
                  1.0e-174
E value
Match length
                  362
% identity
                  81
                  gene M4 protein - Arabidopsis thaliana
NCBI Description
                  >gi 928942 emb CAA62029 (X90381) M4 [Arabidopsis thaliana]
                  116942
Seq. No.
Contig ID
                  337 1.R1010
5'-most EST
                  PLN g928964
                  BLASTX
Method
NCBI GI
                  q2129775
BLAST score
                  1353
E value
                  1.0e-150
                  332
Match length
                  79
% identity
                  Y13 protein - Arabidopsis thaliana >gi_928930_emb_CAA62034_
NCBI Description
                  (X90387) cY13 [Arabidopsis thaliana]
                  >gi 928965 emb_CAA62031_ (X90383) Y13 [Arabidopsis
                  thaliana]
                  116943
Seq. No.
```

>gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting
ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]

338 1.R1010

BLASTX

q2832404

LIB23-069-Q1-E1-F11

```
BLAST score
                   1258
                   1.0e-139
E value
                   273
Match length
% identity
NCBI Description
                   (Y14207) R2R3-MYB transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                   116944
Contig ID
                   338 2.R1010
5'-most EST
                   jC-atXLIB327410P4q03b1
Method
                   BLASTX
NCBI GI
                   q2832404
BLAST score
                   513
E value
                   5.0e-52
Match length
                   118
% identity
NCBI Description
                   (Y14207) R2R3-MYB transcription factor [Arabidopsis
                   thaliana]
                   116945
Seq. No.
Contig ID
                   339 1.R1010
5'-most EST
                   jC-atXLIB327426P1f07b1
Method
                   BLASTX
                   g2129777
NCBI GI
BLAST score
                   1292
                   1.0e-143
E value
Match length
                  269
% identity
                  Y49 protein - Arabidopsis thaliana >gi_928969_emb_CAA62033_
NCBI Description
                   (X90385) Y49 [Arabidopsis thaliana] >gi_10201\overline{57} (\overline{U}26937)
                   DNA-binding protein [Arabidopsis thaliana]
                   >gi 4581115 gb AAD24605.1 AC005825 12 (AC005825) MYB-like
                   protein; very similar to GB:2129777 [Arabidopsis thaliana]
                   116946
Seq. No.
Contig ID
                   341 1.R1010
5'-most EST
                   jC-atXP79CF4H11T7b1
Method
                   BLASTX
                   g1946362
NCBI GI
BLAST score
                   408
                   2.0e-39
E value
Match length
                   120
% identity
NCBI Description
                   (U93215) photosystem II reaction center 6.1KD protein
                   [Arabidopsis thaliana]
                   116947
Seq. No.
Contig ID
                   341_2.R1010
                   jC-alXLIB327436P3d08b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1946362
                   408
BLAST score
E value
                   1.0e-39
Match length
                  120
% identity
NCBI Description
                   (U93215) photosystem II reaction center 6.1KD protein
```

[Arabidopsis thaliana]

Contig ID

```
116948
Seq. No.
                   341_3.R1010
Contig ID
5'-most EST
                  q25\overline{8}1596
                  BLASTX
Method
NCBI GI
                  q1946362
                 ...57
BLAST score
                  5.0e-26
E value
                  88
Match length
% identity
                  81
NCBI Description
                   (U93215) photosystem II reaction center 6.1KD protein
                   [Arabidopsis thaliana]
                  116949
Seq. No.
                   341_4.R1010
Contig ID
5'-most EST
                   jC-atXLIB327426P2f07b1
Method
                  BLASTX
NCBI GI
                  g2129672
                   500
BLAST score
                  3.0e-50
E value
Match length
                  133
% identity.
                  75
NCBI Description
                  photosystem II reaction center protein, 6.1K - Arabidopsis
                  thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1
                  kDa polypeptide of photosystem II reaction center
                   [Arabidopsis thaliana]
                  116950
Seq. No.
                  341 5.R1010
Contig ID .
5'-most EST
                  jC-atXLIB327414P2e06a1
Method
                  BLASTX
NCBI GI
                  g1946362
BLAST score
                   408
                  8.0e-40
E value
Match length
                  120
% identity
                   (U93215) photosystem II reaction center 6.1KD protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  116951
Contig ID
                  344 1.R1010
5'-most EST
                  LIB24-074-Q1-E1-F10
                  BLASTX
Method
NCBI GI
                  g1169277
BLAST score
                  1060
                  1.0e-116
E value
                  246
Match length
% identity
                  DEHYDRIN ERD10 (LOW-TEMPERATURE-INDUCED PROTEIN LTI45)
NCBI Description
                  >gi_2129638_pir__S60480 low temperature-induced protein
                  lit29 - Arabidopsis thaliana >gi_556472_dbj_BAA04568_
                  (D17714) ERD10 protein [Arabidopsis thaliana]
                  >gi_975648_emb_CAA62448_ (X90958) lti29 [Arabidopsis
                  thaliana]
                  116952
Seq. No.
```

344_2.R1010

Method

BLASTX

```
5'-most EST
                  jC-atXLIB327414P3b09a1
Method
                  BLASTX
NCBI GI
                  g1169277
BLAST score
                  965
E value
                  1.0e-105
Match length
                  232
% identity
NCBI Description
                  DEHYDRIN ERD10 (LOW-TEMPERATURE-INDUCED PROTEIN LT145)
                  >gi_2129638_pir__S60480 low temperature-induced protein
                  lit29 - Arabidopsis thaliana >gi_556472_dbj_BAA04568_
                  (D17714) ERD10 protein [Arabidopsis thaliana]
                  >gi_975648_emb_CAA62448_ (X90958) lti29 [Arabidopsis
                  thalianal
                  116953
Seq. No.
                  345 1.R1010
Contig ID
5'-most EST
                  LIB24-059-Q1-E1-A6
Method
                  BLASTX
                  q1174852
NCBI GI
BLAST score
                  815
E value
                  4.0e-87
Match length
                  167
% identity
                  92
                  UBIQUITIN-CONJUGATING ENZYME E2-19 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) (TAYO29)
                  >gi 2129757 pir S46656 ubiquitin carrier protein E2 (clone
                  TAY029) - Arabidopsis thaliana >gi_600389_emb_CAA51200_
                  (X72625) ubiquitin conjugating enzyme E2 [Arabidopsis
                  thaliana] >gi 992708 (U33759) UBC14 [Arabidopsis thaliana]
                  116954
Seq. No.
Contig ID
                  348 1.R1010
5'-most EST
                  LIB24-027-Q1-E1-D3
Method
                  BLASTX
NCBI GI
                  q2342427
BLAST score
                  3113
                  0.0e+00
E value
Match length
                  651
% identity
                  93
NCBI Description
                  (AB000799) NPK1-related protein kinase 3 [Arabidopsis
                  thalianal
Seq. No.
                  116955
Contig ID
                  349 1.R1010
5'-most EST
                  jC-atXLIB327411P1f05b1
Method
                  BLASTX
NCBI GI
                  q1465368
BLAST score
                  2778
E value
                  0.0e+00
Match length
                  623
% identity
NCBI Description
                  (X99548) bHLH protein [Arabidopsis thaliana]
Seq. No.
                  116956
Contig ID
                  349 2.R1010
5'-most EST
                  jC-atXLIB327408P1d10b1
```

```
NCBI GI
                   q2245029
BLAST score
                   521
E value
                   5.0e-53
Match length
                   111
% identity
                   95
                  (Z97341) limonene cyclase homolog [Arabidopsis thaliana]
NCBI Description
                   116957
Seq. No.
Contig ID
                   349 4.R1010
5'-most EST
                   q1268778
Method
                   BLASTX
NCBI GI
                   q1465368
BLAST score
                   324
                   8.0e-30
E value
                   85
Match length
% identity
                   86
NCBI Description
                   (X99548) bHLH protein [Arabidopsis thaliana]
Seq. No.
                   116958
                   349 7.R1010
Contig ID
                   jC-atXLIB327429P1e01b2
5'-most EST
Method
                   BLASTN
                   g1465367
NCBI GI
BLAST score
                   362
                   0.0e + 00
E value
                   506
Match length
                   93
% identity
NCBI Description A.thaliana mRNA for RAP-1 protein
                   116959
Seq. No.
                   350 1.R1010
Contig ID
                  LIB3175-068-P1-K1-G8
5'-most EST
Method
                   BLASTX
                   g2760606
NCBI GI
BLAST score
                   884
E value
                   3.0e-95
Match length
                   169
% identity
                   100
NCBI Description
                   (AB001568) phospholipid hydroperoxide glutathione
                  peroxidase-like protein [Arabidopsis thaliana] >gi_3004869
                   (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis
                   thaliana] >gi 4539451 emb CAB39931.1 (AL049500)
                   phospholipid hydroperoxide glutathione peroxidase
                   [Arabidopsis thaliana]
                   116960
Seq. No.
Contig ID
                   351_1.R1010
5'-most EST
                   PLN_g2281779
Method
                  BLASTX
NCBI GI
                   q2281780
BLAST score
                   1543
                  1.0e-172
E value
                   404
Match length
% identity .
                   79
NCBI Description
                   (AB003041) O-acetylserine (thiol) lyase [Arabidopsis
```

thaliana]

5'-most EST

```
Seq. No.
                  116961
                  353 1.R1010
Contig ID.
                 → PLN g2114105
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2114104
BLAST score
                  3196
                  :0.0e+00 4
E value
Match length
                  677
% identity
                  93
NCBI Description
                  (AB003590) sulfate transporter [Arabidopsis thaliana]
                  >gi_2114106_dbj_BAA20085_ (AB003591) sulfate transporter
                   [Arabidopsis thaliana]
                  116962
Seq. No.
                  354 1.R1010
Contig ID
5'-most EST
                  PLN g2804279
Method
                  BLASTX
NCBI GI
                  q2804280
BLAST score
                  2804
                  0.0e + 00
E value
                  537
Match length
% identity
NCBI Description
                  (AB003687) 6-4 photolyase [Arabidopsis thaliana]
                  >gi_3929918_dbj_BAA34711_ (AB017331) 6-4 photolyase
                  [Arabidopsis thaliana]
                  116963
Seq. No.
Contig ID
                  355 1.R1010
                  LIB25-098-Q1-E1-E12
5'-most EST
Method
                  BLASTX
                  q2130944
NCBI GI
                  3068
BLAST score
E value
                  0.0e + 00
Match length
                  646
% identity
NCBI Description
                  (AB004060) sulfate transporter [Arabidopsis thaliana]
                  >gi_2262137_gb_AAC78252.1_AAC78252 (AC002330) sulfate
                  transporter protein [Arabidopsis thaliana]
Seq. No.
                  116964
                  356 1.R1010
Contig ID
                  jC-atXLIB327437P4b06b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2443357
BLAST score
                  2517
E value
                  0.0e + 00
Match length
                  572
% identity
                  88
NCBI Description
                  (AB004293) SigB [Arabidopsis thaliana]
                  >gi_2597831_emb_CAA75584_ (Y15362) sigma factor
                  [Arabidopsis thaliana] >gi_2879922_dbj_BAA24825_ (AB004820)
                  plastid RNA polymerase sigma-subunīt [Ārabidopsīs thaliana]
                  >gi 3063440 (AC003981) F22013.2 [Arabidopsis thaliana]
Seq. No.
                  116965
                  356 2.R1010
Contig ID
```

jC-atXP79CF4G7T7b1

```
Method
                   BLASTX
NCBI GI
                   q2353173
BLAST score
                   565
E value
                   1.0e-61
Match length
                   137
% identity
                   92
NCBI Description (AF015543) sigma factor 2 [Arabidopsis thaliana]
                   116966
Seq. No.
                   356 3.R1010
Contig ID
5'-most EST
                   LIB24-112-Q1-E1-C3
Method
                   BLASTX
NCBI GI
                   q4455235
BLAST score
                   274
E value
                   3.0e-24
                   69
Match length
% identity
                   83
                   (AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA
NCBI Description
                   SUBUNIT-like [Arabidopsis thaliana]
Seq. No.
                   116967
Contig ID
                   358_1.R1010
5'-most EST
                   PLN_g2196703
Method
                   BLASTX
NCBI GI
                   q2196704
                   1849
BLAST score
E value
                   0.0e + 00
Match length
                   354
% identity
                   100
NCBI Description
                   (AF000977) MEK1 [Arabidopsis thaliana]
                   >gi_2723388_dbj_BAA24079_ (AB004796) mitogen activated
                   protein kinase kinase [Arabidopsis thaliana]
                   >gi_4538936_emb_CAB39672.1_ (AL049483) mitogen activated
                   protein kinase kinase (nMAPKK) [Arabidopsis thaliana]
                   116968
Seq. No.
Contig ID
                   360_1.R1010
5'-most EST
                   PLN_g2398850
Method
                   BLASTX
NCBI GI
                   q2353171
BLAST score
                   2455
E value
                   0.0e + 00
Match length
                   502
% identity
                   97
NCBI Description
                   (AF015542) sigma factor 1 [Arabidopsis thaliana]
                   >gi_2443408_dbj_BAA22421_ (D89993) SigA [Arabidopsis
thaliana] >gi_2558514_emb_CAA74640_ (Y14252) plastid RNA
                   polymerase sigma factor [Arabidopsis thaliana]
Seq. No.
                   116969
Contig ID
                   361_1.R1010
5'-most EST
                   PLN_g2463553
Method
                   BLASTX
NCBI GI
                   q2353175
BLAST score
                   2536
E value
                   0.0e + 00
Match length
                   571
```

Contig ID

```
% identity
                   (AF015544) sigma factor 3 [Arabidopsis thaliana]
NCBI Description
                  >gi 2463554 dbj_BAA22530_ (D89994) SigC [Arabidopsis
                  thaliana]
Seq. No.
                  116970
                  363_1.R1010
Contig ID
5'-most EST
                  PLN_g2244708
                  BLASTX
Method
NCBI GI
                  g2244709
BLAST score
                  563
                  1.0e-57
E value
Match length
                  168
                   72
% identity
                   (AB005295) HY5 [Arabidopsis thaliana]
NCBI Description
                  >gi 2251085 dbj BAA21327 (AB005456) HY5 [Arabidopsis
                  thaliana]
                   116971
Seq. No.
                   364_1.R1010
Contig ID
5'-most EST
                  PLN_g1655423
Method
                  BLASTX
NCBI GI
                   q1655424
BLAST score
                   2332
                  0.0e + 00
E value
Match length
                   445
                  100
% identity
                   (D83531) GDP dissociation inhibitor [Arabidopsis thaliana]
NCBI Description
                  >gi 3212878 (AC004005) GDP dissociation inhibitor
                   [Arabidopsis thaliana]
                   116972
Seq. No.
Contig ID
                   364_2.R1010
5'-most EST
                   PLN_g2569935
Method
                  BLASTX
NCBI GI
                   g2446981
                   2289
BLAST score
                   0.0e + 00
E value
Match length
                   436
% identity
                   100
                   (AB005560) AtGDI2 [Arabidopsis thaliana]
NCBI Description
                  >gi 2569936 emb CAA04727 (AJ001397) GDI2 [Arabidopsis
                   thaliana]
                   116973
Seq. No.
Contig ID
                   365_1.R1010
5'-most EST
                   PLN_g3172022
Method
                  BLASTX
                   q3172023
NCBI GI
BLAST score
                   1584
                   0.0e + 00
E value
                   1367
Match length
                   95
% identity
                  (AB005804) aldehyde oxidase [Arabidopsis thaliana]
NCBI Description
                   116974
Seq. No.
```

366 1.R1010

5'-most EST

```
5'-most EST
                   PLN g3172024
                   BLASTX
Method
NCBI GI
                   q3172025
BLAST score
                   6640
E value
                   0.0e + 00
Match length
                   1321
% identity
                   (AB005805) aldehyde oxidase [Arabidopsis thaliana]
NCBI Description
                   116975
Seq. No.
Contig ID
                   367 2.R1010
5'-most EST
                   jC-atX24027Q1E1D10b1
Method
                   BLASTX
                   q2280528
NCBI GI
                   178
BLAST score
                   6.0e-13
E value
Match length
                   33
                   100
% identity
                   (AB005888) ATMYB3 [Arabidopsis thaliana]
NCBI Description
                   116976
Seq. No.
Contig ID
                   368_1.R1010
5'-most EST
                   PLN_g2280529
                   BLASTX
Method
                   g2280530
NCBI GI
                   1784
BLAST score
                   0.0e + 00
E value
Match length
                   352
% identity
                   94
                  (AB005889) ATMYB4 [Arabidopsis thaliana]
NCBI Description
                   116977
Seq. No.
Contig ID
                   369 1.R1010
5'-most EST
                   LIB25-104-Q1-E1-D2
Method
                   BLASTX
                   g3702691
NCBI GI
                   3554
BLAST score
                   0.0e + 00
E value
Match length
                   678
                   97
% identity
                   (AB005902) AtPIP5K1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   116978
Contig ID
                   373 1.R1010
5'-most EST
                   PLN_g3219163
                   BLASTX
Method
                   g3219164
NCBI GI
BLAST score
                   2945
                   0.0e + 00
E value
Match length
                   593
% identity
NCBI Description
                   (AB006210) glutamine amidotransferase/cyclase [Arabidopsis
                   thaliana]
Seq. No.
                   116979
                   374_1.R1010
Contig ID
```

PLN g2351096

```
Method
                  BLASTX
                  q2351097
NCBI GI
                  2039
BLAST score
                  0.0e + 00
E value
                  391
Match length
% identity
                  97
                  (AB006810) ATMRK1 [Arabidopsis thaliana]
NCBI Description
                  116980
Seq. No.
Contig ID
                  375_1.R1010
5'-most EST
                  PLN_g3738227
Method
                  BLASTX
NCBI GI
                  q3660552
BLAST score
                  1087
E value
                  1.0e-119
Match length
                  216
                  94
% identity
NCBI Description
                  (AB013817) DREB1C [Arabidopsis thaliana]
                  >gi 3738228 dbj BAA33793 (AB007789) DREB1C [Arabidopsis
                  thaliana] >gi 3907541 (AF062925) transcriptional activator
                  CBF1 homolog [Arabidopsis thaliana]
                  >gi_4322228_gb_AAD15976_ (AF074601) CRT/DRE binding factor
                  2 [Arabidopsis thaliana]
                  116981
Seq. No.
                  375 2.R1010
Contig ID
5'-most EST
                  PLN g3738225
                  BLASTX
Method
                  g1899058
NCBI GI
BLAST score
                  1046
                  1.0e-114
E value
                  213
Match length
% identity
                  (U77378) transcriptional activator CBF1 [Arabidopsis
NCBI Description
                  thaliana] >gi 4091982 gb AAC99369 (AF076155) CRT/CRE
                  binding factor 1 [Arabidopsis thaliana]
                  116982
Seq. No.
Contig ID
                  375_3.R1010
                  PLN_g3738223
5'-most EST
                  BLASTX
Method
                  g2980802
NCBI GI
BLAST score
                  1035
E value
                  1.0e-117
Match length
                  234
                  89
% identity
                  (AL022197) transcriptional activator CBF1 - like protein
NCBI Description
                  [Arabidopsis thaliana]
                  116983
Seq. No.
Contig ID
                  378 1.R1010
5'-most EST
                  jC-atXLIB327430P4d12b1
Method
                  BLASTX
                  q3738230
NCBI GI
BLAST score
                  1503
E value
                  1.0e-167
Match length
                  335
```

Method

BLASTX

```
% identity
                   (AB007790) DREB2A [Arabidopsis thaliana]
NCBI Description
                   >gi 4126706 dbj BAA36705 (AB016570) DREB2A [Arabidopsis
                   thaliana]
Seq. No.
                   116984
                   380 1.R1010
Contig ID
                   LIB3177-006-P1-K2-G1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4240116
BLAST score
                   1377
E value
                   1.0e-153
Match length
                   281
                   93
% identity
                   (AB007799) NADH-cytochrome b5 reductase [Arabidopsis
NCBI Description
                   thaliana] >gi_4240118_dbj_BAA74838_ (AB007800)
                  NADH-cytochrome b5 reductase [Arabidopsis thaliana]
                   116985
Seq. No.
                   380 2.R1010
Contig ID
                   jC-atXLIB327424P1f06b2
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4240116
BLAST score
                   279
E value
                   2.0e-29
Match length
                  71
                   93
% identity
                   (AB007799) NADH-cytochrome b5 reductase [Arabidopsis
NCBI Description
                   thaliana] >gi 4240118 dbj BAA74838 (AB007800)
                  NADH-cytochrome b5 reductase [Arabidopsis thaliana]
                  116986
Seq. No.
Contig ID
                  381_1.R1010
5'-most EST
                   jC-atXLIB327422P3a11b2
Method
                  BLASTX
NCBI GI
                   g4240120
BLAST score
                   700
E value
                  9.0e-74
Match length
                  134
% identity
                  100
                  (AB007801) cytochrome b5 [Arabidopsis thaliana]
NCBI Description
                  116987
Seq. No.
                   382 1.R1010
Contig ID
                   jC-atXLIB327406P2f03b1
5'-most EST
Method
                  BLASTX
                  g4240122
NCBI GI
BLAST score
                   721
E value
                  3.0e-76
Match length
                  140
% identity
                  100
                  (AB007802) cytochrome b5 [Arabidopsis thaliana]
NCBI Description
                  116988
Seq. No.
Contig ID
                  382 2.R1010
5'-most EST
                  g907003
```

Contig ID

```
NCBI GI
                  q4240122
BLAST score
                  377
                  5.0e-36
E value
                  99
Match length
                  76
% identity
                  (AB007802) cytochrome b5 [Arabidopsis thaliana]
NCBI Description
                  116989
Seq. No.
                  383_1.R1010
Contig ID
5'-most EST
                 - PLN_g3928757
                  BLASTX
Method
NCBI GI
                  q3928758
                  1739
BLAST score
                  0.0e + 00
E value
Match length
                  374
                  91
% identity
                  (AB007987) Lipoic acid synthase [Arabidopsis thaliana]
NCBI Description
                  >gi 4454462_gb AAD20909 (AC006234) putative lipoic acid
                  synthase [Arabidopsis thaliana]
                  116990
Seq. No.
                  384 1.R1010
Contig ID
5'-most EST
                  LIB25-090-Q1-E1-F11
Method
                  BLASTX
                  g4176420
NCBI GI
BLAST score
                  2559
                  0.0e + 00
E value
                  524
Match length
% identity
                  95
                  (AB008097) cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  116991
Seq. No.
                  385_1.R1010
Contig ID
5'-most EST
                  g2722607
                  BLASTX
Method
                  g3434967
NCBI GI
BLAST score
                  1152
                  1.0e-126
E value
Match length
                  262
% identity
                  85
                  (AB008103) ethylene responsive element binding factor 1
NCBI Description
                  [Arabidopsis thaliana]
                  116992
Seq. No.
                  386 1.R1010
Contig ID
                  LIB25-108-Q1-E1-B7
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3434969
BLAST score
                  1030
E value
                  1.0e-112
Match length
                  241
                  83
% identity
                  (AB008104) ethylene responsive element binding factor 2
NCBI Description
                  ·[Arabidopsis thaliana]
Seq. No.
                  116993
```

386 2.R1010

NCBI Description

```
5'-most EST
                   jC-atXLIB327414P2h03a1
Method
                   BLASTX
NCBI GI
                   g3434969
BLAST score
                   771
                   4.0e-82
E value
Match length
                   180 -.
                   84
% identity
                   (AB008104) ethylene responsive element binding factor 2
NCBI Description
                   [Arabidopsis thaliana]
                   116994
Seq. No.
Contig ID
                   387_1.R1010
5'-most EST
                  PLN_g3434970
                  BLASTX
Method
NCBI GI
                  q3434971
                  857
BLAST score
E value
                  7.0e-92
Match length
                  222
                  73
% identity
                   (AB008105) ethylene responsive element binding factor 3
NCBI Description
                   [Arabidopsis thaliana]
                  116995
Seq. No.
Contig ID
                   388 1.R1010
5'-most EST
                   jC-atXLIB327431P1g03b1
                  BLASTX
Method
NCBI GI
                  g3434973
BLAST score
                  920
E value
                  2.0e-99
Match length
                  222
                  81
% identity
NCBI Description
                   (AB008106) ethylene responsive element binding factor 4
                   [Arabidopsis thaliana]
                  116996
Seq. No.
Contig ID
                  389_1.R1010
5'-most EST
                  LIB22-086-Q1-E1-G3
Method
                  BLASTX
NCBI GI
                  g3434975
                 - 1073
BLAST score
E value
                  1.0e-117
Match length
                  296
                  71
% identity
                   (AB008107) ethylene responsive element binding factor 5
NCBI Description
                   [Arabidopsis thaliana]
                  116997
Seq. No.
Contig ID
                  390_1.R1010
5'-most EST
                  PLN_g2654867
Method
                  BLASTX
NCBI GI
                  q3242456
BLAST score
                   4925
E value
                  0.0e + 0.0
Match length
                  944
                  100
% identity
                  (AB008111) Atrboh F [Arabidopsis thaliana]
```

BLAST score

3062

```
Seq. No.
                  116998
                  391_1.R1010
Contig ID
                  PLN_g3273195
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3273196
BLAST score
                  1029
E value
                  1.0e-112
Match length
                  259
% identity
                  82
NCBI Description
                  (AB010915) responce regulator1 [Arabidopsis thaliana]
                  >gi_3323583 (AF057282) two-component response regulator
                  homolog [Arabidopsis thaliana] >gi_3953597_dbj_BAA34726_
                  (AB008487) response regulator 4 [Arabidopsis thaliana]
                  116999
Seq. No.
                  393 1.R1010
Contig ID
5'-most EST
                  PLN_g3273197
Method
                  BLASTX
NCBI GI
                  g3273198
BLAST score
                  908
                  7.0e-98
E value
                  184
Match length
% identity
                  100
NCBI Description
                  (AB010916) responce reactor2 [Arabidopsis thaliana]
                  >gi_4678318_emb_CAB41129.1_ (AL049658) responce reactor2
                  [Arabidopsis thaliana]
                  117000
Seq. No.
Contig ID
                  395 1.R1010
5'-most EST
                  LIB25-105-Q1-E1-A2
Method
                  BLASTX
                  g3953603
NCBI GI
BLAST score
                  919
E value
                  2.0e-99
                  206
Match length
% identity
                  91
NCBI Description
                  (AB008490) response regulator 7 [Arabidopsis thaliana]
                  117001
Seq. No.
                  396 1.R1010
Contig ID
5'-most EST
                  PLN_g3164221
Method
                  BLASTX
NCBI GI
                  q3164222
BLAST score
                  1185
E value
                  1.0e-130
Match length
                  234
% identity
                  95
                  (AB008518) RMA1 [Arabidopsis thaliana]
NCBI Description
                  >gi 4206205 gb AAD11593.1 AAD11593 (AF071527) RMA1 RING
                  zinc finger protein [Arabidopsis thaliana]
                  117002
Seq. No.
Contig ID
                  397 1.R1010
5'-most EST
                  PLN g2626752
Method
                  BLASTX
NCBI GI
                  g2626753
```

```
0.0e+00
E value
                   685
Match length
                  89
% identity
                   (AB008782) sulfate transporter [Arabidopsis thaliana]
NCBI Description
                   117003
Seq. No.
                   397 2.R1010
Contig ID
5'-most EST
                   jC-atXP98CH2H3T7029d1
Method
                  BLASTX
                   q2626753
NCBI GI
BLAST score
                   706
                   2.0e-74
E value
                   170
Match length
% identity
                  81
                  (AB008782) sulfate transporter [Arabidopsis thaliana]
NCBI Description
                   117004
Seq. No.
                   399 1.R1010
Contig ID
                   jC-atXLIB327433P1h11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3218550
BLAST score
                   2523
                  0.0e+00
E value
                   479
Match length
% identity
                   100
NCBI Description
                  (AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]
Seq. No.
                   117005
                   400 1.R1010
Contig ID
                   jC-atXLIB327408P4d02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3149952
BLAST score
                   2528
E value
                   0.0e + 00
Match length
                   605
% identity
                   83
                   (AB010259) DRH1 [Arabidopsis thaliana]
NCBI Description
                   117006
Seq. No.
                   400 2.R1010
Contig ID
                   jC-alXLIB327436P2b03b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3149952
                   582
BLAST score
                   5.0e-60
E value
Match length
                   116
% identity
                   98
                   (AB010259) DRH1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117007
                   403 1.R1010
Contig ID
                   PLN g3273199
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3273200
                   993
BLAST score
                  1.0e-108
E value
```

225

Match length

BLAST score

796

```
% identity
                   90
NCBI Description
                   (AB010917) responce reactor3 [Arabidopsis thaliana]
                  >gi 3894192 (AC005662) response regulator 3 (Arabidopsis
                  thaliana]
Seq. No.
                   117008
                   403_2.R1010
Contig ID
5'-most EST
                  PLN_g3273201
Method
                  BLASTX
NCBI GI
                  q3273202
BLAST score
                   1054
E value
                   1.0e-115
Match length
                   234
% identity
                   91
                   (AB010918) responce reactor4 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117009
                   405 1.R1010
Contig ID
5',-most EST
                  LIB3176-061-P1-K1-A8
                  BLASTX
Method
NCBI GI
                  q2865175
BLAST score
                  854
E value
                  8.0e-92
                  191
Match length
% identity
                  (AB010945) AtRerlA [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117010
                   406_1.R1010
Contig ID
5'-most EST
                  PLN_g4160668
                  BLASTX
Method
NCBI GI
                  q2865177
BLAST score
                   914
                   1.0e-98
E value
Match length
                  195
% identity
                  89
                  (AB010946) AtRer1B [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117011
                   407 1.R1010
Contig ID
5'-most EST
                  g2048812
Method
                  BLASTX
NCBI GI
                  g3551052
BLAST score
                   1334
E value
                  1.0e-148
Match length
                  263
                  100
% identity
NCBI Description
                   (AB011545) GF14 mu [Arabidopsis thaliana]
                  >gi_4559343_gb_AAD23005.1_AC007087 24 (AC007087) DNA
                  regulatory protein GF14 mu [Arabidopsis thaliana]
                  117012
Seq. No.
Contig ID
                   408_1.R1010
5'-most EST
                  PLN g4107100
Method
                  BLASTX
NCBI GI
                  q4107101
```

```
E value
                  5.0e-85
Match length
                  156
                  100
% identity
                  (AB015142) AHP2 [Arabidopsis thaliana]
NCBI Description
                  >gi 4156241 dbj BAA37110 (AB012568) ATHP1 [Arabidopsis
                  thaliana]
                  117013
Seq. No.
                  409_1.R1010
Contig ID
5'-most EST
                  PLN_g4156242
Method
                  BLASTX
NCBI GI
                  g4156243
                  791
BLAST score
                  2.0e-84
E value
Match length
                  152
                  100
% identity
NCBI Description
                  (AB012569) ATHP2 [Arabidopsis thaliana]
                  117014
Seq. No.
                  410 1.R1010
Contig ID
5'-most EST
                  LIB3175-001-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g4107099
BLAST score
                  727
E value
                  6.0e-77
                  154
Match length
                  94
% identity
                  (AB015141) AHP1 [Arabidopsis thaliana]
NCBI Description
                  >gi 4156245 dbj BAA37112 (AB012570) ATHP3 [Arabidopsis
                  thaliana]
                  117015
Seq. No.
                  411_1.R1010
Contig ID
5'-most EST
                  PLN_g3327867
                  BLASTX
Method
NCBI GI
                  q3327868
BLAST score
                  4780
E value
                  0.0e + 00
Match length
                  1058
% identity
                  89
NCBI Description
                  (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis
                  thaliana]
                  117016
Seq. No.
Contig ID
                  412_1.R1010
5'-most EST
                  PLN_g3298497
Method
                 . BLASTX
NCBI GI
                  g2245108
BLAST score
                  1112
E value
                  1.0e-134
Match length
                  300
                  83
% identity
NCBI Description
                  (Z97343) EREBP-4 homolog [Arabidopsis thaliana]
                  117017
Seq. No.
Contig ID
                  413 1.R1010
5'-most EST
                  LIB22-009-Q1-E1-A10
```

```
Method
                  BLASTX
NCBI GI
                  a3868857
                  1657
BLAST score
                  0.0e + 00
E value
                   329
Match length
% identity
                   98
                  (AB013886) RAV1 [Arabidopsis thaliana]
NCBI Description
                  117018
Seq. No.
Contig ID
                  413_3.R1010
5'-most EST
                  jC-atXLIB327405P1c08a2
Method
                  BLASTN
                  a3868856
NCBI GI
BLAST score
                  156
E value
                  3.0e-82
Match length
                  247
% identity
                  100
NCBI Description Arabidopsis thaliana mRNA for RAV1, complete cds
                  117019
Seq. No.
                  413 4.R1010
Contig ID
5'-most EST
                  ARABL1-037-Q1-E1-F8
Seq. No.
                  117020
Contig ID
                  414_1.R1010
5'-most EST
                  g931044
Method
                  BLASTX
NCBI GI
                  g3868859
BLAST score
                  1664
E value
                  0.0e + 00
Match length
                  319
                  100
% identity
NCBI Description
                  (AB013887) RAV2 [Arabidopsis thaliana]
                  117021
Seq. No.
                  415_1.R1010
Contig ID
5'-most EST
                  LIB25-035-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                  q3096918
BLAST score
                  2125
                  0.0e + 00
E value
                  469
Match length
% identity
                  89
NCBI Description
                  (AL023094) putative cyclase associated protein CAP
                   [Arabidopsis thaliana] >gi_3169136_dbj_BAA28621_ (AB014759)
                  Atcap1 [Arabidopsis thaliana]
Seq. No.
                  117022
                  419 1.R1010
Contig ID
5'-most EST
                  g2597127
Method
                  BLASTX
NCBI GI
                  g3228219
BLAST score
                  1800
                  0.0e + 00
E value
Match length
                  363
% identity
                  (AJ006871) MAP2k beta [Arabidopsis thaliana] >gi 3859486
NCBI Description
```

```
(AF067792) MAP kinase kinase 1 [Arabidopsis thaliana]
                   117023
Seq. No.
Contig ID
                   419 3.R1010
5'-most EST
                   g23\overline{9}3212
Method
                   BLASTX
NCBI GI
                   q3219267
BLAST score
                   215
E value
                   5.0e-39
Match length
                   86
% identity
                   92
NCBI Description
                  (AB015313) MAP kinase kinase 2 [Arabidopsis thaliana]
                   117024
Seq. No.
                   421_1.R1010
PLN_g3219270
Contig ID
5'-most EST
Method
                   BLASTX
                   q3219271
NCBI GI
                   1519
BLAST score
                   1.0e-169
E value
                   321
Match length
% identity
                   91
NCBI Description
                  (AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]
Seq. No.
                   117025
                   421 2.R1010
Contig ID
                   jC-atX25002Q1E1H04b1
5'-most EST
Method
                   BLASTX
                   q1523800
NCBI GI
                   809
BLAST score
                   1.0e-168
E value
                   331
Match length
% identity
                   90
                   (Y07694) MAP kinase kinase alpha protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   117026
Seq. No.
                   421 5.R1010
·Contig ID
5'-most EST
                   jC-atXLIB327410P1a11a1
                   BLASTX
Method
NCBI GI
                   q3219271
BLAST score
                   444
                   1.0e-43
E value
Match length
                   84
                   98
% identity
NCBI Description (AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]
Seq. No.
                   117027
                   423 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327439P2b09b2
                   BLASTX
Method
                   a3928543
NCBI GI
BLAST score
                   2493
E value
                   0.0e+00
Match length
                   481
% identity
NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
```

Match length

% identity

456

 $Y_{i_1} = X_i = X_i$

84

```
thaliana]
Seq. No.:
                   117028
Contig ID
                   423 4.R1010
5'-most EST
                   jC-atXP29C139E24T7044d1
Method
                   BLASTX
NCBI GI
                   q3928543
                                                                     4ť...
BLAST score
                   448
E value
                   1.0e-120
Match length
                   261
% identity
                   88
NCBI Description
                   (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
                   thaliana]
                   117029
Seq. No.
                   423_7.R1010
Contig ID
5'-most EST
                   g20<del>6</del>2788
                   BLASTN
Method
NCBI GI
                   g3928542
                   256
BLAST score
                   1.0e-142
E value
Match length
                   396
% identity
                   93
                   Arabidopsis thaliana mRNA for UDP-glucose
NCBI Description
                   glucosyltransferase, complete cds
                   117030
Seq. No.
Contig ID
                   424 1.R1010
                   g89<del>9</del>187
5'-most EST
Method
                   BLASTX
                   g3608261
NCBI GI
BLAST score
                   898
E value
                   8.0e-97
Match length
                   194
                   87
% identity
NCBI Description
                   (AB017564) dof zinc finger protein [Arabidopsis thaliana]
                   117031
Seq. No.
Contig ID
                   425_1.R1010
                   jC-alx25078Q1E1G01b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3608263
BLAST score
                   647
E value
                   2.0e-67
Match length
                   198
% identity
                   62
                   (AB017565) Dof zinc finger protein [Arabidopsis thaliana]
NCBI Description
                   117032
Seq. No.
Contig ID
                   426 1.R1010
5'-most EST
                   PLN_g4519791
Method
                   BLASTX
NCBI GI
                   g3236238
BLAST score
                   1945
E value
                   0.0e+00
```

5'-most EST

```
NCBI Description (AC004684) putative ARF1 GTPase activating protein
                  [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_
                   (AB017876) Aspl [Arabidopsis thaliana]
                  117033
Seq. No.
Contig ID
                  426 3.R1010
                  jC-atXLIB327425P3h06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3236238
BLAST score
                  447
E value
                  1.0e-76
Match length
                  152
% identity
                  94
NCBI Description
                  (AC004684) putative ARF1 GTPase activating protein
                   [Arabidopsis thaliana] >gi 4519792 dbj BAA75744.1
                   (AB017876) Aspl [Arabidopsis thaliana]
                  117034
Seq. No.
                  427 1.R1010
Contig ID
5'-most EST
                  PLN_g3759176
Method
                  BLASTX
                  g3759177
NCBI GI
BLAST score
                  1505
E value .
                  1.0e-168
Match length
                  295
% identity
                  100
                  (AB018408) 3-phosphoserine phosphatase [Arabidopsis
NCBI Description
                  thaliana] >gi_3759179_dbj_BAA33807.1_ (AB018409)
                  3-phosphoserin phosphatase [Arabidopsis thaliana]
                  117035
Seq. No.
                  427 2.R1010
Contig ID
                  jC-atXLIB327416P1c06b1
5'-most EST
Method
                  BLASTX
                  g3759177
NCBI GI
BLAST score
                  388
                  2.0e-37
E value
Match length
                  79
                  97
% identity
NCBI Description
                  (AB018408) 3-phosphoserine phosphatase [Arabidopsis
                  thaliana] >gi_3759179_dbj_BAA33807.1_ (AB018409)
                  3-phosphoserin phosphatase [Arabidopsis thaliana]
                  117036
Seq. No.
Contig ID
                  428 1.R1010
5'-most EST
                  LIB25-105-Q1-E1-F7
Method
                  BLASTX
                  g3769300
NCBI GI
BLAST score
                  1015
E value
                  1.0e-110
Match length
                  212
% identity
                  92
                  (AB018552) AtRERIC [Arabidopsis thaliana]
NCBI Description
                  117037
Seq. No.
                  430 1.R1010
Contig ID
```

LIB22-033-Q1-E2-F10

Contig ID



```
Method
                  BLASTX
NCBI GI
                  q4063007
                   1438
BLAST score
                   1.0e-160
E value
                   305
Match length
% identity
                   92
                  (AB021706) uncoupling protein [Arabidopsis thaliana]
NCBI Description
                  117038
Seq. No.
                   432_1.R1010
Contig ID
5'-most EST
                  PLN_g2959780
Method
                  BLASTX
NCBI GI
                   g2959781
BLAST score
                   4707
                  0.0e + 00
E value
Match length
                  988
                  92
% identity
                  (AJ223508) Zwille protein [Arabidopsis thaliana]
NCBI Description
                  117039
Seq. No.
                  433 1.R1010
Contig ID
5'-most EST
                  LIB3168-066-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g4210330
BLAST score
                  5433
                  0.0e+00
E value
                  1027
Match length
                  100
% identity
NCBI Description
                   (AJ223802) 2-oxoglutarate dehydrogenase, El subunit
                   [Arabidopsis thaliana]
                  117040
Seq. No.
                   434 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327427P3h12b2
Method
                  BLASTX
NCBI GI
                  g4210332
BLAST score
                  1919
                  0.0e + 00
E value
                   462
Match length
% identity
                  84
                   (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  117041
Contig ID
                   434 2.R1010
5'-most EST
                  jC-atXLIB327429P4a10b2
Method
                  BLASTX
NCBI GI
                  g4455214
BLAST score
                   479
E value
                  3.0e-61
Match length
                  193
% identity
                  63
                   (AL035440) putative dihydrolipoamide succinyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  117042
```

434 4.R1010

NCBI Description

```
5'-most EST
                   jC-atXLIB327408P1f08b1
                   BLASTX
Method
NCBI GI
                   q4210332
BLAST score
                   66
                   3.0e-20.
E value
Match length
                   56
                   100
% identity
                   (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit
NCBI Description
                   [Arabidopsis thaliana]
                   117043
Seq. No.
Contig ID
                   435 1.R1010
                   LIB\overline{2}3-056-Q1-E1-B7
5'-most EST
                   BLASTX
Method
                   g4210334
NCBI GI
BLAST score
                   2244
E value
                   0.0e + 00
Match length
                   472
                   94
% identity
                   (AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit
NCBI Description
                   [Arabidopsis thaliana]
                 117044
Seq. No.
Contig ID
                   435 2.R1010
5'-most EST
                   g3449456
Method
                   BLASTX
                   g4210334
NCBI GI
BLAST score
                   371
E value
                   2.0e-35
                   76
Match length
                   93
% identity
                   (AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit
NCBI Description
                   [Arabidopsis thaliana]
                   117045
Seq. No.
                   437 1.R1010
Contig ID
5'-most EST
                   PLN g3256074
                   BLASTX
Method
NCBI GI
                   g2129610
BLAST score
                   716
                   9.0e-76
E value
Match length
                   156
                   92
% identity
                   heat shock protein 17.6K - Arabidopsis thaliana
NCBI Description
                   >gi_984044_emb_CAA61675_ (X89504) 17.6 kD HSP [Arabidopsis
                   thaliana]
                   117046
Seq. No.
Contig ID
                   438 1.R1010
5'-most EST
                   jC-atXLIB327432P3d07b1
Method
                   BLASTX
                   g1834353
NCBI GI
BLAST score
                   1902
E value
                   0.0e + 00
Match length
                   425
% identity
                   (Y10986) hypothetical protein 194 [Arabidopsis thaliana]
```

5'-most EST Method

```
Seq. No.
                   117047
Contig ID
                   439_1.R1010
5'-most EST
                   PLN_g599621
                   BLASTX
Method
NCBI GI
                   g2129516
BLAST score
                   1906
                   0.0e + 00
E value
                   361
Match length
% identity
                   100
NCBI Description
                   1-aminocyclopropane-1-carboxylate oxidase homolog (clone
                   2A6) - Arabidopsis thaliana >gi_599622_emb_CAA58151
                   (X83096) 2A6 [Arabidopsis thaliana] >gi_2809261 (AC002560)
                   F21B7.30 [Arabidopsis thaliana]
                   117048
Seq. No.
Contig ID
                   440 1.R1010
                   jC-atXLIB327413P1h07b1
5'-most EST
Method
                   BLASTX
                   g3121825
NCBI GI
                   1036
BLAST score
E value
                   1.0e-113
Match length
                   250
% identity
                   82
                   2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
NCBI Description
                   ANTIOXIDANT PROTEIN) >gi 1498247 emb CAA63910_ (X94219)
                   bas1 protein [Spinacia oleracea]
                   117049
Seq. No.
Contig ID
                   443 1.R1010
                   jC-atXLIB327428P1d01b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4337177
                   1886
BLAST score
E value
                   0.0e + 00
Match length
                   369
% identity
                   (AC006416) Identical to gb_Y10557 g5bf gene from
NCBI Description
                   Arabidopsis thaliana. ESTs gb_R30578, gb_R90475, gb_T22384, gb_T22425, gb_N64934 and gb_T46767 come from
                   this gene. [Arabidopsis thaliana]
                   117050
Seq. No.
Contig ID
                   443 2.R1010
                   LIB23-048-Q1-E1-A6
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2765081
BLAST score
                   490
                   6.0e-55
E value
Match length
                   144
% identity
                   (Y10557) q5bf [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117051
Contig ID
                   445_1.R1010
```

jC-atXLIB327437P3d12a2

BLASTX

```
g1710530
NCBI GI
                   752
BLAST score
                   5.0e-80
E value
                   142
Match length
                   97
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
                   ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
                   117052
Seq. No.
                   445 2.R1010
Contig ID
5'-most EST
                   LIB25-009-Q1-E1-B2
                   BLASTX
Method
                   g1710530
NCBI GI
BLAST score
                   790
                   2.0e-84
E value
Match length
                   146
                   100
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256
                   ribosomal protein L27a - Arabidopsis thaliana
                   >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
                                                                            ₹
                 ... 117053
Seq. No.
Contig ID
                  445 5.R1010
5'-most EST
                   q906433
                   BLASTX
Method
NCBI GI
                   q1710530
BLAST score
                   174
                   7.0e-30
E value
                   78
Match length
                   86
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256
                   ribosomal protein L27a - Arabidopsis thaliana
                   >gi 1107487 emb CAA63025 (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
Seq. No.
                   117054
Contig ID
                   445 7.R1010
5'-most EST
                   jC-atXLIB327425P2f07a1
Method
                   BLASTX
                   g1710530
NCBI GI
BLAST score
                   58
E value
                   3.0e-21
Match length
                   114
                   71
% identity
                   60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256
NCBI Description
                   ribosomal protein L27a - Arabidopsis thaliana
                   >gi 1107487 emb CAA63025 (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
                  117055
Seq. No.
Contig ID
                   445 10.R1010
5'-most EST
                   g2412883
Method
                   BLASTN
NCBI GI
                   g4585952
```

```
BLAST score
                   212
 E value
                   1.0e-116
                                                ·:^.
. Match length
                   250
                   95
 % identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F26F24,
                   complete sequence
                   117056
 Seq. No.
                   446 1.R1010
 Contig ID
 5'-most EST
                   jC-atXLIB327408P2f02b1
Method
                   BLASTX
NCBI GI
                   q1710581
                   856
BLAST score
                   6.0e-92
, E value
Match length
                   183
 % identity
                   93
NCBI Description
                   60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal
                   protein L9 - Arabidopsis thaliana >gi 1107489 emb CAA63024
                   (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]
                   117057
Seq. No.
                   446 2.R1010
 Contig ID
 5'-most EST
                   jC-atXP44C171E8T7079a1
Method
                   BLASTX
NCBI GI
                   g4539405
BLAST score
                   553
                   1.0e-56
E value
Match length
                   147
                   76
% identity
                   (ALO49524) putative ribosomal protein L9, cytosolic
NCBI Description
                   [Arabidopsis thaliana]
                   117058
Seq. No.
Contig ID
                   446 3.R1010
 5'-most EST
                   LIB146-030-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   g4539405
BLAST score
                   977
E value
                   1.0e-106
Match length
                   194
 % identity
                   100
                   (ALO49524) putative ribosomal protein L9, cytosolic
NCBI Description
                   [Arabidopsis thaliana]
                   117059
Seq. No.
                   447 1.R1010
 Contig ID
 5'-most EST
                   jC-atXLIB327409P2f07b1
                   BLASTX
Method
NCBI GI
                   g1076389
BLAST score
                   2961
E value
                   0.0e + 00
Match length
                   587
                   100
 % identity
                   protein phosphatase 2A pDF1 - Arabidopsis thaliana
NCBI Description
                   >gi 683502 emb CAA57528 (X82002) protein phosphatase 2A 65
```

kDa regulatory subunit [Arabidopsis thaliana]

```
Seq. No.
                  117060
                   447 2.R1010
Contig ID
                  LIB22-044-Q1-E1-F1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1076389
BLAST score
                   2786
E value
                   0.0e + 00
Match length
                   582
                   93
% identity
NCBI Description
                  protein phosphatase 2A pDF1 - Arabidopsis thaliana
                  >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65
                   kDa regulatory subunit [Arabidopsis thaliana]
                   117061
Seq. No.
                   449_1.R1010
Contig ID
5'-most EST
                  PLN_g3717945
Method
                  BLASTX
NCBI GI
                  q3717946
BLAST score
                   444
                   5.0e-44
E value
Match length
                   110
% identity
                  85
NCBI Description
                  (AJ005901) vag1 [Arabidopsis thaliana]
Seq. No.
                  117062
Contig ID
                  450_1.R1010
5'-most EST
                  PLN_g3717947
Method
                 BLASTX
                  g3717948
NCBI GI
BLAST score
                   410
                   9.0e-40
E value
                  99
Match length
% identity
                  88
                  (AJ005902) vag2 [Arabidopsis thaliana]
NCBI Description
                  117063
Seq. No.
                   452_1.R1010
Contig ID
5'-most- EST
                   jC-atXmonuni27Be06b1
Method
                  BLASTX
                  q1076287
NCBI GI
                   2345
BLAST score
                  0.0e+00
E value
                   493
Match length
% identity
NCBI Description
                  amine acid permease - Arabidopsis thaliana
                  >gi_510236_emb_CAA50672_ (X71787) amine acid permease
                   [Arabidopsis thaliana]
                  117064
Seq. No.
Contig ID
                  452 2.R1010
                  q90\overline{5}729
5'-most EST
Method
                  BLASTX
                  q1076287
NCBI GI
BLAST score .
                  405
E value
                  1.0e-42
                  121
Match length
                  84
% identity
```

5'-most EST

```
NCBI Description amine acid permease - Arabidopsis thaliana
                    >gi_510236_emb_CAA50672_ (X71787) amine acid permease
                    [Arabidopsis thaliana]
                    117065
 Seq. No.
 Contig ID
                    452 3.R1010
                    g27\overline{3}3105
 5'-most EST
 Method
                    BLASTX
                    g1076287
 NCBI GI
 BLAST score
                    374
 E value
                    1.0e-35
 Match length
                    132
 % identity
                    62
                   amine acid permease - Arabidopsis thaliana
 NCBI Description
                    >gi_510236_emb_CAA50672_ (X71787) amine acid permease
                    [Arabidopsis thaliana]
 Seq. No.
                    117066
                    452 5.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327429P3d12b2
 Method
                    BLASTX
 NCBI GI
                    g1076287
 BLAST score
                    602
 E value
                    2.0e-62
 Match length
                    131
 % identity
                   amine acid permease - Arabidopsis thaliana
 NCBI Description
                    >gi_510236_emb_CAA50672_ (X71787) amine acid permease
                   [Arabidopsis thaliana]
                    117067
 Seq. No.
 Contig ID
                    452 7.R1010
 5'-most EST
                    jC-atXmonuni27Be06a1
 Method
                    BLASTX
 NCBI GI
                    g1076287
 BLAST score
                    283
 E value
                    6.0e-37
 Match length
                    124
 % identity
 NCBI Description
                   amine acid permease - Arabidopsis thaliana
                    >gi_510236_emb_CAA50672_ (X71787) amine acid permease
                    [Arabidopsis thaliana]
                    117068
 Seq. No.
 Contig ID
                    453_1.R1010
 5'-most EST
                   PLN_g1769886
Method
                   BLASTX
 NCBI GI
                   g1769887
 BLAST score
                    2478
 E value
                    0.0e + 00
 Match length
                    481
                    97
 % identity
 NCBI Description
                    (X95736) amino acid permease 6 [Arabidopsis thaliana]
                   117069
 Seq. No.
 Contig ID
                    454 1.R1010
```

PLN g531554

5'-most EST

```
Method
                     BLASTX
  NCBI GI
                     q2827636
  BLAST score
                     2268
  E value
                     0.0e + 00
  Match length
                     439
  % identity
                     100
                     (AL021636) aspartate aminotransferase [Arabidopsis
  NCBI Description
                     thaliana]
                     117070
  Seq. No.
  Contig ID
                     454_3.R1010
                     jC-atXLIB327425P1h10b1
  5'-most EST
  Method
                     BLASTX
  NCBI GI
                     g2827636
  BLAST score
                     507
  E value
                     2.0e-51
  Match length
                     102
  % identity
                     98
                     (AL021636) aspartate aminotransferase [Arabidopsis
  NCBI Description
                     thaliana]
                     117071
  Seq. No.
  Contig ID
                     455_1.R1010
  5'-most EST
                     jC-atXLIB327412P2f03b1
  Method
                     BLASTX
  NCBI GI
                     q1076294
  BLAST score
                     953
 · E value
                     1.0e-103
  Match length
                     189
                     94
  % identity
  NCBI Description ATAF2 protein - Arabidopsis thaliana
                     117072
  Seq. No.
  Contig ID
                     456_1.R1010
  5'-most EST
                     jC-atXLIB327430P4d10b1
  Method
                     BLASTX
  NCBI GI
                     g1707364
BLAST score
                     2381
  E value
                     0.0e + 00
  Match length
                     570
  % identity
                     85
                    (X94626) AATP2 [Arabidopsis thaliana]
  NCBI Description
                     117073
  Seq. No.
  Contig ID
                     456 2.R1010
  5'-most EST
                     LIB23-041-Q1-E1-E10
  Method
                     BLASTX
                     g4138583
  NCBI GI
  BLAST score
                     138
  E value
                     0.0e + 00
  Match length
                     555
                     79
  % identity
  NCBI Description
                     (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
                     117074
  Seq. No.
                     458_1.R1010
  Contig ID
```

PLN g16145

```
Method
                    BLASTX
 NCBI GI
                    q584707
 BLAST score
                    2868
 E value
                    0.0e + 00
Match length
                    720
 % identity
                    ABSCISIC ACID-INSENSITIVE PROTEIN 3 >gi_320551_pir__JQ1676
ABI3 protein - Arabidopsis thaliana >gi_16146_emb_CAA48241_
 NCBI Description
                    (X68141) ABI3-protein [Arabidopsis thaliana]
Seq. No.
                    117075
 Contig ID
                    460 1.R1010
                    jC-atXLIB327432P3d10b1
 5'-most EST
Method
                    BLASTX
                    g2129550
NCBI GI
- BLAST score
                    2503
 E value
                    0.0e + 00
                    529
Match length
 % identity
                    calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -
NCBI Description
                    Arabidopsis thaliana >gi_2129554_pir__S71901
                    calcium-dependent protein kinase 6 - Arabidopsis thaliana
                    >gi 836940 (U20623) calcium-dependent protein kinase
                    [Arabidopsis thaliana] >gi_836944 (U20625)
                    calcium-dependent protein \overline{k}inase [Arabidopsis thaliana]
                    >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent
                    protein kinase (CDPK6) [Arabidopsis thaliana]
                    117076
Seq. No.
                    461 1.R1010
Contig ID
                    LIB22-078-Q1-E1-B7
 5'-most EST
Method
                    BLASTX
NCBI GI
                    g2129548
                    2350
BLAST score
E value
                    0.0e + 00
Match length
                    490
 % identity
NCBI Description
                    calcium-dependent protein kinase (EC 2.7.1,-) - Arabidopsis
                    thaliana >gi_2129556_pir__S71902 calcium-dependent protein
                    kinase 9 - Arabidopsis thaliana >gi_836938 (U20388)
                    calcium-dependent protein kinase [Arabidopsis thaliana]
                    >gi 836946 (U20626) calcium-dependent protein kinase
                    [Arabidopsis thaliana]
                    117077
Seq. No.
                    462 1.R1010
Contig ID
 5'-most EST
                    LIB22-010-Q1-E1-H10
Method
                    BLASTX
NCBI GI
                    q1076282
BLAST score
                    4711
                    0.0e + 00
E value
Match length
                    919
 % identity
                    aconitate hydratase (EC 4.2.1.3) - Arabidopsis thaliana
NCBI Description
                    (fragment) >gi_599625_emb_CAA58046_ (X82839) aconitase
```

[Arabidopsis thaliana]



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117078
  Seq. No.
  Contig ID
                    463 1.R1010
  5'-most EST
                    LIB146-010-Q1-E1-D5
                    BLASTX
  Method
  NCBI GI
                    q1076361
  BLAST score
                    1863
  E value
                    0.0e+00
                    362
  Match length
                    99
  % identity
                    oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) -
  NCBI Description
                    Arabidopsis thaliana >gi 2129660 pir S69197
                    oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14)
                    (clone TE 1-7) - Arabidopsis thaliana
                    >qi 804946 emb CAA85389 (Z36912) acyl-(acyl carrier
                    protein) thioesterase [Arabidopsis thaliana]
                    117079
  Seq. No.
                    465 1.R1010
  Contig ID
                    PLN_g1143387
  5'-most EST
                    BLASTX
  Method
                    g2129562
  NCBI GI
  BLAST score
                    1082
                    0.0e + 00
  E value
                    376
  Match length
  % identity
                    100
                    class III ADH, glutathione-dependent formaldehyde
  NCBI Description
                    dehydrogenase. - Arabidopsis thaliana
                    >gi 1143388 emb_CAA57973_ (X82647) class III ADH,
                    glutathione-dependent formaldehyde dehydrogenase.
                    [Arabidopsis thaliana]
                    117080
  Seq. No.
  Contig ID
                    466 1.R1010
                    LIB3176-012-P1-K1-C12
  5'-most EST
                    BLASTX
 Method
                    g728882
  NCBI GI
  BLAST score
                    941
                    1.0e-102
  E value
 Match length
                    182
  % identity
                    100
                    ADP-RIBOSYLATION FACTOR 3 >gi 541846 pir S41938
  NCBI Description
                    ADP-ribosylation factor 3 - Arabidopsis thaliana
                    >gi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3
                    [Arabidopsis thaliana]
                    117081
  Seq. No.
  Contig ID
                    467 1.R1010
  5'-most EST
                    LIB25-046-Q1-E1-C10
 Method
                    BLASTX
                    g2598227
 NCBI GI
 BLAST score
                    1545
 E value
                    1.0e-172
                    351
 Match length
* % identity
 NCBI Description
                    (AJ222585) AT-hook protein 1 [Arabidopsis thaliana]
```

12547

117082

Seq. No.

```
468 1.R1010
Contig ID
5'-most EST
                  LIB22-004-Q1-E1-E4
Method
                  BLASTX
                  g2791900
NCBI GI
BLAST score
                  2069
E value
                  0.0e + 00
Match length
                  413
% identity
                  93
NCBI Description
                  (AJ000057) PP7 [Arabidopsis thaliana]
Seq. No.
                  117083
Contig ID
                  469 1.R1010
5'-most EST
                  jC-atXLIB327430P3e10b1
                  BLASTX
Method -
NCBI GI
                  q3036819
BLAST score
                  3876
E value
                  0.0e + 00
Match length
                  776
                  98
% identity
NCBI Description (AJ000058) MCM3 homolog [Arabidopsis thaliana]
Seq. No.
                  117084
Contig ID
                  470 1.R1010
5'-most EST
                  LIB35-052-Q1-E1-G6
                  BLASTX
Method
NCBI GI
                  q2281631
BLAST score
                  1075
E value
                  1.0e-117
Match length
                  248
                  85
% identity
NCBI Description
                  (AF003096) AP2 domain containing protein RAP2.3
                  [Arabidopsis thaliana]
                  117085
Seq. No.
Contig ID
                  470 2.R1010
5'-most EST
                  ARABL1-047-Q1-B1-D11
                  BLASTX
Method
NCBI GI
                  q2467088
BLAST score
                  1014
E value
                  1.0e-110
Match length
                  246
                  80
% identity
NCBI Description
                  (AJ001911) putative Ckc2 [Arabidopsis thaliana]
                  117086
Seq. No.
                  470 5.R1010
Contig ID
5'-most EST
                  g24<u>1</u>4092
Method
                  BLASTX
                  q2281631
NCBI GI
BLAST score
                  516
E value
                  3.0e-52
Match length
                  171
% identity
                  (AF003096) AP2 domain containing protein RAP2.3
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  117087
```

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470 7.R1010
Contig ID
5'-most EST
                   iC-atXP78C229K16T7b1
                   BLASTX
Method
NCBI GI
                   q2281631
BLAST score
                   467
E value
                   2.0e-53
                   147
Match length
% identity
                   76
                   (AF003096) AP2 domain containing protein RAP2.3
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   117088
                   470 8.R1010
Contig ID
                   g10\overline{5}3593
5'-most EST
Method
                   BLASTX
                   q2281631
NCBI GI
BLAST score
                   562
                   9.0e-58
E value
Match length
                   174
                   70
% identity
                   (AF003096) AP2 domain containing protein RAP2.3
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   117089
                   471 1.R1010
Contig ID
                   jC-atXLIB327403P3a10b2
5'-most EST
                   BLASTX
Method
                   g2569931
NCBI GI
BLAST score
                   2206
                   0.0e + 00
E value
Match length
                   431
% identity
                   (AJ002280) shaggy-like kinase beta [Arabidopsis thaliana]
NCBI Description
                   117090
Seq. No.
                   472 1.R1010
Contig ID
5'-most EST
                   LIB24-004-Q1-E1-G1
                   BLASTX
Method
NCBI GI
                   q4127417
BLAST score
                   2307
                   0.0e + 00
E value
Match length
                   514
% identity
                   (AJ002399) monosaccharide transporter [Arabidopsis
NCBI Description
                   thaliana]
                   117091
Seq. No.
                   473 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327412P2b03b1
Method
                   BLASTX
NCBI GI
                   g2459445
BLAST score
                   578
                   6.0e-59
E value
                   411
Match length
                   36
% identity
                   (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                   thaliana]
```

```
117092
Seq. No.
                  473 2.R1010
Contig ID
5'-most EST
                  LIB25-038-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                  g2459445
                  205
BLAST score
                  6.0e-16
E value
Match length
                  57
                  33
% identity
NCBI Description
                  (AC002332) putative ribonucleoprotein [Arabidopsis
                  thaliana]
                  117093
Seq. No.
                   474 1.R1010
Contig ID
5'-most EST
                  PLN_g3962376
                  BLASTX.
Method
                  g3962377
NCBI GI
BLAST score
                  3067
                  0.0e + 00
E value
                  650
Match length
                  93
% identity
NCBI Description
                  (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
                  117094
Seq. No.
                  475 1.R1010
Contig ID
                  jC-atXP19C111P2T7d2
5'-most EST
                  BLASTX
Method
                  g4006869
NCBI GI
                  1881
BLAST score
                  0.0e + 00
E value
                   400
Match length
                  93
% identity
                  (Z99707) patatin-like protein [Arabidopsis thaliana]
NCBI Description
                  117095
Seq. No.
Contig ID
                  475 2.R1010
5'-most EST
                  jC-atXP62C203B6T7d2
                  BLASTX
Method
                  g4006871
NCBI GI
BLAST score
                  332
                  3.0e-66
E value
                  219
Match length
% identity
NCBI Description
                  (Z99707) patatin-like protein [Arabidopsis thaliana]
                  117096
Seq. No.
                  476 1.R1010
Contig ID
5'-most EST
                  g2764343
Method
                  BLASTX
NCBI GI
                  g2632061
BLAST score
                  2168
                  0.0e + 00
E value
Match length
                  419
                  100
% identity
                  (AJ002597) membrane-associated salt-inducible protein like
NCBI Description
```

[Arabidopsis thaliana]

Match length

.

```
117097
Seq. No.
                  477 1.R1010
Contig ID
                  jC-atXLIB327424P1b08b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2281645
                  811
BLAST score
                  1.0e-86
E value
Match length
                  259
                  64
% identity
                   (AF003103) AP2 domain containing protein RAP2.10
NCBI Description
                   [Arabidopsis thaliana] >gi_2632063_emb_CAA05630_ (AJ002598)
                  TINY-like protein [Arabidopsis thaliana]
                  117098
Seq. No.
                  478 1.R1010
Contig ID
                  jC-atXLIB327408P1g07b1
5'-most EST
Method
                  BLASTX
                  g2826811
NCBI GI
BLAST score
                  618
                  4.0e-64
E value
                  120
Match length
                  100
% identity
NCBI Description
                  (AJ002892) AtGRP2 [Arabidopsis thaliana]
                  117099
Seq. No.
                  478 3.R1010
Contig ID
5'-most EST
                  g16\overline{5}81
                  BLASTX
Method
                  g4455314
NCBI GI
                  271
BLAST score
                  2.0e-23
E value
Match length
                  174
                   99
% identity
                   (AL035528) glycine-rich RNA-binding protein AtGRP2-like
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  117100
                   479 1.R1010
Contig ID
5'-most EST
                  PLN_g2654225
Method
                  BLASTX
                  g2654226
NCBI GI
BLAST score
                   5088
                  0.0e + 00
E value
Match length
                  1067
% identity
                   (AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis
NCBI Description
                  thaliana]
                  117101
Seq. No.
Contig ID
                   479 2.R1010
5'-most EST
                   jC-atXLIB327422P4d04b1
Method
                  BLASTX
                  g2654226
NCBI GI
BLAST score
                   258
E value
                   3.0e-22
                   75
```

NCBI GI

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% identity
                    (AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis
 NCBI Description
                   thaliana]
                   117102
Seq. No.
                   481 1.R1010
 Contig ID
                   LIB23-057-Q1-E1-H9
 5'-most EST
                   BLASTX
 Method
                   q2956690
 NCBI GI
 BLAST score
                    584
 E value
                    4.0e-60
 Match length
                   180
 % identity
                    (AJ223306) PSBY [Arabidopsis thaliana] >gi 3414928
 NCBI Description
                    (AF079800) PsbY precursor [Arabidopsis thaliana]
                   117103
 Seq. No.
                   482 1.R1010
 Contig ID
 5'-most EST
                   PLN g3641844
                   BLASTX
 Method
                   g3641845
 NCBI GI
 BLAST score
                    4079
                   0.0e+00
 E value
                   811
 Match length
 % identity
                   98
                   (AJ223358) stelar K+ outward rectifying channel
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    117104
                    483 1.R1010
 Contig ID
                    jC-\overline{a}lXLIB327435P4d02b1
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   q2826882
 BLAST score
                    538
                   1.0e-54
 E value
 Match length
                   106
 % identity
                    100
                    (AJ223634) transcription factor IIA small subunit .
 NCBI Description
                    [Arabidopsis thaliana]
                    117105
 Seq. No.
                    484_1.R1010
 Contig ID
                    PLN_g1429225
 5'-most EST
 Method
                    BLASTX
                    q2826884
 NCBI GI
 BLAST score
                    1593
                    1.0e-178
 E value
 Match length
                    375
                    83
 % identity
 NCBI Description
                    (AJ223635) transcription factor IIA large subunit
                    [Arabidopsis thaliana]
                    117106
 Seq. No.
                    484 2.R1010
 Contig ID
 5'-most EST
                    jC-atXP34C149G7T7a1
 Method
                    BLASTX
```

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g2826884

Method

BLASTX

```
281
BLAST score
                   1.0e-38
E value
Match length
                   115
% identity
                   68
NCBI Description
                   (AJ223635) transcription factor IIA large subunit
                   [Arabidopsis thaliana]
Seq. No.
                  117107
                   484_3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327422P2h08b2
Method
                  BLASTX
NCBI GI
                  q1429226
BLAST score
                   455
E value
                   3.0e-45
Match length
                  103
% identity
                  86
NCBI Description
                  (X98861) TFIIA [Arabidopsis thaliana]
                  117108
Seq. No.
                   484 4.R1010
Contig ID
                   jC-atXLIB327433P1f02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2826884
BLAST score
                  55.8
                   2.0e-57
E value
                                                                     ... ↑ .
                  123
Match length
% identity
                  85
NCBI Description
                   (AJ223635) transcription factor IIA large subunit
                   [Arabidopsis thaliana]
                  117109
Seq. No.
                   485 1.R1010
Contig ID
5'-most EST
                  PLN_g2916771
Method
                  BLASTX
NCBI GI
                  q2894604
BLAST score
                  1361
                  0.0e + 00
E value
                  436
Match length
                                        6
% identity
                  78
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
                  117110
Seq. No.
                   486 1.R1010
Contig ID
                  jC-atXLIB327421P3a01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3819710
                  2375
BLAST score
E value
                  0.0e + 00
Match length
                  449
% identity
                  (AJ224161) delta-8 sphingolipid desaturase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  117111
Contig ID
                  486 2.R1010
5'-most EST
                  jC-alXLIB327436P4b09b1
```

```
NCBI GI
                   q3819710
BLAST score
                   422
                   3.0e-44
E value
Match length
                   100
% identity
                   91
                   (AJ224161) delta-8 sphingolipid desaturase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   117112
                   487 1.R1010
Contig ID
                   PLN_g3549638
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3549639
BLAST score
                   2150
E value
                   0.0e + 00
Match length
                   444
                   93:
% identity
NCBI Description
                  (AJ005194) receiver-like protein 3 [Arabidopsis thaliana]
                   117113
Seq. No.
Contig ID
                   490 1.R1010
5'-most EST
                   LIB23-036-Q1-E1-H5
Method
                   BLASTX
NCBI GI
                   q3046700
BLAST score
                   1510
E value
                   1.0e-168
Match length
                   301
% identity
                   (AJ005261) cytidine deaminase [Arabidopsis thaliana]
NCBI Description
                   >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase
                   [Arabidopsis thaliana] >gi_4191787 (AC005917) putative
                   cytidine deaminase [Arabidopsis thaliana]
                   117114
Seq. No.
Contig ID
                   491_1.R1010
5'-most EST
                   jC-atX23022Q2E1C11a1
                   BLASTX
Method
NCBI GI
                   q3123331
BLAST score
                   2412
E value
                   0.0e + 00
Match length
                   509
% identity
                   93
                   (AJ005930) squalene epoxidase homologue [Arabidopsis
NCBI Description
                   thaliana]
                   117115
Seq. No.
Contig ID
                   492_1.R1010
5'-most EST
                  PLN_g3123328
                   BLASTX
Method
NCBI GI
                   q3123329
BLAST score
                   2632
E value
                   0.0e + 00
Match length
                   516
% identity
                   100
NCBI Description
                   (AJ005929) squalene epoxidase homologue [Arabidopsis
```

thaliana)

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Seq. No.
                   117116
                   494 1.R1010
Contig ID
                   PLN g3281845
 5'-most EST
                   BLASTX
Method
NCBI GI
                   g3281846
BLAST score
                   2702
E value
                   0.0e+00 /
Match length
                   645
                   83
 % identity
NCBI Description
                   (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]
Seq. No.
                   117117
                   495 1.R1010
Contig ID
 5'-most EST
                   iC-atXP89C242K5T7033d1
                   BLASTX
Method
NCBI GI
                   g2664210
BLAST score
                   2683
                   0.0e + 00
E value
                   565
Match length
 % identity
                   (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   117118
                   496_1.R1010
Contig ID
 5'-most EST
                   PLN g2664211
                   BLASTX
Method
NCBI GI
                   g2664212
 BLAST score
                   1438
                   1.0e-160
 E value
                   276
Match length
                   100
 % identity
NCBI Description
                   (AJ222645) asparaginyl-tRNA synthetase [Arabidopsis
                   thaliana]
 Seq. No.
                   117119
                   497_1.R1010
 Contig ID
 5'-most EST
                   PLN g2664213
 Method
                   BLASTX
                   q2664214
 NCBI GI
 BLAST score
                   4502
 E value
                   0.0e + 00
                   940
Match length
 % identity
 NCBI Description
                   (AJ222646) G2484-1 [Arabidopsis thaliana]
Seq. No.
                   117120
                   498_1.R1010
 Contig ID
                   PLN_g2243115
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   q4376158
 BLAST score
                   2773
 E value
                   0.0e + 00
 Match length
                   569
 % identity
                   98
                   (X98873) aspartate kinase [Arabidopsis thaliana]
 NCBI Description
```

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Seq. No.
                   117121
                499 1.R1010
Contig ID
5'-most EST
                  LIB22-021-Q1-E1-A4
                  BLASTX
Method
NCBI GI
                   g1890152
BLAST score
                   2513
                 .0.0e+00
E value
Match length
                   517
% identity
                   95
NCBI Description
                  (X92510) allene oxide synthase [Arabidopsis thaliana]
Seq. No.
                   117122
Contig ID
                   500_1.R1010
                  jC-atXLIB327413P4a06b1
5'-most EST
                   BLASTX
Method
NCBI GI
                  g1888357
BLAST score
                   5072
E value
                   0.0e + 00
Match length
                   1019
                   96
% identity
NCBI Description
                  (X98130) alpha-mannosidase [Arabidopsis thaliana]
                  >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
                   117123
Seq. No.
Contig ID
                  500 4.R1010
5'-most EST
                  g2393269
Method
                  BLASTN
                  g1890153
NCBI GI
BLAST score
                   350
E value
                   0.0e + 00
Match length
                   382
                  98
% identity
NCBI Description A.thaliana mRNA for alpha-mannosidase precursor
Seq. No.
                  117124
Contig ID
                   501_1.R1010
5'-most EST
                  PLN_g2462926
Method
                  BLASTX
NCBI GI
                  g2462927
BLAST score
                  2296
E value
                  0.0e + 00
Match length
                   457
                   96
% identity
NCBI Description
                  (Y10342) putative amidase [Arabidopsis thaliana]
                  117125
Seq. No.
                  502 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P4b12b1
Method
                  BLASTX
NCBI GI
                  g1703292
BLAST score
                  2291
                 0.0e+00
E value
Match length
                  501
                  87
% identity
NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER >gi 551219 emb CAA53473_
                   (X75879) amt1 [Arabidopsis thaliana]
```

NCBI Description

```
>gi_4678377_emb_CAB41109.1_ (AL049656) ammonium transport
                   protein (AMT1) [Arabidopsis thaliana]
                   117126
Seq. No.
                   503 1.R1010
Contig ID
                   jC-atXLIB327430P4f12b1
5'-most EST
                   BLASTX
Method
                   q1621539
NCBI GI
BLAST score
                   1585
E value
                   1.0e-177
Match length
                   317
% identity
                   98
                   (U28415) annexin-like protein [Arabidopsis thaliana]
NCBI Description
                   117127
Seq. No.
                   503 2.R1010
Contig ID
                   jC-\overline{a}tXP96C248D24T7b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1621539
BLAST score
                   867
E value
                   2.0e-93
Match length
                   177
% identity
                   97
                  (U28415) annexin-like protein [Arabidopsis thaliana]
NCBI Description
                   117128
Seq. No.
Contig ID
                   503_3.R1010
5'-most EST
                  LIB23-046-Q1-E1-C11
Method
                   BLASTX
NCBI GI
                   q1621539
BLAST score
                   573
                   5.0e-59
E value
Match length
                   119
% identity
                   44
NCBI Description
                   (U28415) annexin-like protein [Arabidopsis thaliana]
Seq. No.
                   117129
Contig ID
                   503 4.R1010
5'-most EST
                  LIB3234-071-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q1621539
BLAST score
                   295
E value
                   2.0e-61
Match length
                   167
% identity
                   78
                  (U28415) annexin-like protein [Arabidopsis thaliana]
NCBI Description
                   117130
Seq. No.
                   503 7.R1010
Contig ID
5'-most EST
                  LIB23-028-Q1-E1-E1
Method
                  BLASTX
NCBI GI
                   q1429207
BLAST score
                   765
                   2.0e-81
E value
Match length
                  152
% identity
                   69
                  (X99224) annexin [Arabidopsis thaliana]
```

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117131
Seq. No.
Contig ID
                  503 8.R1010
5'-most EST
                  jC-atXLIB327438P2f08a1
Method
                  BLASTX
NCBI GI
                  q1429207
BLAST score
                   123
                   2.0e-62
E value
                   162
Match length
% identity
NCBI Description
                   (X99224) annexin [Arabidopsis thaliana]
                  117132
Seq. No.
                   504_1.R1010
Contig ID
                  PLN_g2959319
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2959320
                   1031
BLAST score
                  1.0e-112
E value
                  234
Match length
                  90
% identity
NCBI Description
                  (Z97057) ANR1, MADS-box protein [Arabidopsis thaliana]
Seq. No.
                  117133
                   507_1.R1010
Contig ID
5'-most EST
                  q2763811
Method
                  BLASTX
NCBI GI
                  q3915600
BLAST score
                   377
                   3.0e-36
E value
                  80
Match length
% identity
                  85
NCBI Description
                  CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 PRECURSOR (AFP1)
                   (ANTHER-SPECIFIC PROTEIN HOMOLOG) >gi_1592668_emb_CAA63009_
                   (X91916) anther-specific protein homologue [Arabidopsis
                  thaliana] >gi_4105700_gb_AAD02502_ (AF049870) antifungal
                  protein [Arabidopsis thaliana]
Seq. No.
                   117134
Contig ID
                   508 1.R1010
5'-most EST
                   jC-atXLIB327416P3d09b1
Method
                  BLASTX
NCBI GI
                   g478713
BLAST score
                   1232
E value
                   1.0e-136
Match length
                  256
                  95
% identity
                  AP1 protein - Arabidopsis thaliana >gi 383297 prf 1902329A
NCBI Description
                  APETALA1 gene [Arabidopsis thaliana]
                  117135
Seq. No.
Contig ID
                  510 1.R1010
5'-most EST
                  jC-atXLIB327406P2g12b1
Method
                  BLASTX
NCBI GI
                  g2129629
BLAST score
                  1348
E value
                  1.0e-149
```

```
Match length
                   287
% identity
                   91
NCBI Description
                   L-ascorbate peroxidase (EC 1.11.1.11) - Arabidopsis
                   thaliana >gi_1332439_emb_CAA66640_ (X98003) ascorbate peroxidase [Arabidopsis thaliana] >gi_1523791_emb_CAA66926_
                   (X98276) L-ascorbate peroxidase [Arabidopsis thaliana]
                   >gi_2444019 (U69138) ascorbate peroxidase 3 [Arabidopsis
                   thaliana] >gi_2924511_emb_CAA17765.1_ (AL022023)
                   L-ascorbate peroxidase [Arabidopsis thaliana]
                   117136
Seq. No.
Contig ID
                   511 1.R1010
5'-most EST
                   LIB24-087-Q1-E1-A7
                   BLASTX
Method
NCBI GI
                   q399046
BLAST score
                   910
E value
                   3.0e-98
Match length
                   183
                   100
% identity
                   ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT)
NCBI Description
                   >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC
                   2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_
                   (X58640) adenine phosphoribosyltransferase [Arabidopsis
                   thaliana] >gi_433050 (L19637) adenine
                   phosphoribosyltransferase [Arabidopsis thaliana]
                   >gi 3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]
                   117137
Seq. No.
Contig ID
                   511 2.R1010
5'-most EST
                   jC-atXLIB327433P1f06b1
                   BLASTX
Method
NCBI GI
                   q399046
BLAST score
                   440
E value
                   1.0e-43
Match length
                   89
                   99
% identity
NCBI Description
                   ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT)
                   >gi 99657 pir S20867 adenine phosphoribosyltransferase (EC
                   2.4.2.7) - Arabidopsis thaliana >gi_16164 emb_CAA41497
                   (X58640) adenine phosphoribosyltransferase [Arabidopsis
                   thaliana] >gi 433050 (L19637) adenine
                   phosphoribosyltransferase [Arabidopsis thaliana]
                   >gi 3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]
                   117138
Seq. No.
                   512 1.R1010
Contig ID
5'-most EST
                   LIB23-036-Q1-E1-E4
Method
                   BLASTX
                   g2499931
NCBI GI
BLAST score
                   899
E value
                   4.0e-97
Match length
                   192
% identity
                   93
.NCBI Description
                   ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)
                   >gi 2129534 pir S71272 adenine phosphoribosyltransferase
                   (EC 2.4.2.7) - Arabidopsis thaliana
```

Method

NCBI GI BLAST score BLASTX q99735

869

phosphoribosyltransferase [Arabidopsis thaliana] 117139 Seq. No. 514 1.R1010 Contig ID LIB3168-043-P1-K1-B1 5'-most EST BLASTX Method NCBI GI q3176874 BLAST score 3641 0.0e + 00E value 742 Match length % identity 95 (AF065639) cucumisin-like serine protease [Arabidopsis NCBI Description thaliana] 117140 Seq. No. 514 2.R1010 Contig ID :: jC-atXLIB327440P1f11a1 5'-most EST Method BLASTX g1076414 NCBI GI BLAST score 754 E value 2.0e-80 Match length 153 % identity 94 subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis NCBI Description thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974) subtilisin-like protease [Arabidopsis thaliana] Seq. No. 117141 515 1.R1010 Contig ID 5'-most EST jC-atXLIB327422P3f09b2 Method BLASTX NCBI GI q99735 BLAST score 788 E value 1.0e-130 Match length 263 % identity 87 L-ascorbate peroxidase (EC 1.11.1.11) precursor -NCBI Description Arabidopsis thaliana (fragment) 117142 Seq. No. 515 2.R1010 Contig ID 5'-most EST jC-atXP112C129P9T7d2 Method BLASTX NCBI GI q99735 BLAST score 754 E value 4.0e-80 Match length 191 % identity NCBI Description L-ascorbate peroxidase (EC 1.11.1.11) precursor -Arabidopsis thaliana (fragment) 117143 Seq. No. Contig ID 515 5.R1010 5'-most EST g2763232

garage .

Seq. No.

117148

```
2.0e-93
E value
                   272
Match length
                   69
% identity
                   L-ascorbate peroxidase (EC 1.11.1.11) precursor -
NCBI Description
                   Arabidopsis thaliana (fragment)
                                       4
                   117144
Seq. No.
                   515 7.R1010
Contig ID
                   g27<del>6</del>3935
5'-most EST
Method
                   BLASTX
NCBI GI
                   q99735
BLAST score
                   537
E value
                   8.0e-55
Match length
                   147
% identity
                   78
NCBI Description
                   L-ascorbate peroxidase (EC 1.11.1.11) precursor -
                   Arabidopsis thaliana (fragment)
Seq. No.
                   117145
                   516 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327410P2a05b1
Method
                   BLASTX
NCBI GI
                   g2129738
BLAST score
                   2097
E value
                   0.0e+00
Match length
                   393
% identity
                   100
                   shaggy-like kinase dzeta - Arabidopsis thaliana
>gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta
NCBI Description
                   [Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300)
                   serine/threonine kinase [Arabidopsis thaliana]
Seq. No.
                   117146
                   517_1.R1010
Contig ID
                   PLN_g1480077
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1480078
BLAST score
                   2042
E value
                   0.0e + 00
Match length
                   387
% identity
                   100
NCBI Description
                   (X99696) shaggy-like protein kinase iota [Arabidopsis
                   thaliana] >gi 2444277 gb AAB71545.1 (AF019927)
                   GSK3/shaggy-like protein kinase [Arabidopsis thaliana]
                   117147
Seq. No.
                   518_1.R1010
Contig ID
5'-most EST
                   PLN_g1504062
Method
                   BLASTX
NCBI GI
                   q1504063
BLAST score
                   1996
E value
                   0.0e + 00
Match length
                   375
% identity
NCBI Description
                  (Y07597) shaggy-like kinase kappa [Arabidopsis thaliana]
```

```
Contig ID
                   519 1.R1010
5'-most EST
                   jC-atXP27C134D1T7d2
Method
                   BLASTX
NCBI GI
                   g2129739
BLAST score
                   2000
E value
                   0.0e + 00
Match length
                   380
% identity
                   shaggy-like kinase etha - Arabidopsis thaliana
>gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha
NCBI Description
                   [Arabidopsis thaliana] >gi_1627516_emb_CAA70144 (Y08947)
                   shaggy-like kinase etha [Arabidopsis thaliana]
                   117149
Seq. No.
                   519_2.R1010
Contig ID
5'-most EST
                   jC-a1X25087Q1E1B05b1
Method
                   BLASTX
NCBI GI
                   g4539390
BLAST score
                   268
E value
                   2.0e-23
Match length
                   89
                   66
% identity
NCBI Description
                   (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-)
                   [Arabidopsis thaliana]
Seq. No.
                   117150
Contig ID
                   520 1.R1010
5'-most EST
                   jC-atXP85C241G2T7b1
Method
                   BLASTX
NCBI GI
                   q399013
BLAST score
                   1820
E value
                   0.0e + 00
Match length
                   378
% identity
                   93
                   ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                   >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                   thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549)
                   adenylate translocator [Arabidopsis thaliana]
                   >gi 445607 prf 1909354A adenylate translocator
                   [Arabidopsis thaliana]
Seq. No.
                   117151
Contig ID
                   520 3.R1010
5'-most EST
                   g931298
Method
                   BLASTX
                   g399013
NCBI GI
BLAST score
                   372
E value
                   2.0e-35
Match length
                   138
% identity
                   ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                   >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                   thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549)
                   adenylate translocator [Arabidopsis thaliana]
```

>gi 445607 prf 1909354A adenylate translocator

Contig ID 5'-most EST

Method

q2446131

BLASTX

[Arabidopsis thaliana]

```
Seq. No.
                     117152
                     520 4.R1010
Contig ID
5'-most EST
                     jC-atXLIB327437P3f08a1
Method
                     BLASTX
                     q399013
NCBI GI
BLAST score
                     533
E value
                     3.0e-54
Match length
                     109
% identity
                     60
                     ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                     (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                     >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                     thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana]
                     >gi 445607 prf 1909354A adenylate translocator
                     [Arabidopsis thaliana]
                     117153
Seq. No.
Contig ID
                     520 5.R1010
5'-most EST
                     g1269239
Method
                     BLASTX
NCBI GI
                     q399013
BLAST score
                     480
                     3.0e-48
E value
Match length
                     103
% identity
                     ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                     (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                     >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                     thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana]
                     >gi_445607_prf__1909354A adenylate translocator
                     [Arabidopsis thaliana]
                     117154
Seq. No.
Contig ID
                     520 6.R1010
5'-most EST
                     jC-atXP73C223F9T7d2
Method
                     BLASTX
NCBI GI
                     g399013
BLAST score
                     303
E value
                     1.0e-106
Match length
                     393
% identity
                     59
NCBI Description
                     ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                     (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                     >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                     thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana]
                     >gi 445607 prf__1909354A adenylate translocator
                     [Arabidopsis thaliana]
                     117155
Seq. No.
                     520 7.R1010
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NCBI GI
                  q444790
BLAST score
                  206
E value
                  5.0e-16
Match length
                  70
                  67
% identity
NCBI Description nucleotide translocator [Arabidopsis thaliana]
Seq. No.
                  117156
                  521_1.R1010
Contig ID
5'-most EST
                  PLN_g398603
Method
                  BLASTX
                  q480618
NCBI GI
                  1253
BLAST score
                  1.0e-138
E value
                  229
Match length
                  100
% identity
NCBI Description
                  ATAF1 protein - Arabidopsis thaliana (fragment)
                  >gi 1345506 emb CAA52771 (X74755) ATAF1 [Arabidopsis
                  thaliana]
                  117157
Seq. No.
                  523 1.R1010
Contig ID
                  jC-atXLIB327413P1e08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1168546
BLAST score
                  1361
E value
                  1.0e-151
Match length
                  312
% identity
                  86
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-5 (HD-ZIP PROTEIN
NCBI Description
                  ATHB-5) >gi_629504_pir__S47135 homeotic protein Athb-5 -
                  Arabidopsis thaliana >gi_499160_emb_CAA47426_ (X67033)
                  Athb-5 [Arabidopsis thaliana]
                  117158
Seq. No.
                  524 1.R1010
Contig ID
                  jC-atXLIB327409P1c04b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1168547
BLAST score
                  1196
E value
                  1.0e-131
Match length
                  311
% identity
                  77
NCBI Description
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-6 (HD-ZIP PROTEIN
                  ATHB-6) >gi_629505_pir__S47136 homeotic protein Athb-6 -
                  Arabidopsis thaliana >gi_499162_emb_CAA47427_ (X67034)
                  Athb-6 [Arabidopsis thaliana]
Seq. No.
                  117159
Contig ID
                  524 2.R1010
5'-most EST
                  jC-atXLIB327423P1e04b1
Method
                  BLASTX
NCBI GI
                  q1168547
BLAST score
                  208
E value
                  1.0e-100
Match length
                  233
% identity
                  79
```

```
NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-6 (HD-ZIP PROTEIN
                  ATHB-6) >gi_629505_pir___S47136 homeotic protein Athb-6 -. Arabidopsis thaliana >gi_499162_emb_CAA47427_ (X67034)
                   Athb-6 [Arabidopsis thaliana]
Seq. No.
                   117160
                   524 3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327423P2e04b1
Method
                   BLASTX
NCBI GI
                   q4544459
BLAST score
                   382
E value
                   2.0e-36
Match length
                   161
                   57
% identity
                   (AC006592) homeobox-leucine zipper protein ATHB-6
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   117161
                   525_1.R1010
Contig ID
                   jC-atXLIB327417P2b07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1168548
BLAST score
                   1106
E value
                   1.0e-121
Match length
                   260
% identity
                   82
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-7 (HD-ZIP PROTEIN
NCBI Description
                  ATHB-7) >gi_629527_pir__S47137 homeotic protein Athb-7 -
                  Arabidopsis thaliana >gi 499164 emb CAA47425 (X67032) orf
                   [Arabidopsis thaliana]
                   117162
Seq. No.
Contig ID
                   526 1.R1010
                   jC-atXLIB327403P3g09b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1361991
BLAST score
                   1551
E value
                   1.0e-173
Match length
                   311
% identity
                   95
NCBI Description
                  homeotic protein ATK1 - Arabidopsis thaliana
                   >gi 984046 emb CAA57122 (X81354) ATK1 [Arabidopsis
                   thaliana] >gi 984048 emb CAA57121 (X81353) ATK1
                   [Arabidopsis thaliana]
                   117163
Seq. No.
                   527_1.R1010
Contig ID
5'-most EST
                  PLN_g297068
Method
                  BLASTX
NCBI GI
                   q479413
                   5690
BLAST score
E value
                   0.0e + 00
Match length
                  1159
% identity
                  97
NCBI Description myosin-like protein - Arabidopsis thaliana
```

117164

Seq. No.

```
Contig ID
                  530 1.R1010
5'-most EST
                  jC-atXLIB327433P1g02b1
                  BLASTX
Method
NCBI GI
                  q1546688
BLAST score
                  1530
E value
                1.0e-171
                  325
Match length
% identity
                  (X98802) peroxidase ATP11a [Arabidopsis thaliana]
NCBI Description
                  >gi_2388572 (AC000098) Strong similarity to Arabidopsis
                  peroxidase ATP11A (gb_X98802). [Arabidopsis thaliana]
                  >gi_2388573 (AC000098) Strong similarity to Arabidopsis
                  peroxidase ATP11A (gb_X98802). [Arabidopsis thaliana]
                  117165
Seq. No.
Contig ID
                  531 1.R1010
5'-most EST
                  LIB3177-016-P1-K2-E5
Method
                  BLASTX
                  g1546690
NCBI GI
BLAST score
                  1691
E value
                  0.0e + 00
Match length
                  331
% identity
                  100
NCBI Description
                  (X98803) peroxidase ATP14a [Arabidopsis thaliana]
                  117166
Seq. No.
                  532_1.R1010
Contig ID
                  PLN_g1546691
5'-most EST
Method .
                  BLASTX
NCBI GI
                  g1546692
BLAST score
                  1687
                  0.0e+00
E value
Match length
                  326
% identity
                  100
NCBI Description
                  (X98805) peroxidase ATP19a [Arabidopsis thaliana]
                  117167
Seq. No.
                  533_1.R1010
Contig ID
5'-most EST
                  PLN_g1546693
Method
                  BLASTX
NCBI GI
                  g1546694
BLAST score
                  1522
E value
                  1.0e-170
Match length
                  330
                  91
% identity
NCBI Description
                  (X98806) peroxidase ATP20a [Arabidopsis thaliana]
Seq. No.
                  117168
                  534_1.R1010
Contig ID
5'-most EST
                  jC-atXP118C155J23T7016d2
Method
                  BLASTX
NCBI GI
                  g1546696
BLAST score
                  1705
                  0.0e+00
E value
Match length
                  329
% identity
NCBI Description (X98807) peroxidase ATP21a [Arabidopsis thaliana]
```

```
Seq. No.
                   117169
                   535 1.R1010
 Contig ID
 5'-most EST
                   jC-atXP74C224N7T7071d1
 Method
                   BLASTX
 NCBI GI
                   g1546698
BLAST score
                   1524
 E value
                   1.0e-170
Match length
                   296
 % identity
                   100
NCBI Description (X98808) peroxidase ATP3a [Arabidopsis thaliana]
                   117170
 Seq. No.
 Contig ID
                   535 2.R1010
 5'-most EST
                   g2759567
                   BLASTX
Method
NCBI GI
                   q1546698
BLAST score
                   266
                   3.0e-30
E value
Match length
                   97
                   77
 % identity
NCBI Description
                   (X98808) peroxidase ATP3a [Arabidopsis thaliana]
Seq. No.
                   117171
                   535 3.R1010
Contig ID
 5'-most EST
                   jC-atXLIB327412P4d11b1
Method
                   BLASTX
NCBI GI
                   g1546698
BLAST score
                   661
                   3.0e-69
E value
                   176
Match length
 % identity
                   83
NCBI Description
                   (X98808) peroxidase ATP3a [Arabidopsis thaliana]
Seq. No.
                   117172
 Contig ID
                   536 1.R1010
                   jC-atXLIB327404P2b02b1
 5'-most EST
Method
                   BLASTX
NCBI GI
                   g1546700
BLAST score
                   1735
                   0.0e + 00
E value
Match length
                   346
                   96
 % identity
NCBI Description
                   (X98804) peroxidase ATP18a [Arabidopsis thaliana]
 Seq. No.
                   117173
                   537_1.R1010
 Contig ID
 5'-most EST
                   PLN_g1546701
Method
                   BLASTX
NCBI GI
                   q1546702
BLAST score
                   1599
                   1.0e-179
E value
Match length
                   350
 % identity
                   89
NCBI Description
                   (X98809) peroxidase ATP5a [Arabidopsis thaliana]
                   117174
 Seq. No.
```

Match length

138

```
538 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327440P1a05b1
Method
                   BLASTX
NCBI GI
                   g1403134
BLAST score
                   1671
                   0.0e + 00
E value
Match length
                   328
% identity
                   100
NCBI Description
                   (X98453) peroxidase [Arabidopsis thaliana]
Seq. No.
                   117175
                   539 1.R1010
Contig ID
                   LIB22-019-Q1-E1-A12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q99736
BLAST score
                   3423
                   0.0e + 00
E value
Match length
                   692
% identity
                   96
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
NCBI Description
                   Arabidopsis thaliana >gi_16187_emb_CAA46814_ (X66016)
                   NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
                   117176
Seq. No.
                   540 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327413P1c04b1
Method
                   BLASTX
NCBI GI
                  q99737
BLAST score
                   3432
                   0.0e + 00
E value
Match length
                   700
% identity
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
NCBI Description
                   Arabidopsis thaliana >gi 16189 emb CAA46815 (X66017)
                   NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
                   117177
Seq. No.
                   540 3.R1010
Contig ID
                   jC-atXP95CG11G5T7023d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q99737
BLAST score
                   687
E value
                   2.0e-72
Match length
                   156
% identity
                   85
NCBI Description
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
                - Arabidopsis thaliana >gi 16189 emb CAA46815 (X66017)
                  NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
                  117178
Seq. No.
                   540 5.R1010
Contig ID
                   jC-atXLIB327429P2b12b1
5'-most EST
                   BLASTX
Method
                  g99737
NCBI GI
                  730 ·
BLAST score
                   1.0e-77
E value
```

```
97
% identity
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
NCBI Description
                  Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017)
                  NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
Seq. No.
                   117179
                   541 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327438P4a05b2
Method
                   BLASTX
NCBI GI
                   q4678921
BLAST score
                   759
E value
                   1.0e-80
Match length
                   150
                   99
% identity
                   (AL049711) putative calmodulin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117180
                   541_2.R1010
Contig ID
                   PLN_g1359492
5'-most EST
                  BLASTX
Method
                   g4581965
NCBI GI
BLAST score
                   1258
E value
                   1.0e-139
                   231
Match length
% identity
                   100
                  (AJ224122) DNA-binding protein [Arabidopsis thaliana]
NCBI Description
                   117181
Seq. No.
                   541 4.R1010
Contig ID
                   jC-atXLIB327410P3b02b1
5'-most EST
Method
                   BLASTX
                   g4581965
NCBI GI
BLAST score
                   649
                   7.0e-96
E value
Match length
                  192
% identity
                  83
                   (AJ224122) DNA-binding protein [Arabidopsis thaliana]
NCBI Description
                   117182
Seq. No.
Contig ID
                   541 5.R1010
                   g937679
5'-most EST
Method
                   BLASTX
                   g4678921
NCBI GI
BLAST score
                   354
                   1.0e-38
E value
Match length
                  109
% identity
                   56
NCBI Description
                  (AL049711) putative calmodulin [Arabidopsis thaliana]
Seq. No.
                  117183
                   542 1.R1010
Contig ID
5'-most EST
                   jC-atXP69C217G17T7089d1
Method
                  BLASTX
                  g4586264
NCBI GI
BLAST score
                   678
                   3.0e-71
E value
Match length
                  126
```

```
% identity
                  .100
NCBI Description (AL049640) blue copper-binding protein, 15K (lamin)
                   [Arabidopsis thaliana]
Seq. No.
                   117184
                   542 2.R1010
Contig ID
                   PLN g1262751
-5'-most EST
Method
                   BLASTX
NCBI GI
                   q4586264
BLAST score
                   683
E value
                   6.0e-72
Match length
                   127
% identity
                   100
NCBI Description
                   (AL049640) blue copper-binding protein, 15K (lamin)
                   [Arabidopsis thaliana]
Seq. No.
                   117185
                   543 1.R1010
Contig ID
                   g2749072
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1429209
BLAST score
                   2915
E value
                   0.0e + 00
                   643
Match length
                   98
% identity
                  (X99111) beta-fructosidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117186
                   543 2.R1010
Contig ID
                   jC-atXP123C118K15T7014d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4827253
BLAST score
                   711
                   4.0e-75
E value
Match length
                   151
% identity
                   89
                   (AB027002) plastidic aldolase [Nicotiana paniculata]
NCBI Description
Seq. No.
                   117187
                   543 3.R1010
Contig ID
                   jC-atXLIB327417P3h05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4567268
BLAST score
                   1494
                   1.0e-177
E value
Match length
                   352
% identity
                   (AC006841) putative fructose biphosphate aldolase
NCBI Description
                   [Arabidopsis thaliana]
                   117188
Seq. No.
                   543 4.R1010
Contig ID
                   jC-atXP85CG8B6T7b1
5'-most EST
Method
                   BLASTX
                                       4. 7%
NCBI GI
                   q1871503
BLAST score
                   291
                  1.0e-38
E value
```

```
Match length
                  134
% identity
                  74
                  (Y11559) beta-fructosidase [Arabidopsis thaliana]
NCBI Description
                  117189
Seq. No.
Contig ID
                  543 6.R1010
                  jC-atXLIB327431P3c10a1
5'-most EST
                  BLASTX
Method
                  g4539316
NCBI GI
BLAST score
                  545
                  9.0e-70
E value
Match length
                  146
% identity
                  99
                  (AL035679) putative fructose-bisphosphate aldolase
NCBI Description
                  [Arabidopsis thaliana]
                  117190
Seq. No.
                  543 7.R1010
Contig ID
                  jC-atXLIB327409P2d12a1
5'-most EST
Method
                  BLASTN
                  g16472
NCBI GI
                  503
BLAST score
                  0.0e+00
E value
                  1095
Match length
                  98
% identity
NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type
                  117191
Seq. No.
                  543 8.R1010
Contig ID
5'-most EST
                  LIB24-022-Q1-E1-C12
                  BLASTX
Method
NCBI GI
                  q4827253
BLAST score
                  621
E value
                  1.0e-64
Match length
                  133
                  89
% identity
                  (AB027002) plastidic aldolase [Nicotiana paniculata]
NCBI Description
                  117192
Seq. No.
Contig ID
                  543 9.R1010
5'-most EST
                  g2446124
Method
                  BLASTX
NCBI GI
                  g1781348
BLAST score
                  129
                  6.0e-38
E value
Match length
                  110
% identity
                  78
                  (Y10380) homologous to plastidic aldolases [Solanum
NCBI Description
                  tuberosum]
                  117193
Seq. No.
Contig ID
                  543 10.R1010
5'-most EST
                  ARABL1-022-Q1-B1-F6
                  BLASTX
Method
                  g4309738
NCBI GI
BLAST score
                  1096
```

1.0e-120

E value

Match length

```
Match length
                   234
% identity
                   93
NCBI Description
                   (AC006439) putative tubby protein [Arabidopsis thaliana]
                   117194
Seq. No.
Contig ID
                   543 11.R1010
                   jC-atXLIB327437P2e06a1
5'-most EST
                   BLASTX
Method
                   q4539316
NCBI GI
BLAST score
                   592
E value
                   2.0e-61
Match length
                   128.
% identity
                   95
NCBI Description
                   (AL035679) putațive fructose-bisphosphate aldolase
                   [Arabidopsis thaliana]
                   117195
Seq. No.
                   543 12.R1010
Contig ID
                   jC-alXLIB327434P4a09b1
5'-most EST
Method
                   BLASTX
                   g4827253
NCBI GI
BLAST score
                  741
E value
                   1.0e-78
Match length
                   158
% identity
                   89
                  (AB027002) plastidic aldolase [Nicotiana paniculata]
NCBI Description
                   117196
Seq. No.
Contig ID
                   543 15.R1010
5'-most EST
                   jC-atX24056Q1E2D11b1
Method
                   BLASTX
NCBI GI
                   g1429209
BLAST score
                   513
E value
                   5.0e-52
Match length
                   105
% identity
                   98
NCBI Description
                   (X99111) beta-fructosidase [Arabidopsis thaliana]
                   117197
Seq. No.
                   544_1.R1010
Contig ID
                   jC-\overline{a}tXLIB327407P4c11b1
5'-most EST
Method
                   BLASTX
                   g1871503
NCBI GI
BLAST score
                   3462
                   0.0e + 00
E value
Match length
                   664
% identity
                   98
NCBI Description
                  (Y11559) beta-fructosidase [Arabidopsis thaliana]
Seq. No.
                   117198
Contig ID
                   544 2.R1010
5'-most EST
                   jC-atXmonuni27Cf10a1
Method
                   BLASTX
NCBI GI
                   g1871503
BLAST score
                   503
                   7.0e-51
E value
```

```
100 -
% identity
NCBI Description (Y11559) beta-fructosidase [Arabidopsis thaliana]
                  117199
Seq. No.
                  546 1.R1010
Contig ID
5'-most EST *
                  jC-atXLIB327408P2g11b1
                  BLASTX
Method
NCBI GI
                  q4454461
                  586
BLAST score
                  2.0e-60
E value
                  105
Match length
                  100
% identity
                   (AC006234) putative cell wall protein precursor
NCBI Description
                   [Arabidopsis thaliana]
                  117200
Seq. No.
                  547 1.R1010
Contig ID
                  jC-atXLIB327405P2c06b2
5'-most EST
Method
                  BLASTX
                  g2213622
NCBI GI
BLAST score
                  1304
E value
                  1.0e-144
                  312
Match length
% identity
                  87
NCBI Description (AC000103) F21J9.25 [Arabidopsis thaliana]
Seq. No.
                  117201
                  548 1.R1010
Contig ID
                  LIB35-039-Q1-E1-D9
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4406816
BLAST score
                  1323
                  1.0e-146
E value
Match length
                  249
                  100
% identity
NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]
Seq. No.
                  117202
                  548 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327426P2g05b1
Method
                  BLASTX
                  g2961372
NCBI GI
                  745
BLAST score
                  3.0e-84
E value
Match length
                  165
% identity
                  97
                  (AL022141) putative ribosomal protein L8 [Arabidopsis
NCBI Description
                  thaliana] >gi 3036817 emb CAA18507 (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
                  117203
Seq. No.
                  548 3.R1010
Contig ID
                  g2722794
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2961372
BLAST score
                  345
                  3.0e - 32
E value
```

```
Match length
                   119
% identity
                   66
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
NCBI Description
                   thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
                   117204
Seq. No.
Contig ID
                   549 1.R1010
                  LIB22-063-Q1-E1-A12
5'-most EST
Method
                   BLASTX
NCBI GI
                  q1402879
BLAST score
                   2865
E value
                  0.0e + 00
                   615
Match length
                   95
% identity
                   (X98130) unknown [Arabidopsis thaliana]
NCBI Description
                  >gi 1495247 emb CAA66220 (X97616) orf 05 [Arabidopsis
                  thaliana]
                   117205
Seq. No.
Contig ID
                   551_1.R1010
5'-most EST
                  PLN_g534901
Method
                  BLASTN
                  g534901
NCBI GI
BLAST score
                   844
E value
                  0.0e + 00
Match length
                   1018
                  100
% identity
NCBI Description
                  A.thaliana cadmium-induced mRNA
                  117206
Seq. No.
                   553 1.R1010
Contig ID
5'-most EST
                  LIB3168-032-P1-K1-B1
Method
                   BLASTX
                  q1769895
NCBI GI
BLAST score
                   2119
E value
                  0.0e + 00
Match length
                   493
% identity
                   86
                  (X96598) CaLB protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117207
                   554 1.R1010
Contig ID
5'-most EST
                  LIB25-041-Q1-E1-E3
Method
                  BLASTX
NCBI GI
                   q231700
BLAST score
                   982
E value
                  1.0e-107
                   191
Match length
% identity
                   100
NCBI Description
                  22 KD CALMODULIN-LIKE CALCIUM-BINDING PROTEIN (CABP-22)
                  >gi 479694 pir S35188 calmodulin-related protein (clone
                  CaBP-22) - Arabidopsis thaliana >gi 16209 emb CAA78124
                   (Z12136) calcium binding protein [Arabidopsis thaliana]
```

thaliana]

>gi 3402708 (AC004261) calcium binding protein [Arabidopsis

```
117208
Seq. No.
                   555 1.R1010
Contig ID
                   jC-alXLIB327434P2c05b1
5'-most EST
                   BLASTX
Method
                   g3894183
NCBI GI
BLAST score
                   829
                                                   P. . . .
                   9.0e-89
E value
Match length
                   213
                   78 💠
% identity
                   (AC005662) calmodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   117209
Seq. No.
                   556 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327420P1f05a1
Method
                   BLASTX
NCBI GI
                   g115470
                   1381
BLAST score
                   1.0e-153
E value
                   332
Match length
% identity
                   CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
NCBI Description
                   DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase
                   (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase
                   [Arabidopsis thaliana]
                   117210
Seq. No.
                   556 2.R1010
Contig ID
                   LIB24-005-Q1-E1-E4
5'-most EST
                   BLASTX
Method
                   g1168739
NCBI GI
BLAST score
                   401
                   1.0e-125
E value
Match length
                   260
% identity
                   88
                   CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi 438449
NCBI Description
                   (L18901) carbonic anhydrase [Arabidopsis thaliana]
Seq. No.
                  a 117211
                   556 3.R1010
Contig ID
                   jC-atXP86CG9G5T7d2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1168739
BLAST score
                   730
                   3.0e-77
E value
Match length
                   170
% identity
                   96
NCBI Description CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >qi 438449
                   (L18901) carbonic anhydrase [Arabidopsis thaliana]
                   117212
Seq. No.
                   556 5.R1010
Contig ID
                   g1268727
5'-most EST
Method
                   BLASTX
                   g1168739
NCBI GI
BLAST score
                   409
                   8.0e-40
E value
```

```
Match length
                   104
% identity
                   82
                   CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi 438449
NCBI Description
                   (L18901) carbonic anhydrase [Arabidopsis thaliana]
                   117213
Seq. No.
Contig ID
                   556 6.R1010
5'-most EST
                   jC-atXP96C249J9T7b1
Method
                   BLASTX
NCBI GI
                   g1168739
BLAST score
                   1105
E value
                   1.0e-121
Match length
                   229
                   93
% identity
NCBI Description
                   CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi 438449
                   (L18901) carbonic anhydrase [Arabidopsis thaliana]
                   117214
Seq. No.
                   556 10.R1010
Contig ID
5'-most EST
                   jC-atXP27C134A15T7d2
Method
                   BLASTX
                   g115470
NCBI GI
BLAST score
                   302
E value
                   3.0e-27
Match length
                   169
% identity
                   49
                   CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
NCBI Description
                   DEHYDRATASE) >gi_320554_pir__$28412 carbonate dehydratase
                   (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase
                   [Arabidopsis thaliana]
                   117215
Seq. No.
Contig ID
                   556 11.R1010
5'-most EST
                   g15\overline{2}0289
                   BLASTX
Method
NCBI GI
                   g1168739
BLAST score
                   393
E value
                   7.0e-38
Match length
                   104
                   79
% identity
                   CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi 438449
NCBI Description
                   (L18901) carbonic anhydrase [Arabidopsis thaliana]
Seq. No.
                   117216
                   556_18.R1010
Contig ID
5'-most EST
                   jC-atXLIB327404P1h10b1
Method
                   BLASTX
                   g115470
NCBI GI
BLAST score
                   65
E value
                   1.0e-36
Match length
                   159
                   59
% identity
NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
                   DEHYDRATASE) >gi 320554_pir__S28412 carbonate dehydratase
                   (EC 4.2.1.1) precursor - Arabidopsis thaliana
```

>gi 14343 emb CAA46508 (X65541) carbonic anhydrase

[Arabidopsis thaliana]

```
117217
Seq. No.
                   557 1.R1010
Contig ID
                   LIB24-134-Q1-E1-F12
5'-most EST
Method
                   BLASTX
                   g3702368
NCBI GI
                   1471
BLAST score
                   1.0e-164
E value
Match length
                   295
                   96
% identity
                   (AJ001855) alpha subunit of F-actin capping protein
NCBI Description
                   [Arabidopsis thaliana]
                   117218
Seq. No.
                   557 2.R1010
Contig ID
                   jC-atXLIB327409P3d03a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3702367
BLAST score
                   321
                   1.0e-180
E value
Match length
                   333
% identity
                   99
NCBI Description Arabidopsis thaliana mRNA for alpha subunit of F-actin
                   capping protein (CAPZ alpha)
                   117219
Seq. No.
                   558 1.R1010
Contig ID
                   jC-\overline{a}tXLIB327428P1a09b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g416755
                   1769
BLAST score
                   0.0e + 00
E value
Match length
                   492
                   86
% identity
                   CATALASE >gi_218322_dbj_BAA02755.1_ (D13557) catalase
NCBI Description
                   [Vigna radiata]
                   117220
Seq. No.
                   558 5.R1010
 Contig ID
 5'-most EST
                   g936207
Method
                   BLASTX
NCBI GI
                   q2924519
BLAST score
                   136
                   2.0e-14
E value
Match length
                   49
                   90
 % identity
                   (AL022023) catalase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117221
 Contig ID
                   559 1.R1010
 5'-most EST
                   PLN g2995129
Method
                   BLASTX
NCBI GI
                   g3915635
BLAST score
                   1735
                   0.0e+00
E value
Match length
                   335
```

```
% identity
                  100
                  CYCLIN DELTA-1 >gi 2995130 emb CAA58285_ (X83369) cyclin
NCBI Description
                  delta-1 [Arabidopsis thaliana]
Seq. No.
                  117222
                  560 1.R1010
Contig ID
5'-most EST
                  LIB23-037-Q1-E1-E12
Method
                  BLASTX
NCBI GI
                  q1076312
BLAST score
                  1413
E value
                  1.0e-166
Match length
                  362
                  83
% identity
NCBI Description cyclin delta-2 - Arabidopsis thaliana
Seq. No.
                  117223
                  561 1.R1010
Contig ID
                  jC-atXLIB327432P2a03b2
5'-most EST
                  BLASTX
Method
                  q3915637
NCBI GI
                  1528
BLAST score
E value
                  1.0e-170
Match length
                  376
% identity
                  81
                  CYCLIN DELTA-3 >gi 2995134 emb CAA58287 (X83371) cyclin
NCBI Description
                  delta-3 [Arabidopsis thaliana]
                  117224
Seq. No.
                  562 1.R1010
Contig ID
                  jC-atXLIB327440P1e08b1
5'-most EST
Method
                  BLASTX
                  g3121836
NCBI GI
BLAST score
                  2229
                  0.0e + 00
E value
Match length
                  421
% identity
                  100
                  PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE
NCBI Description
                  SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE)
                  (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE
                  CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE)
                  >gi 2181182 emb CAA63969 (X94306) CDP-diacylglycerol
                  synthetase [Arabidopsis thaliana]
Seq. No.
                  117225
Contig ID
                  563 1.R1010
5'-most EST
                  LIB25-064-Q1-E1-D9
Method
                  BLASTX
                  q116229
NCBI GI
                  2761
BLAST score
E value
                  0.0e + 00
                  577
Match length
% identity
                  MITOCHONDRIAL CHAPERONIN HSP60 PRECURSOR
NCBI Description
                  >gi 99676 pir S20876 chaperonin hsp60 precursor -
                  Arabidopsis thaliana >gi_16221_emb_CAA77646_ (Z11547)
```

chaperonin hsp60 [Arabidopsis thaliana]

```
Seq. No.
                  117226
                  564 1.R1010
Contig ID
                  jC-atXLIB327429P3h04a2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2274857
BLAST score
                   1124
                  1.0e-123
E value
                  231
Match length
                  94
% identity
NCBI Description
                   (AJ000469) glutathione peroxidase [Arabidopsis thaliana]
                  >gi_3482968_emb_CAA20524.1_ (AL031369) glutathione
                  peroxidase precursor [Arabidopsis thaliana]
                  117227
Seq. No.
                   564 2.R1010
Contig ID
5'-most EST
                   jC-atXP71CF1A8T7007d1
Method
                  BLASTX
                  q1708062
NCBI GI
                   600
BLAST score
                   4.0e-62
E value
                   195
Match length
% identity
                   64
NCBI Description
                  GLUTATHIONE PEROXIDASE HOMOLOG PRECURSOR
                  >gi_2129599_pir__S71250 glutathione peroxidase -
                  Arabidopsis thaliana >gi_1061036_emb_CAA61965_ (X89866)
                  qlutathione peroxidase [Arabidopsis thaliana]
                   117228
Seq. No.
                   566 1.R1010
Contig ID
5'-most EST
                  LIB22-010-Q1-E1-G7
                   BLASTX
Method
                   q1103318
NCBI GI
BLAST score
                   2240
                   0.0e + 00
E value
Match length
                   451
% identity
                   (X78818) casein kinase I [Arabidopsis thaliana]
NCBI Description
                   >gi 2244791 emb CAB10213.1 (Z97336) casein kinase I
                   [Arabidopsis thaliana]
                   117229
Seq. No.
                   566 2.R1010
Contig ID
5'-most EST
                   g2445928
Method
                   BLASTX
NCBI GI
                   g2244790
BLAST score
                   161
E value
                   9.0e-11
Match length
                   77
                   68
% identity
NCBI Description
                   (Z97336) kinesin homolog [Arabidopsis thaliana]
                   117230
Seq. No.
                   566 3.R1010
Contig ID
5'-most EST
                   jC-atXmonuni26Ce04b1
Method
                   BLASTX
                   g1103318
NCBI GI
                   592
BLAST score
```

```
E value
                   2.0e-61
Match length
                   118
                   100
% identity
                   (X78818) casein kinase I [Arabidopsis thaliana]
NCBI Description
                   >gi 2244791 emb CAB10213.1 (Z97336) casein kinase I
                   [Arabidopsis thaliana]
                   117231
Seq. No.
Contig ID
                   568_1.R1010
5'-most EST
                   PLN_g1103321
Method
                   BLASTX
NCBI GI
                   q1103322
BLAST score
                   1609
                   1.0e-180
E value
                   364
Match length
% identity
                   85
NCBI Description
                   (X78820) casein kinase I [Arabidopsis thaliana]
                   117232
Seq. No.
                   568 3.R1010
Contig ID
                   jC-atXLIB327412P1d01b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1103322
BLAST score
                   137
E value
                   6.0e-67
Match length
                   177
                   77
% identity
NCBI Description
                   (X78820) casein kinase I [Arabidopsis thaliana]
                   117233
Seq. No.
Contig ID
                   568 4.R1010
5'-most EST
                   jC-\overline{a}tXLIB327420P3c12b1
Method
                   BLASTX
NCBI GI
                   q2341031
BLAST score
                   181
                   4.0e-13
E value
Match length
                   151
                   93
% identity
NCBI Description
                   (AC000104) F19P19.10 [Arabidopsis thaliana]
                   117234
Seq. No.
Contig ID
                   569 1.R1010
                   jC-atXP22C119K19T7013a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2274859
                   394
BLAST score
                   6.0e-38
E value
Match length
                   87
% identity
                   86
NCBI Description
                   (AJ000016) Cksl protein [Arabidopsis thaliana]
                   >gi_4510420_gb_AAD21506.1_ (AC006929) putative
                   cyclin-dependent kinase regulatory subunit [Arabidopsis
                   thaliana]
                   117235
Seq. No.
                   569_2.R1010
Contig ID
```

g935985

5'-most EST

```
Method
                     BLASTX
                    q2274859
NCBI GI
                     100
BLAST score
                     2.0e-03
E value
Match length
                     72
% identity
                     81
                     (AJ000016) Cksl protein [Arabidopsis thaliana]
NCBI Description
                     >gi_4510420_gb_AAD21506.1_ (AC006929) putative
                     cyclin-dependent kinase regulatory subunit [Arabidopsis
                    thaliana]
                    117236
Seq. No.
Contig ID
                     570 1.R1010
5'-most EST
                    LIB24-034-Q1-E1-C12
Method
                     BLASTX
NCBI GI
                     g1076283
BLAST score
                     1331
E value
                    1.0e-147
Match length
                     276
                     93
% identity
                    adenylylsulfate kinase (EC 2.7.1.25) precursor -
NCBI Description
                     Arabidopsis thaliana >gi_414737_emb_CAA53426_ (X75782) APS
                    kinase [Arabidopsis thaliana] >gi_450235 (U05238) APS kinase [Arabidopsis thaliana] >gi_1575322 (U59759) APS kinase [Arabidopsis thaliana] >gi_3252812 (AC004705) APS
                     kinase [Arabidopsis thaliana]
                    117237
Seq. No.
                     571_1.R1010
Contig ID
5'-most EST
                    PLN_g1742952
Method
                     BLASTX
                    g2935344
NCBI GI
BLAST score
                     3765
E value
                     0.0e + 00
Match length
                     775
% identity
                     94
                     (AF044313) anion channel protein [Arabidopsis thaliana]
NCBI Description
                     117238
Seq. No.
                     571 2.R1010
Contig ID
                    q27\overline{5}9703
5'-most EST
Method
                     BLASTX
                    g1742953
NCBI GI
BLAST score
                     777
                     8.0e-83
E value
Match length
                     158
% identity
NCBI Description
                     (Z71445) CLC-a chloride channel protein [Arabidopsis
                     thaliana]
Seq. No.
                     117239
                     571 4.R1010
Contig ID
5'-most EST
                    q27\overline{4}9078
Method
                     BLASTX
                    g1742953
NCBI GI
BLAST score
                     266
E value
                     5.0e-23
```

```
Match length
                   71
% identity
                   (271445) CLC-a chloride channel protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   117240
Contig ID
                   572 1.R1010
5'-most EST
                   PLN_g1742954
                   BLASTX
Method
                   g1742955
NCBI GI
BLAST score
                   3704
E value
                   0.0e + 00
                   780
Match length
% identity
                   92
                   (271446) CLC-b chloride channel protein [Arabidopsis
NCBI Description
                   thaliana
                   117241
Seq. No.
                   573 1.R1010
Contig ID
                   LIB3177-080-P1-K1-A1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1655536
BLAST score
                   3517
                   0.0e + 00
E value
                   779
Match length
                   88
% identity
NCBI Description
                   (Y09095) chloride channel [Arabidopsis thaliana]
                   >gi 1742957_emb_CAA96059_ (Z71447) CLC-c chloride channel
                   protein [Arabidopsis thaliana]
                   117242
Seq. No.
                   574_1.R1010
Contig ID
5'-most EST
                   PLN_g1742958
Method
                   BLASTX
NCBI GI
                   q1742959
BLAST score
                   3556
                   0.0e + 00
E value
                   792
Match length
% identity
                88
                   (Z71450) CLC-d chloride channel protein [Arabidopsis
NCBI Description
                   thaliana]
                   117243
Seq. No.
Contig ID
                   575 1.R1010
                   PLN_g16222
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1168748
BLAST score
                   750
                   1.0e-79
E value
Match length
                   148
% identity
                   66
                   {\tt CALMODULIN-4 > gi\_479693\_pir\_S35185 \ calmodulin \ 4 \ -}
NCBI Description
                   Arabidopsis thal\overline{i}ana >g\overline{i}_16\overline{22}3_emb_CAA78057_ (Z12022)
                   calmodulin [Arabidopsis thaliana]
                   117244
Seq. No.
```

575_2.R1010

Contig ID

```
5'-most EST
                   g2723049
                  BLASTX
Method
                 · q1168748
NCBI GI
BLAST score
                  510
                  6.0e-61
E value
Match length
                   146
% identity
                   57
                  CALMODULIN-4 >gi_479693_pir__S35185 calmodulin 4 -
NCBI Description
                  Arabidopsis thaliana >gi_16223 emb CAA78057 (Z12022)
                   calmodulin [Arabidopsis thaliana]
                   117245
Seq. No.
                   576 1.R1010
Contig ID
5'-most EST
                  LIB35-031-Q1-E1-H4
Method
                  BLASTX
                   q1168749
NCBI GI
                   761°
BLAST score
                   6.0e-81
E value
                   149
Match length
% identity
                   100
                  CALMODULIN-6 >gi 1076298 pir S35187 calmodulin 6 -
NCBI Description
                   Arabidopsis thaliana >gi162\overline{27} emb CAA78059 (Z12024)
                   calmodulin [Arabidopsis thaliana]
Seq. No.
                  117246
Contig ID
                   577 1.R1010
5'-most EST
                   PLN g662870
Method
                  BLASTX
                   q3023535
NCBI GI
                  1981
BLAST score
E value
                   0.0e + 00
                   390
Match length
% identity
                   98
                  MOLYBDOPTERIN BIOSYNTHESIS CNX2 PROTEIN (MOLYBDENUM
NCBI Description
                  COFACTOR BIOSYNTHESIS ENZYME CNX2) >gi 662871 emb CAA88107_
                   (Z48047) Cnx2 [Arabidopsis thaliana]
                  117247
Seq. No.
                   578 1.R1010
Contig ID
5'-most EST
                  PLN g662872
Method
                  BLASTX
NCBI GI
                  q2497964
BLAST score
                   1362
                   1.0e-151
E value
                   270
Match length
                  100
% identity
                  MOLYBDOPTERIN BIOSYNTHESIS CNX3 PROTEIN (MOLYBDENUM
NCBI Description
                  COFACTOR BIOSYNTHESIS ENZYME CNX3) >gi 662873_emb_CAA88106_
                   (Z48046) Cnx3 [Arabidopsis thaliana]
                  117248
Seq. No.
Contig ID
                  584 1.R1010
                   jC-atXLIB327409P1h02b1
5'-most EST
Method
                  BLASTX
                  g2281095
NCBI GI
BLAST score
                  988
                  0.0e+00
E value
```

```
391
Match length
% identity
                 . 89
NCBI Description (AC002333) cysteine synthase, cpACS1 [Arabidopsis thaliana]
Seq. No.
                  117249
                  585 1.R1010
Contig ID
                  LIB25-041-Q1-E1-F10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2154715
BLAST score
                  2807
E value
                  0.0e + 00
Match length
                  601
                  92
% identity
NCBI Description
                  (Y09418) CDPK-related protein kinase [Arabidopsis thaliana]
Seq. No.
                  586 1.R1010
Contig ID
5'-most EST
                  PLN g1488518
Method
                  BLASTX
NCBI GI
                  g2493896
BLAST score
                  1795
E value
                  0.0e + 00
Match length
                  424
% identity
NCBI Description
                  CYSTEINE SYNTHASE MITOCHONDRIAL PRECURSOR (O-ACETYLSERINE
                  SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                  >gi_1488519_emb_CAA57498_ (X81973) cysteine synthase
                  [Arabidopsis thaliana]
                  117251
Seq. No.
                  587 1.R1010
Contig ID
5'-most EST
                  LIB25-034-Q1-E1-E8
Method
                  BLASTX
NCBI GI
                  q1351272
BLAST score
                  1146
E value
                  1.0e-126
Match length
                  243
% identity
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >qi 414550
                  (U02949) cytosolic triose phosphate isomerase [Arabidopsis
                  thaliana] >gi_742408_prf__2009415A triose phosphate
                  isomerase [Arabidopsis thaliana]
Seq. No.
                  117252
                  587 2.R1010
Contig ID
5'-most EST
                  q2722792
Method
                  BLASTX
NCBI GI
                  q1351272
BLAST score
                  190
E value
                  7.0e-14
Match length
                  191
% identity
                  22
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 414550
                  (U02949) cytosolic triose phosphate isomerase [Arabidopsis
                  thaliana] >gi 742408 prf 2009415A triose phosphate
```

isomerase [Arabidopsis thaliana]

```
117253
Seq. No.
                  588 1.R1010
Contig ID
5'-most EST
                  PLN_g2769565
Method
                  BLASTX
NCBI GI
                  q2769566
BLAST score
                  1670
E value
                  0.0e + 00
Match length
                  340
% identity
                  95
                  (Y10477) chloroplast thylakoidal processing peptidase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  117254
                  588 2.R1010
Contig ID
5'-most EST
                  jC-atX35042Q1E1E10a1
                  BLASTN
Method
NCBI GI
                  q1946354
BLAST score
                  133
                  2.0e-68
E value
Match length
                  357
                  95
% identity
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
NCBI Description
                  sequence, complete sequence
                  117255
Seq. No.
Contig ID
                  589 1.R1010
5'-most EST
                  LIB3177-084-P1-K1-C9
                  BLASTX
Method
NCBI GI
                  q1082054
BLAST score
                  493
                  2.0e-49
E value
Match length
                  127
                  76
% identity
NCBI Description
                  (Z49859) copper transporter protein [Arabidopsis thaliana]
Seq. No.
                  117256
Contig ID
                  590 1.R1010
5'-most EST
                  PLN g1903018
Method
                  BLASTX
NCBI GI
                  q1903019
BLAST score
                  4236
E value
                  0.0e + 00
Match length
                  885
% identity
                  91
NCBI Description
                  (Y10580) polycomb group [Arabidopsis thaliana]
                · . 117257
Seq. No.
                  591 1.R1010
Contig ID
5'-most EST
                  jC-atXP78C229L18T7b1
Method
                  BLASTX
                  g2661422
NCBI GI
BLAST score
                  1246
E value
                  1.0e-137
Match length
                  243
% identity
                  100
                  (AJ001342) Putative S-phase-specific ribosomal protein
NCBI Description
```

[Arabidopsis thaliana] >gi 3096936 emb CAA18846.1

```
[Arabidopsis thaliana]
                   117258
Seq. No.
                   591 2.R1010
Contig ID
                   jC-\overline{a}1XLIB327434P2e06b1
5'-most EST
Method
                   BLASTX
                   g4204265
NCBI GI
BLAST score
                   391
                   2.0e-37
E value
Match length
                   99
% identity
                   73
NCBI Description
                   (AC005223) 45643 [Arabidopsis thaliana]
                   117259
Seq. No.
                   591 5.R1010
Contig ID
5'-most EST
                   iC-atXLIB327415P2d11b2
Method
                   BLASTX
NCBI GI
                   g2661422
BLAST score
                   472
                   3.0e-47
E value
Match length
                   92
% identity
                   100
NCBI Description
                   (AJ001342) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_
                   (AL023094) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana]
                  117260
Seq. No.
                   592_1.R1010
Contig ID
5'-most EST
                  LIB24-033-Q1-E1-F6
Method
                  BLASTX
NCBI GI
                   g728519
BLAST score
                   1951
E value
                  0.0e + 00
Match length
                   429
% identity
                   90
NCBI Description
                  (Z31400) cyclin 2a protein [Arabidopsis thaliana]
Seq. No.
                   117261
Contig ID
                   593 1.R1010
5'-most EST
                   PLN g728520
Method
                  BLASTX
NCBI GI
                   g784946
BLAST score
                   2133
E value
                   0.0e + 00
Match length
                   436
% identity
                  97
NCBI Description
                  (Z31402) cyclin 3b [Arabidopsis thaliana]
Seq. No.
                  117262
                  594 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327416P4e01b1
Method
                  BLASTX
NCBI GI
                  g231735
BLAST score
                  2095
```

(AL023094) Putative S-phase-specific ribosomal protein

0.0e + 00

E value

```
428
Match length
% identity
                  96
                  G2/MITOTIC-SPECIFIC CYCLIN (B-LIKE CYCLIN)
NCBI Description
                  >gi 541854 pir A44123 cyclin cycl - Arabidopsis thaliana
                  >gi_166684 (M80190) cyclin [Arabidopsis thaliana]
                  >gi 908816 emb CAA44169 (X62279) cyclin [Arabidopsis
                  thaliana]
                  117263
Seq. No.
                  596 1.R1010
Contig ID
5'-most EST
                  LIB24-027-Q1-E1-A3
Method
                  BLASTX
NCBI GI
                  g2065013
                  952
BLAST score
                  1.0e-103
E value
                  181
Match length
                  100
% identity
                  (Y11650) cyclic phosphodiesterase [Arabidopsis thaliana]
NCBI Description
                  >qi 2832621 emb CAA16750 (AL021711) cyclic
                  phosphodiesterase [Arabidopsis thaliana]
                  117264
Seq. No.
                  597 1.R1010
Contig ID
5'-most EST
                  LIB23-062-Q1-E1-D8
Method
                  BLASTX
NCBI GI
                  g1076315
BLAST score
                  2111
                  0.0e + 00
E value
Match length
                  430
% identity
                  cytochrome P450 - Arabidopsis thaliana
NCBI Description
                  >gi 853719 emb CAA60793 (X87367) CYP90 protein
                   [Arabidopsis thaliana] >gi 871988_emb_CAA60794_ (X87368)
                  CYP90 protein [Arabidopsis thaliana]
                  117265
Seq. No.
Contig ID
                  597 4.R1010
5'-most EST
                  jC-atXP1C63C12T7d1
Method
                  BLASTX
NCBI GI
                  g1076315
BLAST score
                  429
                  3.0e-42
E value
                  144
Match length
                  72
% identity
NCBI Description
                  cytochrome P450 - Arabidopsis thaliana
                  >gi 853719 emb_CAA60793_ (X87367) CYP90 protein
                   [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368)
                  CYP90 protein [Arabidopsis thaliana]
                  117266
Seq. No.
Contig ID
                  597 5.R1010
                  jC-atXLIB327438P4f02a2
5'-most EST
Method
                  BLASTX
                  g1076315
NCBI GI
BLAST score
                  810
E value
                  1.0e-86
                  205
Match length
```

NCBI GI

```
81
% identity
NCBI Description
                  cytochrome P450 - Arabidopsis thaliana
                  >gi 853719 emb CAA60793 (X87367) CYP90 protein
                  [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368)
                  CYP90 protein [Arabidopsis thaliana]
                  117267
Seq. No.
                  598_1.R1010
Contig ID
                  jC-atXLIB327426P1g02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1523796
BLAST score
                  2470
E value
                  0.0e + 00
Match length
                  485
                  98
% identity
                  (X97864) cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  117268
Seq. No.
                  598 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327427P3g09b2
Method
                  BLASTX
                  g1523796
NCBI GI
BLAST score
                  640
E value
                  9.0e-73
                  172
Match length
                  76
% identity
                  (X97864) cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  117269
Seq. No.
                  598 4.R1010
Contig ID
                  jC-atXP33C148I16T7d2
5'-most EST
                  BLASTX
Method
                  g1523796
NCBI GI
BLAST score
                  992
                  1.0e-108
E value
                  246
Match length
                  77
% identity
                  (X97864) cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117270
                  599 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P2g02b2
                  BLASTX
Method
                  g1791309
NCBI GI
BLAST score
                  2583
                  0.0e + 00
E value
                  563
Match length
                  90
% identity
                  (U83500) cystathionine gamma-synthase [Arabidopsis
NCBI Description
                  thaliana] >gi 2852454 dbj BAA24699_ (AB010888)
                  cystathionine gamma-synthase [Arabidopsis thaliana]
                  117271
Seq. No.
                  599 4.R1010
Contig ID
                  jC-atXLIB327427P3d03b2
5'-most EST
Method
                  BLASTX
```

g2507422

```
491
BLAST score
E value
                   2.0e-49
                   114
Match length
                   89
% identity
                  CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS)
NCBI Description
                   (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi 3293261 (AF039206)
                   cystathionine gamma-synthase precursor [Arabidopsis
                   thaliana]
                   117272
Seq. No.
                   600 1.R1010
Contig ID
5'-most EST
                   LIB25-048-Q1-E1-C2
Method
                   BLASTX
NCBI GI
                   g2244845
BLAST score
                   1518
                   1.0e-169
E value
                   322
Match length
                   94
% identity
                   (Z97337) cytosolic O-acetylserine(thiol)lyase (EC 4.2.99.8)
NCBI Description
                   [Arabidopsis thaliana]
                   117273
Seq. No.
                   600 2.R1010
Contig ID
5'-most EST
                   g1328069
                   BLASTX
Method
                   g2118307
NCBI GI
BLAST score
                   64
                   3.0e-45
E value
                   137
Match length
% identity
                   71
                   cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana
NCBI Description
                   >gi 804950 emb CAA58893 (X84097) cysteine synthase
                   [Arabidopsis thaliana] >gi 1096196 prf 2111276A Ser(Ac)
                   thiol lyase [Arabidopsis thaliana]
                   117274
Seq. No.
Contig ID
                   600 3.R1010
5'-most EST
                   jC-atXLIB327423P1e03b1
Method
                   BLASTX
NCBI GI
                   q2244845
BLAST score
                   481
                   7.0e-48
E value
                   264
Match length
                   92
% identity
NCBI Description
                   (Z97337) cytosolic O-acetylserine(thiol)lyase (EC 4.2.99.8)
                   [Arabidopsis thaliana]
                   117275
Seq. No.
Contig ID
                   600 5.R1010
5'-most EST
                   LIB3176-008-P1-K2-A7
Method
                   BLASTX
                   g2243120
NCBI GI
BLAST score
                   262
                   1.0e-22
E value
Match length
                   97
% identity
                   78
                  (Y10845) O-acetylserine(thiol) lyase [Brassica juncea]
NCBI Description
```

Method

BLASTX

```
. 117276
Seq. No.
Contig ID
                  600 6.R1010
5'-most EST
                  jC-atXP96C248J18T7b1
Method
                  BLASTX
                  g2118307
NCBI GI
BLAST score
                  721
E value
                  3.0e-76
Match length
                  158
% identity
NCBI Description
                  cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana
                  >gi_804950_emb_CAA58893_ (X84097) cysteine synthase
                  [Arabidopsis thaliana] >gi_1096196_prf__2111276A Ser(Ac)
                  thiol lyase [Arabidopsis thaliana]
                  117277
Seq. No.
                  602 1.R1010
Contig ID
                  LIB24-092-Q1-E1-A9
5'-most EST
Method
                  BLASTX
                  g1946690
NCBI GI
BLAST score
                  882
E value
                  4.0e-95
Match length
                  169
% identity
                  100
NCBI Description
                  (U94495) glutathione peroxidase [Arabidopsis thaliana]
                  >gi 4582452 gb AAD24836.1 AC007071 8 (AC007071) putative
                  glutathione peroxidase [Arabidopsis thaliana]
Seq. No.
                  117278
                  603 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327414P3e02a1
Method
                  BLASTX
NCBI GI
                  g3063472
BLAST score
                  852
                  2.0e-91
E value
Match length
                  159
% identity
                  100
NCBI Description (AC003981) F22013.34 [Arabidopsis thaliana]
                  117279
Seq. No.
                  603 2.R1010
Contig ID
5'-most EST
                  LIB35-009-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  g134600
BLAST score
                  437
                  5.0e-43
E value
                  83
Match length
                  98
% identity
NCBI Description
                  SUPEROXIDE DISMUTASE (CU-ZN) >gi_66372_pir__DSMUZ
                  superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - Arabidopsis
                  thaliana >gi_16250_emb_CAA43270_ (X60935) superoxide
                  dismutase [Arabidopsis thaliana]
                  117280
Seq. No.
Contig ID
                  603 3.R1010
5'-most EST
                  LIB23-047-Q1-E1-E6
```

```
NCBI GI
                  q134600
                  60
BLAST score
                  2.0e-27
E value
                  73
Match length
                  70
% identity
                  SUPEROXIDE DISMUTASE (CU-ZN) >gi 66372 pir DSMUZ
NCBI Description
                  superoxide dismutase (EC 1.15.\overline{1.1}) (Cu-Zn) - Arabidopsis
                  thaliana >gi 16250 emb CAA43270 (X60935) superoxide
                  dismutase [Arabidopsis thaliana]
Seq. No.
                  117281
                  604 1.R1010
Contig ID
                  jC-atXLIB327416P4f06b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2129578
BLAST score
                  2271
E value
                  0.0e+00
                  432
Match length
                  100
% identity
                  dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
NCBI Description
                  thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of
                  dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
                  >gi 1585435_prf__2124427B diamide resistance gene
                   [Arabidopsis thaliana]
Seq. No.
                  117282
                  604 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327426P2g12b1
                  BLASTX
Method
                  g3522929
NCBI GI
BLAST score
                  230
                  2.0e-94
E value
Match length
                  180
% identity
                   (AC002535) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana] >gi_3738279 (AC005309) putative
                  dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.
                  117283
                   604 3.R1010 ·
Contig ID
                   jC-atXLIB327416P1g10b1
5'-most EST
                  BLASTX
Method
                  q3522929
NCBI GI
BLAST score
                   424
                  1.0e-41
E value
                  95
Match length
% identity
NCBI Description
                   (AC002535) putative dTDP-glucose 4-6-dehydratase
                   [Arabidopsis thaliana] >gi_3738279 (AC005309) putative
                  dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.
                  117284
                  604 4.R1010
Contig ID
5'-most EST
                  ARABL1-029-Q1-B1-D6
Method
                  BLASTX
                  q3522929
NCBI GI
```

615

BLAST score

E value

5.0e-64

```
Match length
                  120
                   99
% identity
                  (AC002535) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana] >gi_3738279 (AC005309) putative
                  dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No. :
                  117285
                  604_5.R1010
Contig ID
                  jC-atXLIB327401P3h09b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3522929
BLAST score
                  916
                  1.0e-105
E value
Match length
                  232
                  83
% identity
                  (AC002535) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana] >gi 3738279 (AC005309) putative
                  dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
                  117286
Seq. No.
Contig ID
                  604 7.R1010
5'-most EST
                  jC-atXLIB327416P1g10a1
Method
                  BLASTX
NCBI GI
                  g3522929
BLAST score
                  183
                  2.0e-13
E value
Match length
                  60
% identity
                  68
NCBI Description
                   (AC002535) putative dTDP-glucose 4-6-dehydratase
                  [Arabidopsis thaliana] >gi 3738279 (AC005309) putative
                  dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.
                  117287
Contig ID
                  604 8.R1010
5'-most EST
                  jC-atXP6C90L20T7d1
Method
                  BLASTX
NCBI GI
                  g3522929
BLAST score
                  627
E value
                  1.0e-65
Match length
                  133
                  91
% identity
                  (AC002535) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana] >gi 3738279 (AC005309) putative
                  dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
                  117288
Seq. No.
                  605_1.R1010
Contig ID
5'-most EST
                  PLN_g928933
Method
                  BLASTX
NCBI GI
                  g2129587
BLAST score
                  2836
                  0.0e + 00
E value
Match length
                  568
% identity
                  gamma-glutamyltransferase (EC 2.3.2.2) - Arabidopsis
NCBI Description
                  thaliana >gi 928934 emb CAA89206 (Z49240) gamma-glutamyl
```

5'-most EST

```
>gi 1585436 prf 2124427C gamma-Glu transpeptidase
                   [Arabidopsis thaliana]
Seq. No.
                  117289
                  606_1.R1010
Contig ID
                  PLN_g928935
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2129626
BLAST score
                  2642
E value
                  0.0e + 00
Match length
                  539
                  97
% identity
NCBI Description
                  J-domain protein - Arabidopsis thaliana
                  >gi 928936_emb_CAA89204_ (Z49238) J-domain protein
                  [Arabidopsis thaliana] >gi_1585434_prf 2124427A diamide
                  resistance gene [Arabidopsis thaliana]
                  117290
Seq. No.
                  608_1.R1010
Contig ID
                  g3450406
5'-most EST
Method
                  BLASTX
                  g1871577
NCBI GI
                  298
BLAST score
E value
                  8.0e-27
Match length
                  105
% identity
                  54
NCBI Description
                  (Y11553) putative 21kD protein precursor [Medicago sativa]
                  117291
Seq. No.
Contig ID
                  609 1.R1010
5'-most EST
                  PLN_g1592669
Method
                  BLASTX
NCBI GI
                  q1592670
                  509
BLAST score
E value
                  2.0e-51
Match length
                  185
% identity
                  55
NCBI Description
                  (X91920) dehydrin [Arabidopsis thaliana]
                  >gi 4567280 gb AAD23693.1 AC006841 21 (AC006841) putative
                  dehydrin [Arabidopsis thaliana]
                  117292
Seq. No.
Contig ID
                  610 1.R1010
5'-most EST
                  jC-alXLIB327436P4a06b1
Method
                  BLASTX
                  q1076317
NCBI GI
BLAST score
                  1747
E value
                  0.0e + 00
Match length
                  365
% identity
                  92
                  dihydrodipicolinate synthase (EC 4.2.1.52) precursor -
NCBI Description
                  Arabidopsis thaliana
                  117293
Seq. No.
Contig ID
                  611 1.R1010
```

transpeptidase [Arabidopsis thaliana]

jC-alXLIB327436P1f03b1

```
Method
                  BLASTX
NCBI GI
                  q4678949
BLAST score
                  2889
E value
                  0.0e+00
Match length
                  637
% identity
                  91
                   (AL049711) dihydrolipoamide S-acetyltransferase precursor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  117294
Contig ID
                  612_1.R1010
5'-most EST
                  jC-atXLIB327422P4g07b1
Method
                  BLASTX
NCBI GI
                  q1076316
                  1043
BLAST score
                  1.0e-114
E value
Match length
                  206
% identity
                  100
NCBI Description
                  drought-induced protein Di19 - Arabidopsis thaliana
                  >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis
                  thaliana]
Seq. No. -
                  117295
                  612 6.R1010
Contig ID
5!-most EST
                  ARABL1-033-Q1-B1-H11
Method
                  BLASTN
NCBI GI
                  g469109
BLAST score
                  266
E value
                  1.0e-148
Match length
                  482
% identity
                  99
NCBI Description A.thaliana (Columbia) Di19 mRNA
Seq. No.
                  117296
Contig ID
                  613_1.R1010
5'-most EST
                  jC-atXLIB327422P3f07b2
Method
                  BLASTX
                  g1084337
NCBI GI
BLAST score
                  445
E value
                  8.0e-44
Match length
                  104
                  88
% identity
NCBI Description
                  drought-induced protein Di21 - Arabidopsis thaliana
                  >gi 469112 emb CAA55322 (X78585) Di21 [Arabidopsis
                  thaliana]
                  117297
Seq. No.
                  615 1.R1010
Contig ID
5'-most EST
                  LIB22-024-Q1-E1-D9
Method
                  BLASTX
NCBI GI
                  q2230757
                  2064
BLAST score
E value
                  0.0e + 00
Match length
                 426
                  94
% identity
NCBI Description (Y11969) dnaJ-like protein [Arabidopsis thaliana]
```

NCBI GI

q544134

```
Seq. No.
                   117298
                   616 1.R1010
Contig ID
                   LIB24-083-Q1-E1-C1
5'-most EST
Method
                   BLASTX
                   q2494165
NCBI GI
BLAST score
                   4041
                   0.0e + 00
E value
Match length
                   790
% identity
                   100
                   DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))
NCBI Description
                   >gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana
                   >gi_1359495_emb_CAA66599 (X97924) DNA ligase [Arabidopsis
                   thaliana]
                   117299
Seq. No.
Contig ID
                   617 1.R1010
                  LIB22-003-Q1-E1-E9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1084338
BLAST score
                   1090
                   1.0e-119
E value
                   209
Match length
                   100
% identity
NCBI Description
                   drought-induced protein Dr4 - Arabidopsis thaliana
                   >gi 469114_emb_CAA55323_ (X78586) Dr4 [Arabidopsis
                   thaliana]
                   117300
Seq. No.
                   617 2.R1010
Contig ID
5'-most EST
                   g957533
Method
                   BLASTN
NCBI GI
                   g469113
BLAST score
                   269
                   1.0e-149
E value
Match length
                   304
                   98
% identity
                  A.thaliana (Columbia) Dr4 mRNA
NCBI Description
Seq. No.
                   117301
Contig ID
                   618 1.R1010
5'-most EST
                   g2759203
Method
                   BLASTX
NCBI GI
                   q544134
                   807
BLAST score
                   2.0e-90
E value
Match length
                   386
% identity
                   38
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR
NCBI Description
                   >gi 99720 pir__S22863 hypothetical protein - Arabidopsis
                   thaliana \overline{>}gi \overline{42}1844 pir A46260 RecA functional analog
                   DRT100 - Arabidopsis thaliana (fragment)
Seq. No.
                   117302
                   618 2.R1010
Contig ID
5'-most EST
                   g1269339
Method
                  BLASTX
```

NCBI GI BLAST score

E value

```
BLAST score
                  207
E value
                  4.0e-16
Match length
                  162
% identity
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR
                  >gi 99720 pir S22863 hypothetical protein - Arabidopsis
                  thaliana >gi_421844_pir__A46260 RecA functional analog
                  DRT100 - Arabidopsis thaliana (fragment)
                  117303
Seq. No.
Contig ID
                  619 1.R1010
5'-most EST
                  jC-atXLIB327417P3h03b1
Method
                  BLASTX
NCBI GI
                  q4056424
BLAST score
                  1587
E value
                  1.0e-177
Match length
                  323
% identity
                  94
NCBI Description
                  (AC005322) Identical to 1-aminocyclopropane-1-carboxylate
                  oxidase (ACC oxidase) gb X66719 (EAT1). ESTs gb T43073,
                  gb T5714, gb R90435, gb R44023, gb AA597926, gb AI099676,
                  gb AA650810 and gb 29725 come from this gene. [Arabidopsis
                  thaliana]
                  117304
Seq. No.
Contig ID
                  619 2.R1010
5'-most EST
                  jC-atXLIB327429P1h11b2
Method
                  BLASTX
NCBI GI
                  q4056424
BLAST score
                  157
                  3.0e-10
E value
                  166
Match length
% identity
                  30
NCBI Description
                  (AC005322) Identical to 1-aminocyclopropane-1-carboxylate
                  oxidase (ACC oxidase) gb_X66719 (EAT1). ESTs gb_T43073,
                  gb_T5714, gb_R90435, gb_R44023, gb_AA597926, gb_AI099676,
                  gb AA650810 and gb 29725 come from this gene. [Arabidopsis
                  thaliana}
                  117305
Seq. No.
                  620 1.R1010
Contig ID
5'-most EST
                  g453894
Method
                  BLASTX
NCBI GI
                  g2497912
BLAST score
                  414
                  1.0e-40
E value
Match length
                  69
% identity
                  100
NCBI Description
                  EC PROTEIN HOMOLOG
Seq. No.
                  117306
Contig ID
                  622 1.R1010
5'-most EST
                  LIB23-024-Q1-E1-H12
Method
                  BLASTX
```

g3122265

1171 1.0e-129

```
235
Match length
                   92
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)
NCBI Description
                   (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT)
                   (EIF-4F P26 SUBUNIT) >gi 2288883 emb CAA71580_ (Y10548)
                  eIF4E protein [Arabidopsis thaliana]
                  117307
Seq. No.
Contig ID
                   623 1.R1010
5'-most EST
                  LIB24-021-Q1-E1-E8
                  BLASTX
Method
                  g3122263
NCBI GI
BLAST score
                   1011
E value
                   1.0e-110
Match length
                   211
                   90
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)
NCBI Description
                   (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-(ISO)4F 25 KD
                   SUBUNIT) (EIF-(ISO)4F P28 SUBUNIT) >gi_2209274 (U62044)
                   eukaryotic initiation factor (iso)-4F p28 subunit
                   [Arabidopsis thaliana]
                   117308
Seq. No.
                   624 1.R1010
Contig ID
                   LIB23-072-Q1-E1-D9
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4467104
BLAST score
                   1713
                   0.0e + 00
E value
                   357
Match length
% identity
                   93
                   (AL035538) cinnamyl-alcohol dehydrogenase ELI3-1
NCBI Description
                   [Arabidopsis thaliana]
                   117309
Seq. No.
                   624_3.R1010
Contig ID
                   g935600
5'-most EST
                   BLASTX
Method
                   q4467104
NCBI GI
BLAST score
                   439
                   2.0e-44
E value
Match length
                   117
                   79
% identity
                   (AL035538) cinnamyl-alcohol dehydrogenase ELI3-1
NCBI Description
                   [Arabidopsis thaliana]
                   117310
Seq. No.
                   626 1.R1010
Contig ID
                   jC-atXLIB327427P2d03b1
5'-most EST
                   BLASTX
Method
                   g1550738
NCBI GI
BLAST score
                   546
                   2.0e-55
E value
                   178
Match length.
% identity
                   (Y08061) endomembrane-associated protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2982443 emb CAA18251 (AL022224)
```

endomembrane-associated protein [Arabidopsis thaliana] 117311 Seq. No. 626 2.R1010 Contig ID jC-atXP104CE10F10T7b1 5'-most EST Method BLASTN = . g1550737 NCBI GI BLAST score 381 0.0e + 00E value Match length 538 92 % identity NCBI Description A.thaliana mRNA for endomembrane-associated protein 117312 Seq. No. 626_3.R1010 Contig ID $jC-\overline{a}tXLIB327418P1c09b1$ 5'-most EST Method BLASTX NCBI GI g2746341 BLAST score 834 2.0e-89 E value Match length 217 % identity 68 NCBI Description (AF037590) ATA27 [Arabidopsis thaliana] 117313 Seq. No. Contig ID 626 4.R1010 5'-most EST LIB3175-056-P1-K1-G6 BLASTN Method g3059018 NCBI GI BLAST score 41 2.0e-13 E value Match length 515 94 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project) Seq. No. 117314 Contig ID 626 9.R1010 5'-most EST jC-atXLIB327416P2f12b1 Method BLASTX q1076442 NCBI GI BLAST score 1609 E value 1.0e-180 Match length 402 % identity 73 beta-glucosidase (EC 3.2.1.21) - rape NCBI Description >gi_757740_emb_CAA57913_ (X82577) beta-glucosidase

 Seq. No.
 117315

 Contig ID
 626_10.R1010

 5'-most EST
 jC-atXP34C151G24T7a1

 Method
 BLASTX

 NCBI GI
 g3759184

[Brassica napus]

NCBI GI g3759184
BLAST score 53
E value 1.0e-23
Match length 76

Match length

```
% identity
                  69
NCBI Description
                  (AB018441) phi-1 [Nicotiana tabacum]
                  117316
Seq. No.
                  626 11.R1010
Contig ID
5'-most EST
                  LIB22-089-Q1-E1-B7
Method
                  BLASTX
                  g3759184
NCBI GI
BLAST score
                  229
                  1.0e-18
E value
                  103
Match length
                  48
% identity
NCBI Description
                   (AB018441) phi-1 [Nicotiana tabacum]
                  117317
Seq. No.
                  626 12.R1010
Contig ID
5'-most EST
                  jC-atXP41C163H1T7d1
                  BLASTX
Method
                  g3759184
NCBI GI
                  811
BLAST score
                  1.0e-86
E value
                  304
Match length
                  55
% identity
                  (AB018441) phi-1 [Nicotiana tabacum]
NCBI Description
                  117318
Seq. No.
                  626 13.R1010
Contig ID
5'-most EST
                  jC-atXP92C246M10T7041d1
                  BLASTX
Method
NCBI GI
                  g1550738
BLAST score
                  144
                  2.0e-19
E value
Match length
                  87
                  67
% identity
NCBI Description
                   (Y08061) endomembrane-associated protein [Arabidopsis
                  thaliana] >gi 2982443_emb_CAA18251_ (AL022224)
                  endomembrane-associated protein [Arabidopsis thaliana]
                  117319
Seq. No.
                  626 17.R1010
Contig ID
5'-most EST
                  LIB25-075-Q1-E1-E1
Method
                  BLASTX
                  q2746341
NCBI GI
                  57
BLAST score
                  6.0e-39
E value
Match length
                  106
% identity
                  71
                  (AF037590) ATA27 [Arabidopsis thaliana]
NCBI Description
                  117320
Seq. No.
                  626_18.R1010
Contig ID
5'-most EST
                  jC-atXLIB327427P1e05a2
Method
                  BLASTX
                  g2746341
NCBI GI
BLAST score
                  314
                  1.0e-28
E value
```

Method

BLASTX

```
% identity
                     79
 NCBI Description
                    (AF037590) ATA27 [Arabidopsis thaliana]
                     117321
 Seq. No.
                     627 1.R1010
 Contig ID
 5'-most EST.
                    LIB22-026-Q1-E1-H5
 Method
                     BLASTX
 NCBI GI
                    g549010
 BLAST score
                     2239
 E value
                     0.0e + 00
 Match length
                     435
 % identity
                     100
                    EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1)
 NCBI Description
                     (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG)
                    >gi 322554 pir__S31328 omnipotent suppressor protein SUP1
                     homolog (clone G18) - Arabidopsis thaliana
                    >gi_16514_emb_CAA49172_ (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic
                     early release factor subunit 1-like protein [Arabidopsis
                     thaliana] >gi_1495249_emb_CAA66118_ (X97486) eRF1-3
                     [Arabidopsis thaliana]
Seq. No.
                     117322
 Contig ID
                     627 2.R1010
 5'-most EST
                     PLN g16511
                    BLASTX
 Method
 NCBI GI
                    q322525
 BLAST score
                     1568
 E value
                     1.0e-175
 Match length
                     304
 % identity
                     100
 NCBI Description
                    omnipotent suppressor protein SUP1 homolog (clone A18) -
                     Arabidopsis thaliana (fragment) >gi_16512_emb_CAA49171_
                     (X69374) similar to yeast omnipotent suppressor protein
                     SUP1 (SUP45); ORF [Arabidopsis thaliana]
                     117323
 Seq. No.
 Contig ID
                     630 1.R1010
                     jC-atXLIB327413P1f05b1
 5'-most EST
 Method
                     BLASTX
                    g119723
 NCBI GI
 BLAST score
                    1811
 E value
                     0.0e + 00
 Match length
                     382
 % identity
                     92
 NCBI Description
                    FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                     (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                    >gi_99693 pir S16582 fructose-bisphosphatase (EC 3.1.3.11)
                    precursor, chloroplast - Arabidopsis thaliana
                    >gi_11242_emb_CAA41154_ (X58148) fructose-bisphosphatase
                    [Arabidopsis thaliana]
                    117324
 Seq. No.
 Contig ID
                     630 2.R1010
 5'-most EST
                    LIB3177-052-P1-K1-H10
```

```
NCBI GI
                  q119723
BLAST score
                  423
E value
                  1.0e-41
Match length
                  102
                  86
% identity
                  FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi_99693_pir__S16582 fructose-bisphosphatase (EC 3.1.3.11)
                  precursor, chloroplast - Arabidopsis thaliana
                  >gi_11242_emb_CAA41154_ (X58148) fructose-bisphosphatase
                  [Arabidopsis thaliana]
Seq. No.
                  117325
                  631 1.R1010
Contig ID
                  PLN_g3869250
5'-most EST
                  BLASTX
Method
                  q3869251
NCBI GI
BLAST score
                  8156
                  0.0e+00
E value
                  1622
Match length
                  97
% identity
                  (U39287) ferredoxin-dependent glutamate synthase precursor
NCBI Description
                  [Arabidopsis thaliana]
                  117326
Seq. No.
                  631 2.R1010
Contig ID
                  PLN_g1702871
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1702872
BLAST score
                  8312
                  0.0e + 00
E value
                  1648
Match length
                  98
% identity
                  (Y09667) ferredoxin-dependent glutamate synthase
NCBI Description
                  [Arabidopsis thaliana]
                  117327
Seq. No.
                  632 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327412P4c12b1
Method
                  BLASTX
                  g2129583
NCBI GI
BLAST score
                  1233
                  1.0e-136
E value
                  255
Match length
                  95
% identity
                  ferritin - Arabidopsis thaliana >gi_1246401_emb_CAA63932_
NCBI Description
                  (X94248) ferritin [Arabidopsis thaliana]
                  117328
Seq. No.
                  633 1.R1010
Contig ID
5'-most EST
                  LIB24-116-Q1-E1-E4
Method
                  BLASTX
NCBI GI
                  ·g2623990
BLAST score
                  2380
                  0.0e + 00
E value
Match length
                  511
```

91

% identity

```
NCBI Description (Y13156) ferrochelatase [Arabidopsis thaliana]
Seq. No.
                  117329
Contig ID
                  634 1.R1010
5'-most EST
                  g315562
Method
                  BLASTX
NCBI GI
                  q2369690
BLAST score
                  461
                  1.0e-52
E value
Match length
                  110
% identity
                  97
NCBI Description
                  (Y11988) FPF1 protein [Arabidopsis thaliana]
                  117330
Seq. No.
                  635 1.R1010
Contig ID
                  LIB23-037-Q1-E1-H3
5'-most EST
Method
                  BLASTX
                  g1872500
NCBI GI
                  1909
BLAST score
E value
                  0.0e + 00
Match length
                  384
                  95
% identity
NCBI Description
                  (U80605) farnesyl diphosphate synthase precursor
                   [Arabidopsis thaliana]
                  117331
Seq. No.
                  636 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327428P1c02b2
Method
                  BLASTX
                  g2492514
NCBI GI
BLAST score
                  3149
E value
                  0.0e + 00
Match length
                  692
% identity
                  92
                  CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
NCBI Description
                  >gi 1483215_emb_CAA68141_ (X99808) chloroplast FtsH
                  protease [Arabidopsis thaliana]
                  117332
Seq. No.
Contig ID
                  636 2.R1010
                  jC-atXLIB327432P4d09b1
5'-most EST
Method
                  BLASTX
                  g1170939
NCBI GI
BLAST score
                  866
E value
                  8.0e-93
                  192
Match length
                  87
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                  >gi_1084408_pir__S46540 methionine adenosyltransferase (EC
                  2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743)
                  S-adenosyl-L-methionine synthetase [Lycopersicon
                  esculentum]
                  117333
Seq. No.
Contig ID
                  636 3.R1010
5'-most EST
                  LIB3234-071-P1-K1-E7
```

Match length

360

```
Method
                  BLASTX
                  g2492514
NCBI GI
BLAST score
                  779
                  5.0e-83
E value
Match length
                  176
                  88
% identity
                  CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
NCBI Description
                  >gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH
                  protease [Arabidopsis thaliana]
                  117334
Seq. No.
                  637_1.R1010
Contig ID
5'-most EST
                  PLN g1174335
Method
                  BLASTX
                  g3021305
NCBI GI
BLAST score
                  247
                  0.0e+00
E value
                  560
Match length
% identity
                  92
                   (AJ001359) plastidic glucose-6-phosphate dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
                  117335
Seq. No.
                  638_1.R1010
Contig ID
5'-most EST
                  PLN_g1166404
                  BLASTX
Method
NCBI GI
                  g2146735
                  2552
BLAST score
                  0.0e + 00
E value
Match length
                  492
                  100
% identity
                  glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (clone
NCBI Description
                  E5) - Arabidopsis thaliana (fragment)
                  >gi_1166405_emb_CAA59011_ (X84229) glucose-6-phosphate
                  1-dehydrogenase [Arabidopsis thaliana]
                  117336
Seq. No.
                  639 1.R1010
Contig ID
                  jC-atXLIB327420P4e07b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g81615
BLAST score
                  1425
                  1.0e-158
E value
Match length
                  315
                  88
% identity
                  G-box-binding factor 1 - Arabidopsis thaliana
NCBI Description
                  >gi_16286_emb_CAA45356_ (X63894) G-box binding factor 1
                   [Arabidopsis thaliana]
                  117337
Seq. No.
                  640_1.R1010
Contig ID
5'-most EST
                  LIB22-030-Q1-E1-E10
Method
                  BLASTX
NCBI GI
                  g1169861
BLAST score
                  1458
                  1.0e-162
E value
```

5'-most EST

Method

g1565687

BLASTX

```
% identity
                   81
                  G-BOX BINDING FACTOR 2 >gi_81616_pir__S20884 G-box-binding
NCBI Description
                   factor 2 - Arabidopsis thaliana >gi_16288_emb_CAA45357
                   (X63895) G-box binding factor 2 [Arabidopsis thaliana]
                   >qi 3319286 (AF053228) G-box binding factor 2 [Arabidopsis
                   thaliana]
                   117338
Seq. No.
Contig ID
                   641_1.R1010
5'-most EST
                   jC-atXLIB327412P2f05b1
                   BLASTX
Method
NCBI GI
                   g3702322.
BLAST score
                   1780
                   0.0e + 00
E value
Match length
                   361
                   94
% identity
                   (AC005397) G-box binding factor [Arabidopsis thaliana]
NCBI Description
                  117339
Seq. No.
                   642_1.R1010
Contig ID
5'-most EST
                   g2596245
                  BLASTX
Method
NCBI GI
                   g421840
BLAST score
                   1843
E value
                   0.0e + 00
                   341
Match length
                   100
% identity
NCBI Description
                  hypothetical protein (clone GBGa476) - Arabidopsis thaliana
                  >gi. 311339 emb CAA50730 (X71915) unknown [Arabidopsis
                   thaliana]
                   117340
Seq. No.
                   644 1.R1010
Contig ID
5'-most EST
                  PLN g3093293
Method
                  BLASTX
                   g3093294
NCBI GI
BLAST score
                   4866
E value
                   0.0e + 00
Match length
                   974
% identity
                   96
NCBI Description
                   (Y12782) putative villin [Arabidopsis thaliana]
                   117341
Seq. No.
                   645 1.R1010
Contig ID
5'-most EST
                  LIB3175-056-P1-K1-F8
Method
                  BLASTX
NCBI GI
                   g1755162
BLAST score
                   1146
E value
                   1.0e-126
Match length
                   222
% identity
                  100
                  (U75192) germin-like protein [Arabidopsis thaliana]
NCBI Description
                  117342
Seq. No.
Contig ID
                   646 1.R1010
```

NCBI GI BLAST score

E value

```
NCBI GI
                       q1755156
     BLAST score
                       913
   . E value
                       1.0e-98
    Match length
                       194
% identity
                       93
     NCBI Description
                       (U75189) germin-like protein [Arabidopsis thaliana]
                       >gi 1755158 (U75190) germin-like protein [Arabidopsis
                       thaliana] >gi_1755170 (U75196) germin-like protein
                       [Arabidopsis thaliana] >gi_1755172 (U75197) germin-like
                       protein [Arabidopsis thaliana] >gi 1755180 (U75201)
                       germin-like protein [Arabidopsis thaliana] >gi 1755190
                       (U75206) germin-like protein [Arabidopsis thalīana]
                       >gi_1934728 (U95035) germin-like protein [Arabidopsis
                       thaliana] >gi_4154285 (AF090733) germin-like protein 1
                       [Arabidopsis thaliana] >gi 4666248 dbj BAA77207.1 (D89055)
                       germin-like protein precursor [Arabidopsis thaliana]
                       117343
     Seq. No.
                       646 4.R1010
     Contig ID
                       LIB3177-090-P1-K1-A2
     5'-most EST
                       BLASTX
     Method
                       g1934726
     NCBI GI
     BLAST score
                       541
                       2.0e-55
     E value
     Match length
                       145
                       78
     % identity
                       (U95034) germin-like protein [Arabidopsis thaliana]
     NCBI Description
                       117344
     Seq. No.
                       647 1.R1010
     Contig ID.
                       jC-atXLIB327408P3q04b1
     5'-most EST
                       BLASTX
     Method
     NCBI GI
                       g2828267
     BLAST score
                       2212
                       0.0e+00
     E value
     Match length
                       461
                       93
     % identity
                       (Y14044) geranylgeranyl reductase [Arabidopsis thaliana]
     NCBI Description
     Seq. No.
                       117345
                       647 3.R1010
     Contig ID
     5'-most EST
                       ARABL1-023-Q1-B1-D3
                       BLASTX
     Method
     NCBI GI
                       q2828267
     BLAST score
                       762
                       4.0e-81
     E value
     Match length
                       161
     % identity
                       (Y14044) geranylgeranyl reductase [Arabidopsis thaliana]
     NCBI Description
                       117346
     Seq. No.
     Contig ID
                       648 1.R1010
     5'-most EST
                       LIB23-005-Q1-E1-G12
     Method
                       BLASTX
```

q3292836

2740 0.0e + 00

```
Match length
                   522
                   100
% identity
NCBI Description
                   (AL031018) gamma-glutamylcysteine synthetase [Arabidopsis
                   thaliana] >gi_4262277_gb_AAD14544_ (AF068299)
gamma-glutamylcysteine synthetase [Arabidopsis thaliana]
Seq. No.
                   117347
                   648 2.R1010
Contig ID
5'-most EST
                   jC-alXLIB327436P1f04a1
Method
                   BLASTX
NCBI GI
                   q541858
BLAST score
                   1628
E value
                   0.0e + 00
Match length
                   296
                   100
% identity
                  endoxyloglucan transferase - Arabidopsis thaliana
NCBI Description
                   >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
                   transferase [Arabidopsis thaliana] >gi 4063757 (AC005561)
                   endo-xyloglucan transferase [Arabidopsis thaliana]
                   117348
Seq. No.
Contig ID
                   648 5.R1010
5'-most EST
                  ARABL1-047-Q1-E1-H11
Method
                   BLASTX
NCBI GI
                   q541858
                                                ....
BLAST score
                   126
E value
                   2.0e-06
Match length
                   204
% identity
                   86
                  endoxyloglucan transferase - Arabidopsis thaliana
NCBI Description
                   >gi_469484 dbj BAA03921 (D16454) endo-xyloglucan
                   transferase [Arabidopsis thaliana] >qi 4063757 (AC005561)
                   endo-xyloglucan transferase [Arabidopsis thaliana]
                   117349
Seq. No.
                   648 14.R1010
Contig ID
5'-most EST
                   jC-atXP89CG6D12T7046d1
Method
                   BLASTX
NCBI GI
                   g1170034
BLAST score
                   1207
E value
                   1.0e-133
Match length
                   255
% identity
                   93
NCBI Description
                  GLUTAMATE--CYSTEINE LIGASE PRECURSOR
                   (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS)
                   >gi_2129598 pir S60128 glutamate--cysteine ligase (EC
                  6.3.2.2) precursor, chloroplast - Arabidopsis thaliana
                   >gi_488615_emb_CAA82626_ (Z29490) gamma-glutamylcysteine
                   synthetase [Arabidopsis thaliana]
Seq. No.
                  117350
                   649 1.R1010
Contig ID
5'-most EST
                  PLN g1755167
Method
                  BLASTX
NCBI GI
                  g1755164
BLAST score
                   920
                   2.0e-99
E value
```

5'-most EST

```
Match length
                    211
                    87
 % identity
                    (U75193) germin-like protein [Arabidopsis thaliana]
 NCBI Description
                    >gi 1755168 (U75195) germin-like protein [Arabidopsis
                    thaliana] >gi_2239042_emb_CAA73213_ (Y12673) GLP3 protein [Arabidopsis thaliana] >gi_4666250_dbj_BAA77208.1_ (D89374)
                    germin-like protein 2 precursor [Arabidopsis thaliana]
 Seq. No.
                    117351
                    652 1.R1010
 Contig ID
                    LIB23-033-Q1-E1-F2
 5'-most EST
 Method
                    BLASTX
                    q3201613
 NCBI GI
 BLAST score
                    1124
 E value
                    1.0e-123
                    215
 Match length
                    100
 % identity
                    (AC004669) glutathione S-transferase [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    117352
                    652 2.R1010
 Contig ID
 5'-most EST
                    g2739662
 Method
                    BLASTX
                    g2462929
 NCBI GI
"BLAST score
                    490
 E value
                    2.0e-49
 Match length
                    123
 % identity
                    (Y12295) glutathione transferase [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    117353
 Contig ID
                    653 1.R1010
                    jC-atXLIB327408P3g08b1
 5'-most EST
 Method
                    BLASTX
                    g3913733
 NCBI GI
 BLAST score
                    660
                    1.0e-148
 E value
 Match length
                    258
 % identity
                    100
                    HYDROXYACYLGLUTATHIONE HYDROLASE CYTOPLASMIC ISOZYME
 NCBI Description
                    (GLYOXALASE II) (GLX II) >gi 1924921 emb CAA69644 (Y08357)
                    hydroxyacylglutathione hydrolase [Arabidopsis thaliana]
                    117354
 Seq. No.
                    655 1.R1010
 Contig ID
 5'-most EST
                    PLN g1109696
 Method
                    BLASTX
                    g1109697
 NCBI GI
 BLAST score
                    1945
                    0.0e + 00
 E value
                    378
 Match length
 % identity
                    97
                    (X83380) gibberellin 20-oxidase [Arabidopsis thaliana]
 NCBI Description
                    117355
 Seq. No.
                    656 1.R1010
 Contig ID
```

LIB3234-084-Q1-K1-G3

```
Method
                  BLASTX
                  q1109699
NCBI GI
BLAST score
                  2026
E value
                  0.0e + 00
Match length
                  380
% identity
                  100
NCBI Description
                  (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
                  117356
Seq. No.
                  657 1.R1010
Contig ID
5'-most EST
                  PLN g2072987
Method
                  BLASTX
                  g2072986
NCBI GI
                  1678
BLAST score
                  0.0e + 00
E value
                  326
Match length
                  97
% identity
                  (U95142) putative G-protein-coupled receptor [Arabidopsis
NCBI Description
                  thaliana] >gi 2072988 (U95143) putative G-protein-coupled
                  receptor [Arabidopsis thaliana]
                  117357
Seq. No.
                  659 1.R1010
Contig ID
5'-most EST
                  LIB24-031-Q1-E1-B10
Method
                  BLASTN
NCBI GI
                  g16298
                  433
BLAST score
                  0.0e + 00
E value
                  761
Match length
                  93
% identity
                  A.thaliana mRNA encoding glycine rich protein
NCBI Description
                  117358
Seq. No.
                  661 1.R1010
Contig ID
5'-most EST
                  LIB24-077-Q1-E1-D3
Method
                  BLASTX
                   g81629
NCBI GI
BLAST score
                   589
E value
                  2.0e-60
                  186
Match length
                   67
% identity
                  glycine-rich protein atGRP-7 - Arabidopsis thaliana
NCBI Description
                  >gi 16303 emb CAA77894 (Z11868) Glycine-rich protein
                   [Arabidopsis thaliana] >gi 16308 emb CAA77882 (Z11858)
                  Glycine Rich Protein [Arabidopsis thaliana]
                   117359
Seq. No.
                   661 4.R1010
Contig ID
5'-most EST
                   jC-atXLIB327408P2b06b1
Method
                  BLASTN
NCBI GI
                   q16306
BLAST score
                   161
                   3.0e-85
E value
Match length
                  310
                  15
% identity
NCBI Description A.thaliana genes encoding glycine-rich proteins
```

```
117360
Seq. No.
Contig ID
                   663 1.R1010
5'-most EST
                   LIB24-113-Q1-E1-B3
                   BLASTX
Method
                   g2129600
NCBI GI
BLAST score
                   2527
E value
                   0.0e + 00
Match length
                   496
                   99
% identity
                   glutathione synthase (EC 6.3.2.3) 2 - Arabidopsis thaliana
NCBI Description
                   (fragment) >gi_1107503_emb_CAA90515_ (Z50153) glutathione
                   synthetase [Arabidopsis thaliana] >gi_1585560_prf__2201360A
                   glutathione synthetase [Arabidopsis thaliana]
                   117361
Seq. No.
                   663 2.R1010
Contig ID
                   jC-atXLIB327408P4f09b1
 5'-most EST
                   BLASTX
Method
                   g2129600
NCBI GI
                   846
BLAST score
                   8.0e-91
E value
                   166
Match length
                   100
% identity
                   glutathione synthase (EC 6.3.2.3) 2 - Arabidopsis thaliana
NCBI Description
                   (fragment) >gi 1107503 emb CAA90515 (Z50153) glutathione
                   synthetase [Arabidopsis thaliana] >gi_1585560_prf__2201360A
                   glutathione synthetase [Arabidopsis thaliana]
                   117362
Seq. No.
                   663 4.R1010
Contig ID
                   jC-atXP89C244N13T7003d1
5'-most EST
                   BLASTX
Method
                   g2129600
NCBI GI
BLAST score
                   547
                   5.0e-56
E value
                   130
Match length
                   88
% identity
                   glutathione synthase (EC. 6.3.2.3) 2 - Arabidopsis thaliana
NCBI Description
                   (fragment) >gi 1107503 emb CAA90515 (Z50153) glutathione
                   synthetase [Arabidopsis thaliana] >gi_1585560_prf__2201360A
                   glutathione synthetase [Arabidopsis thaliana]
                   117363
 Seq. No.
                   666 1.R1010
 Contig ID
                   LIB25-049-Q1-E1-H4
 5'-most EST
                   BLASTX
Method
                   g3334349
NCBI GI
                   3490
BLAST score
                   0.0e+00
E value
                   729
Match length
                   93
% identity
                   GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)
NCBI Description
                   >gi 2564215 emb CAA05162_ (AJ002062) glycyl-tRNA synthetase
                   [Arabidopsis thaliana]
```

117364

668 1.R1010

Seq. No. Contig ID

5'-most EST

q2393361

```
PLN g4204911
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4204912
BLAST score
                   2781
                   0.0e + 00
E value
                   609
Match length
                   88
% identity
NCBI Description
                   (U58918) MEK kinase [Arabidopsis thaliana]
                   117365
Seq. No.
                   668_3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327437P2f07a1
                   BLASTX
Method
NCBI GI
                   g3688191
BLAST score
                   620
                   1.0e-64
E value
Match length
                   164
                   77
% identity
NCBI Description
                   (AJ010090) MAP3K alpha protein kinase [Arabidopsis
                   thaliana]
                   117366
Seq. No.
Contig ID
                   669 1.R1010
5'-most EST
                   jC-atXP73C223E5T7b1
Method
                   BLASTX
NCBI GI
                   g3775985
BLAST score
                   1997
E value
                   0.0e + 00
Match length
                   391
                   100
% identity
                   (AJ010456) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   117367
Seq. No.
                   669 3.R1010
Contig ID
5'-most EST
                   g1520708
Method
                   BLASTX
                   g3775985
NCBI GI
BLAST score
                   468
E value
                   1.0e-46
Match length
                   92
                   99
% identity
                   (AJ010456) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   117368
Seq. No.
Contig ID
                   670 1.R1010
5'-most EST
                   jC-atXP91CH1F4T7b1
Method .
                   BLASTX
                   q3775987
NCBI GI
BLAST score
                   3352
E value
                   0.0e + 00
Match length
                   748
% identity
                   90
                   (AJ010457) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117369
                   670 2.R1010
Contig ID
```

Method

3.

BLASTX

```
BLASTN
Method:
                  g3775986
NCBI GI
BLAST score
                  354
                  0.0e + 00
E value
                  397
Match length
                  98
% identity
NCBI Description Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
                  117370
Seq. No.
                  671_1.R1010
Contig ID
                  PLN_g3775988
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3775989
BLAST score
                  2004
                  0.0e + 00
E value
                  406
Match length
                  97
% identity
                  (AJ010458) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117371
                  672 1.R1010
Contig ID
                  LIB3168-060-P1-K1-F8
5'-most EST
                  BLASTX
Method
                  g3386613
NCBI GI
BLAST score
                  968
                  1.0e-105
E value
Match length
                  223
% identity
                  86
                  (AC004665) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                  thaliana]
                  117372
Seq. No.
                   672 2.R1010
Contig ID
                  jC-atXLIB327424P4f10b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3775991
                  597
BLAST score
                  1.0e-61
E value
Match length
                  112
                  99
% identity
                  (AJ010459) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  117373
Seq. No.
                  673 1.R1010
Contig ID
                  LIB3168-064-P1-K1-D10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3775993
BLAST score
                  2466
                  0.0e + 00
E value
                  505
Match length
% identity
                  94
NCBI Description
                  (AJ010460) RNA helicase [Arabidopsis thaliana]
                  117374
Seq. No.
                  673 2.R1010
Contig ID
                  LIB3234-085-Q1-K1-A6
5'-most EST
```

NCBI GI

```
g3775993
NCBI GI
BLAST score
                   310
E value
                   6.0e-28
Match length
                  119
                  59
% identity
                  (AJ010460) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  117375
Seq. No.
                   674_1.R1010
Contig ID
5'-most EST
                  PLN_g3775994
                  BLASTX
Method
NCBI GI
                  g3775995
BLAST score
                  1224
E value
                  1.0e-135
                  257
Match length
                  95
% identity
                  (AJ010461) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  117376
Seq. No.
                   675 1.R1010
Contig ID
                  jC-\overline{a}tXLIB327422P2e06b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3775997
BLAST score
                  1859
E value
                  0.0e + 00
Match length
                  365
                  100
% identity
                  (AJ010462) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117377
                   676 1.R1010
Contig ID
5'-most EST
                  LIB3234-058-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g4559339
BLAST score
                  1407
E value
                  1.0e-156
Match length
                  323
% identity
                  (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                  thaliana]
                  117378
Seq. No.
                   677 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327414P4g10b2
Method
                  BLASTX
NCBI GI
                  g3776001
BLAST score
                  2379
                  0.0e + 00
E value
Match length
                  498
                  93
% identity
NCBI Description
                  (AJ010464) RNA helicase [Arabidopsis thaliana]
                  117379
Seq. No.
                  677 2.R1010
Contig ID .
5'-most EST
                  LIB22-085-Q1-E2-F4
Method
                  BLASTX
```

g3193316

```
760
BLAST score
                   2.0e-80
E value
                   410
Match length
                   53
% identity
                   (AF069299) contains similarity to nucleotide sugar
NCBI Description
                  epimerases [Arabidopsis thaliana]
                  117380
Seq. No.
                   677 3.R1010
Contig ID
                  jC-atXLIB327414P4b07a2
5'-most EST
                  BLASTX
Method
                  g3193316
NCBI GI
BLAST score
                   253
E value
                   2.0e-21
Match length
                  125
% identity
                   48
                   (AF069299) contains similarity to nucleotide sugar
NCBI Description
                   epimerases [Arabidopsis thaliana]
Seq. No.
                   117381
Contig ID
                   678 1.R1010
5'-most EST
                  PLN g3776002
Method
                  BLASTX
                  g3776003
NCBI GI
                 2076
BLAST score
                 0.0e+00
E value
Match length
                   444
                   93
% identity
                  (AJ010465) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   117382
Seq. No.
Contig ID
                   679 1.R1010
                   jC-atXLIB327420P1h11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3776005
BLAST score
                   2165
                   0.0e+00
E value
Match length
                   436
                   97
% identity
NCBI Description
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   117383
                   679 3.R1010
Contig ID
                   LIB25-068-Q1-E1-F9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2500532
BLAST score
                   117
E value
                   1.0e-57
Match length
                   177
% identity
                   64
                   PROBABLE ATP-DEPENDENT RNA HELICASE WM6
NCBI Description
                   >gi 1079062 pir S51601 DEAD-box RNA helicase WM6 - fruit
                   fly (Drosophila melanogaster) >gi 158313 (L06018) DECD
                   family putative RNA helicase [Drosophila melanogaster]
                   >gi 505583 emb CAA56197 (X79802) WM6 [Drosophila
```

melanogaster]

```
Seq. No.
                  117384
                  680_1.R1010
Contig ID
                  PLN_g3776006
5'-most EST
                  BLASTX
Method
                  g3776007
NCBI GI
BLAST score
                  1018
E value
                  1.0e-111
Match length
                  259
                  81
% identity
                  (AJ010467) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  117385
Seq. No.
                  681_1.R1010
Contig ID
5'-most EST
                  PLN_g3776008
                  BLASTX
Method
                  q3776009
NCBI GI
                  1422
BLAST score
                  1.0e-158
E value
                  298
Match length
                  94
% identity
                  (AJ010468) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117386
Contig ID
                  682 1.R1010
5'-most EST
                  PLN_g3776010
                  BLASTX
Method
NCBI GI
                  g3776011
                  1737
BLAST score
                  0.0e + 00
E value
                  360
Match length
                   95
% identity
                  (AJ010469) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117387
                   683 1.R1010
Contig ID
5'-most EST
                   PLN_g3776012
Method
                  BLASTX
NCBI GI
                   g3776013
                   790
BLAST score
E value
                   3.0e-84
                   172
Match length
                   91
% identity
                   (AJ010470) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117388
                   684 1.R1010
Contig ID
5'-most EST
                  LIB3177-057-P1-K1-F7
Method
                  BLASTX
NCBI GI
                   g3776015
BLAST score
                   2478
E value
                   0.0e + 00
                   505
Match length
                   96
% identity
                   (AJ010471) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  >gi 4249378 gb AAD14475 (AC005966) Identical to
                   gb AJ010471 mRNA for DEAD box RNA helicase (RH22) from
                  Arabidopsis thaliana. EST gb Y11191 comes from this gene.
```

\$40

[Arabidopsis thaliana]

```
117389
Seq. No.
                  685 1.R1010
Contig ID
5'-most EST
                  jC-atXP79C231J2T7d2
                  BLASTX
Method
                  g1170503
NCBI GI
BLAST score
                  2102
                  0.0e + 00
E value
                  412
Match length
                  100
% identity
                  EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
NCBI Description
                  >gi 322503 pir JC1452 translation initiation factor
                  eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188
                   (X65052) eukaryotic translation initiation factor 4A-1
                   [Arabidopsis thaliana]
Seq. No.
                  117390
                   685 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P1g01b2
                  BLASTX
Method
                  g1170505
NCBI GI
BLAST score
                  2111
E value
                  0.0e + 00
                   412.
Match length
% identity
                  100
                  EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2)
NCBI Description
                  >gi 322504 pir JC1453 translation initiation factor
                  eIF-4A2 - Arabidopsis thaliana >gi 16556 emb CAA46189
                   (X65053) eukaryotic translation initiation factor 4A-2
                   [Arabidopsis thaliana] >gi 4585969 gb AAD25605.1 AC005287 7
                   (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis
                   thaliana]
                   117391
Seq. No.
                   685 3.R1010
Contig ID
5'-most EST
                   g2762228
Method.
                  BLASTX
NCBI GI
                   g3776021
BLAST score
                   2239
                   0.0e + 00
E value
                   439
Match length
                   100
% identity
                  (AJ010472) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117392
                   685 4.R1010
Contig ID
                   jC-\overline{a}tXP79C230N6T7b1
5'-most EST
                   BLASTX
Method
                   g1170503
NCBI GI
BLAST score
                   460
                   7.0e-62
E value
                   142
Match length
                   88
% identity
                  EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
NCBI Description
                  >gi 322503 pir JC1452 translation initiation factor
```

eIF-4A1 - Arabidopsis thaliana >gi 16554 emb CAA46188_

% identity

98

```
(X65052) eukaryotic translation initiation factor 4A-1
                   [Arabidopsis thaliana]
                  117393
Seq. No.
                  685 5.R1010
Contig ID
5'-most EST
                  iC-atXP96C248I1T7b1
                  BLASTX
Method
                  g1170503
NCBI GI
BLAST score
                  962
                  1.0e-124
E value
Match length
                  232
% identity
                  100
                  EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
NCBI Description
                  >gi 322503 pir JC1452 translation initiation factor
                  eIF-4A1 - Arabidopsis thaliana >gi 16554 emb CAA46188
                   (X65052) eukaryotic translation in \overline{1}tiation factor 4A-\overline{1}
                   [Arabidopsis thaliana]
                  117394
Seq. No.
Contig ID
                  685 10.R1010
5'-most EST
                  LIB3175-082-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g1170503
BLAST score
                  223
E value
                  9.0e-51
Match length
                  130
% identity
NCBI Description
                  EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
                  >gi 322503 pir JC1452 translation initiation factor
                  eIF-4A1 - Arabidopsis thaliana >gi 16554 emb CAA46188
                   (X65052) eukaryotic translation initiation factor 4A-1
                   [Arabidopsis thaliana]
Seq. No.
                  117395
Contig ID
                   685 11.R1010
5'-most EST
                  jC-atXLIB327414P3a01a1
Method
                  BLASTX
NCBI GI
                  g1170503
BLAST score
                  897
E value
                  7.0e-97
Match length
                  196
% identity
                   93
                  EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
NCBI Description
                  >gi 322503 pir JC1452 translation initiation factor
                  eIF-4A1 - Arabidopsis thaliana >gi 16554 emb CAA46188
                   (X65052) eukaryotic translation initiation factor 4A-1
                   [Arabidopsis thaliana]
Seq. No.
                  117396
Contig ID
                   686 1.R1010
5'-most EST
                  LIB3168-044-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g3776023
BLAST score
                 - 2778
                  0.0e + 00
E value
                  563
Match length
```

75

```
NCBI Description (AJ010473) RNA helicase [Arabidopsis thaliana]
                   117397
Seq. No.
                   686 2.R1010
Contig ID
                   jC-atX24101Q1E1D03b1
5'-most EST
                   BLASTX
Method
                   q3776025
NCBI GI
BLAST score
                   2702
                   0.0e + 00
E value
                   595
Match length
                   91
% identity
                  (AJ010474) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117398
                   688 1.R1010
Contig ID
                   PLN g3776026
5'-most EST
                  BLASTX
Method
                   g3776027
NCBI GI
                   3053
BLAST score
                   0.0e+00
E value
                   780
Match length
% identity
                   81
                   (AJ010475) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117399
                   689 1.R1010
Contig ID
5'-most EST
                   PLN g3776028
Method
                   BLASTX
NCBI GI
                   g3776029
BLAST score
                   1363
                   1.0e-151
E value
Match length
                   263
% identity
                   100
                  (AJ010476) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117400
                   691 1.R1010
Contig ID
                   jC-atX25022Q1E1G02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4127456
BLAST score
                   1241
E value
                   1.0e-137
Match length
                   253
% identity
                   100
                   (AJ010818) Cpn21 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117401 ...
                   691_2.R1010
Contig ID
                   jC-alXLIB327434P2a05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3057150
BLAST score
                   447
E value
                   4.0e-72
Match length
                   149
% identity
                   48
NCBI Description, (AF059037) chaperonin 10 [Arabidopsis thaliana]
```

```
Seq. No.
                  117402
                  692 1.R1010
Contig ID
                  jC-atXLIB327427P2c11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4490321
BLAST score
                  2777
E value
                  0.0e + 00
Match length
                  577
% identity
                  95
NCBI Description
                  (AJ011604) nitrate transporter [Arabidopsis thaliana]
                  117403
Seq. No.
Contig ID
                  696 1.R1010
5'-most EST
                  jC-atXLIB327423P1e10b1
Method
                  BLASTX
NCBI GI
                  q4006934
BLAST score
                  1157
E value
                  1.0e-127
Match length
                  219
                  100
% identity
                  (AJ012571) glutathione transferase [Arabidopsis thaliana]
NCBI Description
                  117404
Seq. No.
Contig ID:
                  696 3.R1010
5'-most EST
                  LIB35-041-Q1-E1-C9
Method
                  BLASTX
                  g4006934
NCBI GI -
BLAST score
                  663
E value
                  1.0e-75
Match length
                  198
% identity
                  76
                  (AJ012571) glutathione transferase [Arabidopsis thaliana]
NCBI Description
                  117405
Seq. No.
                  696 6.R1010
Contig ID
5'-most EST
                  LIB25-064-Q1-E1-D5
Method
                  BLASTX
                  g4006934
NCBI GI
BLAST score
                  496
E value
                  3.0e-50
Match length
                  94
                  100
% identity
NCBI Description
                  (AJ012571) glutathione transferase [Arabidopsis thaliana]
Seq. No.
                  117406
                  697 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327411P3c08b1
Method
                  BLASTX
NCBI GI
                  g121907
BLAST score
                  365
E value
                  3.0e - 34
                  133
Match length
% identity
                  61
                  HISTONE H1.2 >gi_70682_pir__HSMU12 histone H1.2 -
NCBI Description
                  Arabidopsis thaliana >gi_16320_emb_CAA44316_ (X62459)
                  Histone H1-2 [Arabidopsis thaliana] >gi 1946357 (U93215)
```

histone H1-2C [Arabidopsis thaliana]

```
Seq. No.
                   117407
Contig ID
                   697 2.R1010
5'-most EST
                   g2763829
Method
                  BLASTN
                   g16319
NCBI GI
BLAST score
                   282
E value
                   1.0e-157
Match length
                   282
% identity
                   100
                  A.thaliana H1-2C mRNA for histone H1-2
NCBI Description
                   117408
Seq. No.
Contig ID
                   698 1.R1010
5'-most EST
                   jC-alXLIB327436P4d10b1
Method
                   BLASTX
NCBI GI
                   q3929649
BLAST score
                   1632
E value
                   0.0e + 00
Match length
                   341
% identity
                   96
                   (AJ131205) mitochondrial NAD-dependent malate dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
                   117409
Seq. No.
Contig ID
                   699 1.R1010
5'-most EST
                   jC-atXLIB327417P1g06b1
Method
                   BLASTX
NCBI GI
                   q3929651
BLAST score
                   1774
                   0.0e + 00
E value
Match length
                   351
                   100
% identity
                   (AJ131206) microbody NAD-dependent malate dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   117410
                  700 1.R1010
Contig ID
5'-most EST
                   PLN g4140256
Method
                   BLASTX
NCBI GI
                   q4140257
BLAST score
                   1031
E value
                   1.0e-112
Match length
                   287
% identity
                  (AJ131342) LEA-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117411
Contig ID
                  700 2.R1010
5'-most EST
                  LIB3168-065-P1-K1-B4
                  BLASTN
Method
NCBI GI
                  q4159708
BLAST score
                   413
E value
                  0.0e+00
Match length
                  433
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
```

E value

MKP6, complete sequence

```
117412
Seq. No.
                  701 1.R1010
Contig ID
5'-most EST
                  LIB146-030-Q1-K1-E10
Method
                  BLASTX
                  g4006941
NCBI GI
BLAST score
                . 1343
E value
                  1.0e-149
Match length
                  274
% identity
                  96
                 (AJ131391) voltage-dependent anion-selective channel
NCBI Description
                  protein [Arabidopsis thaliana]
                  117413
Seq. No.
                  701 2.R1010
Contig ID
                  jC-atXP96C249J10T7b1
5'-most EST
                  BLASTX
Method
                  q4006941
NCBI GI
BLAST score
                  528
                  1.0e-53
E value
Match length
                  139
% identity
                  79
NCBI Description
                  (AJ131391) voltage-dependent anion-selective channel
                  protein [Arabidopsis thaliana]
                  117414
Seq. No.
                  703_1.R1010
Contig ID
5'-most EST
                  LIB23-056-Q1-E1-H2
Method
                  BLASTX
                  q4218144
NCBI GI
BLAST score
                  535
E value
                  1.0e-127
Match length
                  245
                  95
% identity
                  (AJ132398) glutathione transferase, GST 10b [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  117415
Contig ID
                  703_2.R1010
5'-most EST
                  g949657
Method
                  BLASTX
NCBI GI
                  q4049401
BLAST score
                  89
                  6.0e-60
E value
Match length
                  152
% identity
                  88
                  (AJ131580) glutathione transferase AtGST 10 [Arabidopsis
NCBI Description
                  thaliana]
                  117416
Seq. No.
Contig ID
                  704 1.R1010
5'-most EST
                  PLN g4038490
Method
                  BLASTX
NCBI GI
                  q4038491
BLAST score
                  4760
                  0.0e+00
```

```
983
Match length
% identity
                  93
                  (AJ131705) poly(ADP-ribose) polymerase [Arabidopsis
NCBI Description
                  thaliana]
                  117417
Seq. No.
Contig ID
                  706 1.R1010
5'-most EST
                  LIB22-003-Q1-E1-C11
Method
                  BLASTX
NCBI GI
                  g4185855
BLAST score
                  4868
                  0.0e + 00
E value
Match length
                  983
                  97
% identity
                  (AJ132388) Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
                  117418
Seq. No.
                  708 1.R1010
Contig ID
                  jC-atXP92C246M14T7057d1
5'-most EST
                  BLASTX
Method
                  g2281094
NCBI GI
BLAST score
                  1017
                  1.0e-111
E value
Match length
                  198
                  99
% identity
                  (AC002333) molybdenum cofactor biosynthesis protein E
NCBI Description
                  isolog [Arabidopsis thaliana] >gi 4469121 emb CAB38428
                  (AJ133519) molybdopterin synthase large subunit
                  [Arabidopsis thaliana]
                  117419
Seq. No.
                  708 2.R1010
Contig ID
5'-most EST
                  jC-atX25010Q1E1B01b1
Method
                  BLASTX
                  g2281094
NCBI GI
BLAST score
                  461
                  4.0e-46
E value
                  90
Match length .
                  100
% identity
                  (AC002333) molybdenum cofactor biosynthesis protein E
NCBI Description
                  isolog [Arabidopsis thaliana] >gi 4469121 emb CAB38428
                  (AJ133519) molybdopterin synthase large subunit
                  [Arabidopsis thaliana]
                  117420
Seq. No.
                  709 1.R1010
Contig ID
5'-most EST
                  PLN_g1498119
                  BLASTX
Method
NCBI GI
                  g1498120
BLAST score
                  3029
E value
                  0.0e + 00
                  658
Match length
                  93
% identity
                  (D85416) sulfate transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117421
```

710 1.R1010

Contig ID

```
5'-most EST
                  LIB23-008-Q1-E1-G12
Method
                  BLASTX
NCBI GI
                   g4033838
BLAST score
                   2264
E value
                  0.0e + 00
Match length
                  517
% identity
                  89
                  (Y18550) sigma-like factor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117422
                  711_1.R1010
Contig ID
5'-most EST
                  PLN_g4150962
                  BLASTX
Method
                  g4150963
NCBI GI
                  915
BLAST score
                  8.0e-99
E value
                  181
Match length
                  100
% identity
                  (Y18620) DsPTP1 protein [Arabidopsis thaliana]
NCBI Description
                  117423
Seq. No.
                  711 2.R1010
Contig ID
5'-most EST
                  g501872
Method
                  BLASTN
                  g4220635
NCBI GI
                  547
BLAST score
                  0.0e + 00
E value
                  592
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDB19, complete sequence [Arabidopsis thaliana]
                  117424
Seq. No.
                  712 1.R1010
Contig ID
5'-most EST
                  LIB25-109-Q1-E1-D9
                  BLASTX
Method
                  g266829
NCBI GI
                 : 1691
BLAST score
                  0.0e + 00
E value
Match length
                  318
% identity
                  100
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 1
NCBI Description
                  >gi 81655 pir S20882 phosphoprotein phosphatase (EC
                  3.1.3.16) 1 catalytic chain (clone TOPP1) - Arabidopsis
                  thaliana >gi 16431_emb_CAA45611_ (X64328) protein
                  phosphatase-1 [Arabidopsis thaliana] >gi 166572 (M93408)
                  phosphoprotein phosphatase 1 [Arabidopsis thaliana]
                  >gi 3980395 (AC004561) phosphoprotein phosphatase-type 1
                  catalytic subunit [Arabidopsis thaliana]
Seq. No.
                  117425
Contig ID
                  713 1.R1010
5'-most EST
                  PLN_g685233
                  BLASTX
Method
                  g1351999
NCBI GI
BLAST score
                  2330
                  0.0e+00
E value
```

```
473
Match length
                  96
% identity
                  HOMEOBOX PROTEIN ATH1 >gi_685234_emb_CAA56426_ (X80126) H1
NCBI Description
                  [Arabidopsis thaliana] >gi 3688179 emb CAA21207 (AL031804)
                  homeobox gene ATH1 [Arabidopsis thaliana]
                  117426
Seq. No.
                  714 1.R1010
Contig ID
                  PLN_g3319885
5'-most EST
                  BLASTX
Method
                  g3319884
NCBI GI
BLAST score
                  1932
                  0.0e + 00
E value
Match length
                  390
                  91
% identity
                  (AJ224306) PRT1 [Arabidopsis thaliana]
NCBI Description
                  >gi 3319886 emb CAA11892 (AJ224307) PRT1 [Arabidopsis
                  thaliana]
                  117427
Seq. No.
                  715 1.R1010
Contig ID
                  jC-atXLIB327405P2b04b2
5'-most EST
                  BLASTX
Method
                  g2407800
NCBI GI
BLAST score
                  556
                  7.0e-57
E value
Match length
                  123
% identity
                  93
                  (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117428
                  716 1.R1010
Contig ID
                  LIB3175-019-P1-K1-H10
5'-most EST
                  BLASTX
Method
                  g2407802
NCBI GI
BLAST score
                  451
                  1.0e-44
E value
                  92
Match length
                  100
% identity
NCBI Description
                  (Y12576) histone H2B [Arabidopsis thaliana]
                  117429
Seq. No.
                  716 2.R1010
Contig ID
5'-most EST
                  q931113
Method
                  BLASTX
NCBI GI
                  g2407802
BLAST score
                  330
                  2.0e-30
E value
                  77
Match length
                  99
% identity
NCBI Description
                  (Y12576) histone H2B [Arabidopsis thaliana]
                  117430
Seq. No.
                  716 3.R1010
Contig ID
5'-most EST
                  LIB35-015-Q1-E1-F6
Method
                  BLASTX
NCBI GI
                  g2558962
```

```
449
BLAST score
                   2.0e-44
E value
Match length
                   92
                   99
% identity
                   (AF025667) histone H2B1 [Gossypium hirsutum]
NCBI Description
                   117431
Seq. No.
                   716 4.R1010
Contig ID
                  LIB25-022-Q1-E1-H12
5'-most EST
                   BLASTX
Method
                   g1617013
NCBI GI
BLAST score
                   385
                   3.0e-37
E value
Match length
                   79
                   99
% identity
                   (Y07745) histone H2B like protein [Arabidopsis thaliana]
NCBI Description
                   117432
Seq. No.
                   716 5.R1010
Contig ID
                   jC-atXP110C119E17T7d1
5'-most EST
                   BLASTX
Method
                   g4580384
NCBI GI
                   422
BLAST score
                   4.0e-41
E valúe
Match length
                   86
                   100
% identity
                   (AC007184) putative histone H2B [Arabidopsis thaliana]
NCBI Description
                   117433
Seq. No.
                   716 6.R1010
Contig ID
                   LIB35-038-Q1-E1-E6
5'-most EST
                   BLASTX
Method
                   g4056497
NCBI GI
BLAST score
                   483
                   2.0e-48
E value
Match length
                   108
                   92
% identity
                   (AC005896) putative histone H2B [Arabidopsis thaliana]
NCBI Description
                   117434
Seq. No.
                   717 1.R1010
Contig ID
5'-most EST
                   g2722431
Method
                   BLASTX
                   g2739375
NCBI GI
BLAST score
                   590
E value
                   5.0e-61
Match length
                   119
                   100
% identity
                   (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                   117435
Seq. No.
                   719 1.R1010
Contig ID
                   PLN_g3096909
5'-most EST
                   BLASTX
Method
                   g3096910
NCBI GI
BLAST score
                   2764
                   0.0e + 00
E value
```

```
538
Match length
% identity
                  98
                  (AJ005813) neoxanthin cleavage enzyme [Arabidopsis
NCBI Description
                  thaliana]
                  117436
Seq. No.
                  720 1.R1010
Contig ID
5'-most EST
                  LIB22-027-Q1-E1-H5
Method ·
                  BLASTX
                  g3201477
NCBI GI
                  2230
BLAST score
                  0.0e+00
E value
                  507
Match length
% identity
NCBI Description
                  (AJ006021) putative PRL1 associated protein [Arabidopsis
                  thaliana]
Seq. No.
                  117437
Contig ID
                  721 1.R1010
5'-most EST
                  jC-atXLIB327409P3c11a1
Method
                  BLASTX
NCBI GI
                  g4773885
BLAST score
                  1038
E value
                  1.0e-113
Match length
                  198
% identity
NCBI Description
                  (AF076243) putative aspartic protease [Arabidopsis
                  thaliana]
Seq. No.
                  117438
Contig ID
                  721 2.R1010
5'-most EST
                  LIB23-028-Q1-E1-B1
Method
                  BLASTX
NCBI GI
                  g3980254
BLAST score
                  979
E value
                  1.0e-106
Match length
                  190
% identity
                  100
                  (AJ006053) peroxisomal membrane protein [Arabidopsis
NCBI Description
                  thaliana] >gi 4773886 gb AAD29759.1 AF076243 6 (AF076243)
                  pmp22 peroxisomal membrane protein [Arabidopsis thaliana]
Seq. No.
                  117439
Contig ID
                  721 3.R1010
                  jC-atXLIB327421P3a04b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4773885
BLAST score
                  1011
E value
                  0.0e+00
Match length
                  361
% identity
NCBI Description
                  (AF076243) putative aspartic protease [Arabidopsis
                  thaliana]
                  117440
Seq. No.
Contig ID
                  723 1.R1010
5'-most EST
                  PLN q3559804
```

```
Method
                   BLASTX
NCBI GI
                   q3559805
BLAST score
                   1867
                   0.0e + 00
E value
                   343
Match length
% identity
                   98
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   117441
Seq. No.
Contig ID
                   723 2.R1010
                   jC-\overline{a}1XLIB327436P4h03b1
5'-most EST
Method
                   BLASTX
NCBI GI
                  q2160169
BLAST score
                   569
                   2.0e-58
E value
Match length
                   167
% identity
                   63
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   117442
Seq. No.
                   723 3.R1010
Contig ID
5'-most EST
                   g2047940
Method
                  BLASTN
                 ,..g2618603
NCBI GI
                  296
BLAST score
                   1.0e-165
E value
Match length
                   450
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSL3, complete sequence [Arabidopsis thaliana]
                   117443
Seq. No.
                   723 4.R1010
Contig ID
                   jC-atXLIB327439P1c03b2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3559805
BLAST score
                   492
E value
                   2.0e-57
Match length
                   144
% identity
                   81
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                  thaliana]
                   117444
Seq. No.
                  723 5.R1010
Contig ID
5'-most EST
                  ARABL1-024-Q1-B1-C8
                   BLASTN
Method
NCBI GI
                   g3559804
BLAST score
                   115
E value
                  8.0e-58
Match length
                  256
% identity
                   91
                  Arabidopsis thaliana mRNA for putative phytochelatin
NCBI Description
                   synthetase
```

117445

Seq. No.

```
725_1.R1010
Contig ID
                   PLN_g3242070
5'-most EST
                  BLASTX
Method :
                   q3242071
NCBI GI
                   1520
BLAST score
E value
                   1.0e-169
Match length
                   323
% identity
                   (AJ007289) myb-like protein [Arabidopsis thaliana]
NCBI Description
                   117446
Seq. No.
                   726 1.R1010
Contig ID
5'-most EST
                   LIB23-048-Q1-E1-B4
                   BLASTX
Method:
                   g4049632
NCBI GI
                   1913
BLAST score
                   0.0e + 00
E value
Match length
                   366
                   100
% identity
                   (AF039406) pyruvate dehydrogenase kinase [Arabidopsis
NCBI Description
                   thaliana]
                   117447
Seq. No.
                   727_1.R1010
Contig ID
5'-most EST
                   PLN g3286690
                   BLASTX
Method_
                   g3286691
NCBI GI
                   1687
BLAST score
E value
                   0.0e + 00
                   452
Match length
                   77
% identity
                   (AJ007450) auxilin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117448
                   728_1.R1010
Contig ID
5'-most EST
                   PLN_g3292848
                   BLASTX
Method
                   g3292849
NCBI GI
BLAST score
                   1856
E value
                   0.0e + 00
                   376
Match length
% identity
                   (AJ007582) arginine methyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   117449
Seq. No.
                   728_3.R1010
Contig ID
                   LIB\overline{2}4-078-Q1-E1-E6
5'-most EST
Method
                   BLASTX
                   g3292849
NCBI GI
BLAST score
                   321
                   3.0e - 34
E value
Match length
                   95
                   83.
% identity
                   (AJ007582) arginine methyltransferase [Arabidopsis
NCBI Description
```

thaliana]

```
117450
Seq. No.
                  729 1.R1010
Contig ID
5'-most EST
                  LIB3175-033-P1-K1-F5
                   BLASTN
Method
NCBI GI
                  g3426057
BLAST score
                   613
E value
                   0.0e+00
Match length
                   613
% identity
                   100
NCBI Description Arabidopsis thaliana mRNA for IB1P8-4 protein
                  117451
Seq. No.
                  730 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327409P2a09b1
Method
                   BLASTX
NCBI GI
                   q3426060
BLAST score
                   903
                   3.0e-97
E value
Match length
                   202
% identity
                   88
                  (AJ007586) src2-like protein [Arabidopsis thaliana]
NCBI Description
                  117452
Seq. No.
                  731 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327423P3c09b1
Method
                   BLASTX
NCBI GI
                   g3426062
BLAST score
                   1916
                   0.0e + 00
E value
                   397
Match length
% identity
                   94
NCBI Description (AJ007587) monooxygenase [Arabidopsis thaliana]
Seq. No.
                   117453
                  732 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327409P2h07b1
Method
                   BLASTX
                  g3426064
NCBI GI
BLAST score
                   2024
E value
                   0.0e+00
                   407
Match length
% identity
                   95
                   (AJ007588) monooxygenase [Arabidopsis thaliana]
NCBI Description
                  >gi 4467141 emb CAB37510 (AL035540) monooxygenase 2 (MO2)
                   [Arabidopsis thaliana]
Seq. No.
                  117454 .
                  732 2.R1010
Contig ID
5'-most EST
                  g1269288
Method
                  BLASTX
                  q2739365
NCBI GI
BLAST score
                  908
E value
                  4.0e-98
Match length .
                  199
% identity
                  83
```

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

```
117455
 Seq. No.
 Contig ID
                   732 3.R1010
 5'-most EST
                   LIB35-040-Q1-E1-F3
 Method
                   BLASTX
                   g2244827
 NCBI GI
 BLAST score
                   574
                   1.0e-69
 E value
                   218
Match length
 % identity
                   60
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   117456
 Contig ID
                   732 6.R1010
 5'-most EST
                   jC-atXLIB327402P4b03b1
Method
                   BLASTX
NCBI GI
                   g2244827
BLAST score
                   489
 E value
                   3.0e-49
Match length
                   91
 % identity
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   117457
Seq. No.
Contig ID
                   732 8.R1010
 5'-most EST
                   LIB35-025-Q1-E1-F4
Method
                   BLASTN
NCBI GI
                   q4539331
BLAST score
                   310
E value
                   1.0e-174
Match length
                   318
                   99
 % identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13
 NCBI Description
                   (ESSA project)
Seq. No.
                   117458
 Contig ID
                   734 1.R1010
 5'-most EST
                   LIB3177-022-P1-K2-A5
Method
                   BLASTX
NCBI GI
                   q3688162
 BLAST score
                   864
 E value
                   5.0e-93
Match length
                   169
 % identity
                   100
NCBI Description (AJ009672) centrin [Arabidopsis thaliana]
 Seq. No.
                   117459
 Contig ID
                   734 2.R1010
 5'-most EST
                   LIB3234-071-P1-K1-A12
 Method
                   BLASTN
NCBI GI
                   g3688161
 BLAST score
                   105
 E value
                   6.0e-52
Match length
                   171
 % identity
                   97
 NCBI Description Arabidopsis thaliana mRNA for centrin
```

2

117460

Seq. No.

```
Contig ID
                   735 1.R1010
5'-most EST
                   jC-alXLIB327435P3h07b1
Method
                   BLASTX
                   g541848
NCBI GI
BLAST score
                   2428
E value
                   0.0e + 00
Match length
                   485
% identity
NCBI Description
                   amino acid transport protein I - Arabidopsis thaliana
                   >gi_22641_emb_CAA47603_ (X67124) amino acid permease I
[Arabidopsis thaliana] >gi_404019 (L16240) amino acid
                   transporter [Arabidopsis thaliana]
                   117461
Seq. No.
                   737_1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327420P3c10b1
Method
                   BLASTX
NCBI GI
                   q543841
BLAST score
                   616
                   5.0e-92
E value
Match length
                   180
                   95
% identity
NCBI Description
                   ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir___$28875
                   ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                   >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   tha \overline{\text{liana}} >gi 4630747 gb AAD26597.1 AC007236 2 (AC007236)
                   ADP-ribosylation factor [Arabidopsis thaliana]
                   117462
Seq. No.
                   737 2.R1010
Contig ID
5'-most EST
                   jC-atXP118C155E20T7055d2
Method
                   BLASTX
NCBI GI
                   g543841
BLAST score
                   636
                   2.0e-95
E value
Match length
                   181
                   99
% identity
                   ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir___$28875
NCBI Description
                   ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                   >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   thaliana] >gi 4630747 gb AAD26597.1 AC007236 2 (AC007236)
                   ADP-ribosylation factor [Arabidopsis thaliana]
                   117463
Seq. No.
                   737 4.R1010
Contig ID
5'-most EST
                   jC-alXLIB327436P2h06b1
Method
                   BLASTX
NCBI GI
                   q4056469
BLAST score
                   768
E value
                   1.0e-81
Match length
                   186
% identity
                   84
NCBI Description
                   (ACO05990) Strong similarity to gb M95166 ADP-ribosylation
                   factor from Arabidopsis thaliana. ESTs gb_Z25826,
                   gb R90191, gb N65697, gb AA713150, gb T46332, gb AA040967,
```

NCBI GI

BLAST score E value

1248

1.0e-138

```
gb AA712956, gb T46403, gb T46050, gb AI100391 and
                   gb Z25043 come from t
                   117464
 Seq. No.
                   737 5.R1010
 Contig ID
 5'-most EST
                   jC-atXP80C24001T7d1
                   BLASTX
 Method
                   g4056469
 NCBI GI
 BLAST score
                   383
                   2.0e-96
 E value
                   181
 Match length
                   100
 % identity
                   (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
 NCBI Description
                   factor from Arabidopsis thaliana. ESTs gb_Z25826,
                   gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
                   gb AA712956, gb T46403, gb T46050, gb AI100391 and
                   gb Z25043 come from t
                   117465
 Seq. No.
                   737 8.R1010
 Contig ID
                   g1269524
 5'-most EST
 Method
                   BLASTX
                   g543841
 NCBI GI
 BLAST score
                   132
 E value
                   3.0e-41
                   90
 Match length
                   99
 % identity
                   ADP-RIBOSYLATION FACTOR 1 >gi 322518_pir__S28875
 NCBI Description
                   ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                   >gi 2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   thaliana] >gi 4630747 gb AAD26597.1 AC007236 2 (AC007236)
                   ADP-ribosylation factor [Arabidopsis thaliana]
                   117466
 Seq. No.
 Contig ID
                   737 9.R1010
                   LIB3176-116-P2-K1-A9
 5'-most EST
                   BLASTX -
 Method
                   q543841
 NCBI GI
 BLAST score
                   733
                   7.0e-84
 E value
 Match length
                   174
                   95
 % identity
                   ADP-RIBOSYLATION FACTOR 1 >gi 322518_pir__S28875
 NCBI Description
                   ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                   >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236)
                   ADP-ribosylation factor [Arabidopsis thaliana]
                   117467
 Seq. No.
 Contig ID
                   738 1.R1010
 5'-most EST
                   LIB24-047-Q1-E1-A12
Method
                   BLASTX
                   g113512
```

```
Match length
                   248
 % identity
                   96
                   FLORAL HOMEOTIC PROTEIN AGL2 >gi_81610_pir__B39534 floral
· NCBI Description
                   homeotic protein AGL2 - Arabidopsis thaliana >gi_166591
                   (M55551) transcription factor [Arabidopsis thaliana]
                   117468
 Seq. No.
                   739 1.R1010
 Contig ID
 5'-most EST
                   LIB24-063-Q1-E1-F10
                   BLASTX
 Method
 NCBI GI
                   g113514
BLAST score
                   1308
E value
                   1.0e-145
                   249
Match length
                   100
 % identity
                   FLORAL HOMEOTIC PROTEIN AGL4 >gi 81612 pir D39534 floral
 NCBI Description
                   homeotic protein AGL4 - Arabidopsis thaliana >gi_166594
                   (M55552) transcription factor [Arabidopsis thaliana]
                   117469
 Seq. No.
                   740 1.R1010
 Contig ID
 5'-most EST
                   LIB25-001-Q1-E1-G12
                   BLASTX
 Method
NCBI GI
                   g4512687
                                                                     3 to 1
BLAST score
                   1152
 E value
                   1.0e-126
                   244
Match length
 % identity
                   (ACO06931) floral homeotic protein AGL5 [Arabidopsis
NCBI Description
                   thaliana]
                   117470
 Seq. No.
 Contig ID
                   740 2.R1010
                   jC-atXLIB327420P1e11b1
 5'-most EST
                   BLASTX
Method
                   g113511
NCBI GI
BLAST score
                   760
E value
                   1.0e-110
Match length
                   239
 % identity
                   88
                   FLORAL HOMEOTIC PROTEIN AGL1 >gi 81609_pir__ A39534 floral
NCBI Description
                   homeotic protein AGL1 - Arabidopsis thaliana >gi 166588
                   (M55550) transcription factor [Arabidopsis thaliana]
                   117471
 Seq. No.
                   740 3.R1010
 Contig ID
 5'-most EST .
                   jC-atX24123Q1E2A05b1
 Method
                   BLASTX
 NCBI GI
                   g113511
 BLAST score
                   581
                   4.0e-60
 E value
 Match length
                   114
 % identity
                   100
                   FLORAL HOMEOTIC PROTEIN AGL1 >gi 81609 pir_A39534 floral
 NCBI Description
                   homeotic protein AGL1 - Arabidopsis thaliana >gi 166588
```

(M55550) transcription factor [Arabidopsis thaliana]

```
117472
Seq. No.
Contig ID
                  742 1.R1010
5'-most EST
                  PLN g217826
Method
                  BLASTX
NCBI GI
                  g1170182
BLAST score
                  1332
E value
                  1.0e-147
                  294
Match length
                  91
% identity
                  TRANSCRIPTION FACTOR HBP-1B >gi_479793_pir__S35439
NCBI Description
                  transcription factor HBP-1b homolog - Arabidopsis thaliana
                  >gi 217827 dbj BAA00933 (D10042) AHBP-1b [Arabidopsis
                  thaliana]
                  117473
Seq. No.
                  743_1.R1010
Contig ID
                  PLN_g469192
5'-most EST
                  BLASTX
Method
                  q1076286
NCBI GI
BLAST score
                  2612
                  0.0e + 00
E value
                  506
Match length
                  100
% identity
                  amidophosphoribosyltransferase - Arabidopsis thaliana
NCBI Description
                  >gi 469193 dbj BAA06023 (D28868)
                  amidophosphoribosyltransferase [Arabidopsis thaliana]
Seq. No.
                  117474
                  743 2.R1010
Contig ID
                  jC-atXP72C221P15T7d1
5'-most EST
Method
                  BLASTX
                  g1076285
NCBI GI
BLAST score
                  850
E value
                  2.0e-91
Match length
                  167
% identity
                  98
                  amidophosphoribosyltransferase - Arabidopsis thaliana
NCBI Description
                  >gi 469195 dbj BAA06024 (D28869)
                  amidophosphoribosyltransferase [Arabidopsis thaliana]
                  117475
Seq. No.
Contig ID
                  744 1.R1010
                  LIB146-018-Q1-E1-F9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g113782
BLAST score
                  2571
E value
                  0.0e+00
Match length
                  498
% identity
                  BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE)
NCBI Description
                  >gi 486824 pir S36094 beta-amylase (EC 3.2.1.2) -
                  Arabidopsis thaliana >gi 166602 (M73467) beta-amylase
                   [Arabidopsis thaliana] >gi 228699 prf 1808329A beta
                  amylase [Arabidopsis thaliana]
                  117476
Seq. No.
```

744 2.R1010

Contig ID

```
g1053982
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2244879
BLAST score
                  415
                  2.0e-40
E value
                  79
Match length
                  100
% identity
                  (Z97338) Nucleotide sequence of a cDNA clone encoding a
NCBI Description
                  beta-amylase from Arabidopsis thaliana
                  117477
Seq. No.
                  745 1.R1010
Contig ID
5'-most EST
                  LIB3176-073-P1-K1-A8
Method
                  BLASTX
                  g2398521
NCBI GI
BLAST score
                  1224
                  1.0e-135
E value
                  270
Match length
                  86
% identity
                  (Y13720) transcription factor [Arabidopsis thaliana]
NCBI Description
                  117478
Seq. No.
                  746 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327412P3c10b1
Method
                  BLASTX
                  g2398523
NCBI GI
BLAST score
                  1441
                  1.0e-160
E value
                  295
Match length
                  94
% identity
                  (Y13721) Transcription factor [Arabidopsis thaliana]
NCBI Description
                  117479
Seq. No.
                  747 1.R1010
Contig ID
                  jC-atXLIB327439P1h06b2
5'-most EST
Method
                  BLASTX
                  g2398525
NCBI GI
BLAST score
                  1609
                  1.0e-180
E value
Match length
                  340
% identity
                  91
                  (Y13722) Transcription factor [Arabidopsis thaliana]
NCBI Description
                  117480
Seq. No.
                  748 1.R1010
Contig ID
5'-most EST
                  PLN g2398526
Method
                  BLASTX
                  g2398527
NCBI GI
BLAST score
                  653
                  3.0e-68
E value
Match length
                  141
% identity
                  (Y13723) Transcription factor [Arabidopsis thaliana]
NCBI Description
                  117481
Seq. No.
                  749 1.R1010
Contig ID
5'-most EST
                  jC-atXP91C247D4T7b1
```

```
BLASTX
Method
                  g2398529
NCBI GI
BLAST score
                   614
                  2.0e-63
E value
                  119
Match length
                  100
% identity
                  (Y13724) Transcription factor [Arabidopsis thaliana]
NCBI Description
                  117482
Seq. No.
                  750 1.R1010
Contig ID
                  LIB3177-016-P1-K2-B5
5'-most EST
                  BLASTX
Method
                  g3776575
NCBI GI
BLAST score
                   464
                   5.0e-46
E value
                  119
Match length
                   76
% identity
                   (AC005388) Similar to Schizosaccharomyces CCAAT-binding
NCBI Description
                   factor F7G19.16 gi 1922964 from Arabidopsis thaliana BAC
                   gb AC000106. EST gb H36963 comes from this gene.
                   [Arabidopsis thaliana]
                   117483
Seq. No.
                  750 2.R1010
Contig ID
                   jC-atXmonuni26Aellbl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2398531
BLAST score
                   616
                   9.0e-64
E value
                   132
Match length
% identity
                   90
                  (Y13726) Transcription factor [Arabidopsis thaliana]
NCBI Description
                   117484
Seq. No.
                   751 1.R1010
Contig ID
                   LIB3175-019-P1-K1-B5
5'-most EST
                   BLASTX
Method
                   g2398533
NCBI GI
BLAST score
                   671
E value
                   3.0e-70
Match length
                   129
% identity
                  (Y13725) Transcription factor [Arabidopsis thaliana]
NCBI Description
                   117485
Seq. No.
                   752 1.R1010
Contig ID
5'-most EST
                   PLN g166607
                   BLASTX
Method
                   q543815
NCBI GI
BLAST score
                   1207
                   1.0e-133
E value
Match length
                   232
% identity
                   100
                  FLORAL HOMEOTIC PROTEIN APETALA3 >gi 282855 pir A42095
NCBI Description
                   homeotic protein AP3 - Arabidopsis thaliana >gi_166608
```

(M86357) APETELA3 [Arabidopsis thaliana]

NCBI GI

g114088

```
Seq. No.
                  117486
                  753 1.R1010
Contig ID
                  LIB24-053-Q1-E1-F9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1742965
BLAST score
                  1931
E value
                  0.0e + 00
Match length
                  421
% identity
                  92
NCBI Description (Y09562) HAPp48,5 protein [Arabidopsis thaliana]
                  117487
Seq. No.
Contig ID
                  754 1.R1010
5'-most EST
                  LIB3176-087-P1-K1-F1
                  BLASTX
Method '
NCBI GI
                  g114086
BLAST score
                  1037
E value
                  1.0e-113
                  216
Match length
                  94
% identity
                  RAS-RELATED PROTEIN ARA-2 >gi 320559 pir JS0639
NCBI Description
                  GTP-binding protein ara-2 - Arabidopsis thaliana
                  >gi_217835_dbj_BAA00829_ (D01024) small GTP-binding protein
                  [Arabidopsis thaliana]
                  117488
Seq. No.
                  755 1.R1010
Contig ID
5'-most EST
                  g930727
                  BLASTX
Method
NCBI GI
                  g114088
BLAST score
                  850
E value
                  3.0e-91
                  202
Match length
% identity
                  85
NCBI Description
                  RAS-RELATED PROTEIN ARA-3 >gi_320560_pir__JS0640
                  GTP-binding protein ara-3 - Arabidopsis thaliana
                  >gi_217837_dbj_BAA00830_ (D01025) small GTP-binding protein
                  [Arabidopsis thaliana]
                  117489
Seq. No.
Contig ID
                  755 2.R1010
5'-most EST
                  jC-atXLIB327408P3e11b1
                  BLASTX
Method
NCBI GI
                  g1362066
BLAST score
                  652
                  2.0e-73
E value
                  200
Match length
% identity
                  78
                  small GTP-binding protein - garden pea
NCBI Description
                  >gi 871510 emb CAA90080 (Z49900) small GTP-binding protein
                  [Pisum sativum]
                  117490
Seq. No.
                  755 3.R1010
Contig ID
                  jC-atXLIB327409P1h10b1
5'-most EST
Method
                  BLASTX
```

Match length

276

```
BLAST score
                  902
                  2.0e-97
E value
Match length
                  202
                  90
% identity
                  RAS-RELATED PROTEIN ARA-3 >gi_320560_pir__JS0640
NCBI Description
                  GTP-binding protein ara-3 - Arabidopsis thaliana
                  >gi_217837_dbj_BAA00830_ (D01025) small GTP-binding protein
                  [Arabidopsis thaliana]
                  117491
Seq. No.
Contig ID
                  755 4.R1010
5'-most EST
                  LIB23-058-Q1-E1-F8
Method
                  BLASTX
                  g114088
NCBI GI
BLAST score
                  608
E value
                  4.0e-63
Match length
                  143
% identity
                  85
                  RAS-RELATED PROTEIN ARA-3 >gi 320560 pir JS0640
NCBI Description
                  GTP-binding protein ara-3 - Arabidopsis thaliana
                  >gi 217837 dbj BAA00830 (D01025) small GTP-binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  117492
Contig ID
                  756 1.R1010
5'-most EST
                  jC-atXP71C221I2T7058d1
Method
                  BLASTX
                  g114089
NCBI GI
BLAST score
                  1027
                  1.0e-112
E value
                  204
Match length
                  100
% identity
                  RAS-RELATED PROTEIN ARA-4 >gi 81633 pir JS0641 GTP-binding
NCBI Description
                  protein ara-4 - Arabidopsis thaliana
                  >gi_217839_dbj_BAA00831_ (D01026) small GTP-binding protein
                  [Arabidopsis thaliana] >gi_3763922 (AC004450) GTP-binding
                  protein [Arabidopsis thaliana]
                  117493
Seq. No.
                  757 1.R1010
Contig ID
                  jC-\overline{a}tXP78C229M14T7b1
5'-most EST
Method
                  BLASTX
                  g2252472
NCBI GI
BLAST score
                  2528
E value
                  0.0e + 00
Match length
                  517
                  95
% identity
                  (Z97558) argininosuccinate lyase [Arabidopsis thaliana]
NCBI Description
                  117494
Seq. No.
Contig ID
                  758 1.R1010
5'-most EST
                  jC-atXLIB327438P2d10a1
Method
                  BLASTX
NCBI GI
                  g541849
BLAST score
                  1356
E value
                  1.0e-150
```

```
95
% identity
                  anthranilate synthase (EC 4.1.3.27) beta chain -
NCBI Description
                  Arabidopsis thaliana >gi 403434 (L22585) anthranilate
                  synthase beta subunit [Arabidopsis thaliana]
                  117495
Seq. No.
                  760 1.R1010
Contig ID
                  jC-atXP94CG11D11T7016d1
5'-most EST
Method
                  BLASTX
                  g1399275
NCBI GI
BLAST score
                  2747
                  0.0e + 00
E value
Match length
                  544
% identity
                  97
NCBI Description
                  (U31835) calmodulin-domain protein kinase CDPK isoform 6
                  [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6
                  (calmodulin-domain protein kinase isoform 6) [Arabidopsis
                  thaliana]
                  117496
Seq. No.
Contig ID
                  760 2.R1010
5'-most EST
                  jC-atXP87CG8F3T7b1
                  BLASTX
Method
NCBI GI
                  g1399273
BLAST score
                  2730
E value
                  0.0e + 00
                  556
Match length
% identity
                  (U31834) calmodulin-domain protein kinase CDPK isoform 5
NCBI Description
                  [Arabidopsis thaliana] >gi 3080419 emb CAA18738.1
                   (AL022604) calmodulin-domain protein kinase CDPK isoform 5
                   (CPK5) [Arabidopsis thaliana]
                  117497
Seq. No.
Contig ID
                  760 3.R1010
5'-most EST
                  jC-atXLIB327439P1g09b2
Method
                  BLASTX
                  q967125
NCBI GI
BLAST score
                  58
                  9.0e - 54
E value
Match length
                  187
% identity
                  (U08140) calcium dependent protein kinase [Vigna radiata]
NCBI Description
                  117498
Seq. No.
                  760 4.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P3g02b1
Method
                  BLASTX
NCBI GI
                  g1399275
BLAST score
                  221
                  2.0e-17
E value
                  258
Match length
% identity
NCBI Description (U31835) calmodulin-domain protein kinase CDPK isoform 6
                   [Arabidopsis thaliana] >qi 2623752 (AC002329) CDPK6
                   (calmodulin-domain protein kinase isoform 6) [Arabidopsis
```

thalianal

NCBI GI

```
117499
Seq. No.
                  761 1.R1010
Contig ID
5'-most EST
                  PLN_g1374771
                  BLASTX
Method
                  g2494034
NCBI GI
BLAST score
                  3776
                  0.0e+00
E value
                  728
Match length
% identity
                  DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG
NCBI Description
                  KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase -
                  Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787)
                  diacylglycerol kinase [Arabidopsis thaliana]
                  117500
Seq. No.
                  762 1.R1010
Contig ID
                  jC-atXLIB327424P4b10b1
5'-most EST
Method
                  BLASTX
                  g585421
NCBI GI
BLAST score
                  4685
                  0.0e+00 *
E value
                  896
Match length
% identity
                  99
                  LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879 pir_JQ2391
NCBI Description
                  lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis Thaliana
                  >gi 431258 (L23968) lipoxygenase [Arabidopsis thaliana]
                  117501
Seq. No.
                  762 2.R1010
Contig ID
                  jC-\overline{a}1XLIB327434P3f04b1
5'-most EST
Method
                  BLASTX
                  g585421
NCBI GI
BLAST score
                  1189
                  1.0e-131
E value
Match length
                  221
% identity
                  LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879 pir JQ2391
NCBI Description
                  lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana
                  >gi 431258 (L23968) lipoxygenase [Arabidopsis thaliana]
Seq. No.
                  117502
                  762 5.R1010
Contig ID
                  jC-atXLIB327431P4g11a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g431257
BLAST score
                   408
                  0.0e + 00
E value
Match length
                   452
% identity
                  Arabidopsis thaliana lipoxygenase (Lox2) mRNA, complete cds
NCBI Description
Seq. No.
                  117503
                  763 1.R1010
Contig ID
                  LIB23-053-Q1-E1-B10
5'-most EST
Method
                  BLASTX
```

q1255448

```
2732
BLAST score
                  0.0e+00
E value
                  587
Match length
% identity
                  91
NCBI Description
                  (D50468) mitogen-activated protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  117504
                  764 1.R1010
Contig ID
5'-most EST
                  LIB3168-053-P1-K1-G2
                  BLASTX
Method
                  g2499606
NCBI GI
BLAST score
                  1860
E value
                  0.0e + 00
Match length
                  376
                  94
% identity
NCBI Description
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2 (MAP KINASE 2)
                   (ATMPK2) >gi 533281 dbj BAA03536 (D14714) ATMPK2
                   [Arabidopsis thaliana]
                  117505
Seq. No.
                  764 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327416P2g01b1
Method
                  BLASTX
NCBI GI
                  q2499605
BLAST score
                  1862
E value
                  0.0e + 00
Match length
                  370
% identity
                  96
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 1 (MAP KINASE 1)
NCBI Description
                   (ATMPK1) >qi 533280 dbj BAA03535 (D14713) ATMPK1
                   [Arabidopsis thaliana]
                  117506
Seq. No.
Contig ID
                  766 1.R1010
5'-most EST
                  LIB23-043-Q1-E1-E12
Method
                  BLASTX
                  g2499607
NCBI GI
BLAST score
                  1958
E value
                  0.0e + 00
Match length
                  370
% identity
                  100
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 3 (MAP KINASE 3)
NCBI Description
                  (ATMPK3) >gi 629544 pir S40469 mitogen-activated protein
                  kinase 3 (EC 2.7.1.-) - Arabidopsis thaliana
                  >qi 457398 dbj BAA04866 (D21839) MAP kinase [Arabidopsis
                  thaliana]
                  117507
Seq. No.
                  767 1.R1010
Contig ID
                  LIB24-049-Q1-E1-E1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2499608
BLAST score
                  1899
                  0.0e + 00
E value
Match length
                  376
% identity
                  96
```

4-2-

Match length

368

```
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4)
                   (ATMPK4) >gi_2129645_pir__S40470 mitogen-activated protein
                  kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi 457400 dbj BAA04867 (D21840) MAP kinase [Arabidopsis
                  thalianal
Seq. No.
                  117508
                  768 1.R1010
Contig ID
                  LIB24-001-Q1-E1-B4
5'-most EST
                  BLASTX
Method
                  g2499609
NCBI GI
BLAST score
                  1973
E value
                  0.0e + 00
Match length
                  376
                  100
% identity
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 5 (MAP KINASE 5)
NCBI Description
                   (ATMPK5) >gi 629546 pir S40471 mitogen-activated protein
                  kinase 5 (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi 457402 dbj BAA04868 (D21841) MAP kinase [Arabidopsis
                  thaliana]
                  117509
Seq. No.
                  769 1.R1010
Contig ID
5'-most EST
                  LIB25-014-Q1-E1-D4
Method
                  BLASTX
                  q2499610
NCBI GI
BLAST score
                  2004
                  0.0e+00
E value
                  395
Match length
                  97
% identity
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 6 (MAP KINASE 6)
NCBI Description
                   (ATMPK6) >qi 629547 pir S40472 mitogen-activated protein
                  kinase 6 (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi 457404 dbj BAA04869 (D21842) MAP kinase [Arabidopsis
                  thaliana] >gi 2281091 (AC002333) MAP Kinase 6 [Arabidopsis
                  thaliana]
                  117510
Seq. No.
                  769~3.R1010
Contig ID
5'-most EST
                  g2393457
Method
                  BLASTN
NCBI GI
                  g2281081
BLAST score
                  249
                  1.0e-137
E value
Match length
                  333
% identity
                  94
                  Arabidopsis thaliana chromosome II BAC F18019 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  117511
Seq. No.
                  770 1.R1010
Contig ID
5'-most EST
                  LIB24-074-Q1-E1-G11
Method
                  BLASTX
NCBI GI
                  q2499611
BLAST score
                  1945
                  0.0e + 00
E value
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```
100
% identity
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)
NCBI Description
                  (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein
                  kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana
                  >qi 457406 dbj BAA04870 (D21843) MAP kinase [Arabidopsis
                  thaliana]
                  117512
Seq. No.
                  771 1.R1010
Contig ID
                  jC-atXLIB327404P1g07b1
5'-most EST
                  BLASTX
Method
                  g1709534
NCBI GI
BLAST score
                  3171
                  0.0e + 00
E value
                  717
Match length
% identity
                  DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE A (P5CS A)
NCBI Description
                  [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                  GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                   (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                   (GLUTAMYL-GAMMA-SEMIALDE... >gi_2129572_pir___S66637
                  delta-1-pyrroline-5-carboxylate synthetase - Arabidopsis
                  thaliana >gi 829100 emb CAA60740 (X87330)
                  pyrroline-5-carboxylate synthetase [Arabidopsis thaliana]
                  >qi 870866 emb CAA60446 (X86777) pyrroline-5-carboxylate
                  synthetase A [Arabidopsis thaliana]
                  >gi 1041248_emb_CAA61593_ (X89414) pyrroline-5-carboxylate
                  synthase [Arabidopsis thaliana] >gi 2642162 (AC003000)
                  delta-1-pyrroline 5-carboxylase synthetase, P5C1
                  [Arabidopsis thaliana]
                  117513
Seq. No.
                  771 2.R1010
Contig ID
5'-most EST
                  g2048042
                  117514
Seq. No.
                  771 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327419P2f03b2
Method
                  BLASTX
                  g1709535
NCBI GI
BLAST score
                  3253
                  0.0e + 00
E value
                  726
Match length
% identity
                  DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B)
NCBI Description
                   [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                  GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                   (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                   (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447
                   (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis
                  thaliana] >gi_1669658_emb_CAA70527_ (Y09355)
pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]
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Seq. No. 117515 Contig ID 771 5.R1010

5'-most EST jC-atXLIB327429P4f05a2

Method BLASTX

E value

1.0e-28

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q1709535
NCBI GI
BLAST score
                  732
E value
                  2.0e-77
                  238
Match length
% identity
                  48
                  DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B)
NCBI Description
                  [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                  GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                  (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                   (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447_
                  (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis
                  thaliana] >gi 1669658 emb CAA70527 (Y09355)
                  pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]
Seq. No.
                  117516
Contig ID
                  771 6.R1010
5'-most EST
                  g2763374
                  BLASTX
Method
                  q1709535
NCBI GI
BLAST score
                  506
E value
                  2.0e-51
                  130
Match length
% identity
                  DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B)
NCBI Description
                  [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                  GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                   (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                   (GLUTAMYL-GAMMA-SEMIALDE... >gi 887388 emb CAA60447
                  (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis
                  thaliana] >gi_1669658_emb_CAA70527_ (Y09355)
                  pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]
                  117517
Seq. No.
                  771 7.R1010
Contig ID
5'-most EST
                  g1054019
                  BLASTX
Method
NCBI GI
                  g1709535
BLAST score
                  485
                  6.0e-49
E value
Match length
                  96
% identity
                  DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B)
NCBI Description
                  [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                  GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                   (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                   (GLUTAMYL-GAMMA-SEMIALDE... > gi 887388 emb CAA60447
                  *(X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis
                  thaliana] >gi_1669658_emb_CAA70527_ (Y09355)
                  pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]
                  117518
Seq. No.
                  771 9.R1010
Contig ID
5'-most EST
                  q2708415
Method
                  BLASTX
NCBI GI
                  q1709535
BLAST score
                  315
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% identity

97

```
Match length
                   155
% identity
                   44
                   DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B)
NCBI Description
                   [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                   GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                   (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                   (GLUTAMYL-GAMMA-SEMIALDE... >gi 887388 emb CAA60447
                   (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis
                   thaliana] >gi_1669658_emb_CAA70527_ (Y09355)
pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]
                   117519
Seq. No.
                   771 10.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P4f02b1
                   BLASTX
Method
                   g1709535
NCBI GI
                   1007
BLAST score
                   1.0e-110
E value
                   216
Match length
% identity
                   97
                   DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B)
NCBI Description
                   [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                   GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                   (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                   (GLUTAMYL-GAMMA-SEMIALDE... >gi 887388 emb CAA60447
                   (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis
                   thaliana] >gi_1669658_emb_CAA70527_ (Y09355) pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]
Seq. No.
                   117520
Contig ID
                   772 1.R1010
5'-most EST
                   PLN g508307
Method
                   BLASTX
NCBI GI
                   q1170689
BLAST score
                   2094
E value
                   0.0e + 00
Match length
                   464
% identity
                   SERINE/THREONINE-PROTEIN KINASE ATPK1/ATPK6
NCBI Description
                   >gi 625979 pir A54141 ribosomal protein S6 kinase (EC
                   2.7.1.-) Atpk1 - Arabidopsis thaliana
                   >gi 2129542 pir S68462 ATPK6 protein - Arabidopsis
                   thaliana >qi 914080 bbs 160873 ATPK6=ribosomal-protein S6
                   kinase homolog [Arabidopsis thaliana, Peptide, 465 aa]
                   >qi 508308 (L29030) protein-serine kinase [Arabidopsis
                   thaliana] >gi 867997 dbj BAA07656 (D42056)
                   risosomal-protein S6 kinase homolog [Arabidopsis thaliana]
                   117521
Seq. No.
Contig ID
                   772 2.R1010
5'-most EST
                   PLN g1526412
Method
                   BLASTX
NCBI GI
                   g2129541
BLAST score
                   2382
E value
                   0.0e + 00
Match length
                   471
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•

```
NCBI Description ATPK19 protein - Arabidopsis thaliana >gi 914079 bbs 160872
                  ATPK19=ribosomal-protein S6 kinase homolog [Arabidopsis
                   thaliana, Peptide, 471 aa] >gi 867995 dbj BAA07661
                   (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis
                   thaliana]
Seq. No.
                   117522
                   773 1.R1010
Contig ID
5'-most EST
                  g2748672
                   BLASTX
Method
                  g99749
NCBI GI
BLAST score
                   2358
E value
                   0.0e + 00
Match length
                   498
                   91
% identity
                  probable serine/threonine-specific protein kinase ATPK64
NCBI Description
                   (EC 2.7.1.-) - Arabidopsis thaliana
                   >gi 217843 dbj BAA01731 (D10937) protein kinase
                   [Arabidopsis thaliana]
                   117523
Seq. No.
                   775_1.R1010
Contig ID
5'-most EST
                   PLN_g1526413
Method
                   BLASTX
                   g902923
NCBI GI
BLAST score
                   2910
                   0.0e + 00
E value
                   561
Match length
                   97
% identity
                   (D38544) phosphoinositide specific phospholipase C
NCBI Description
                   [Arabidopsis thaliana]
                   117524
Seq. No.
Contig ID
                   776 1.R1010
5'-most EST
                  LIB22-083-Q1-E2-E7
                   BLASTX
Method
                   g2129670
NCBI GI
BLAST score
                   2982
                   0.0e+00
E value
Match length
                   581
% identity
                  phosphoinositide-specific phospholipase C - Arabidopsis
NCBI Description
                   thaliana >qi 857374 dbj BAA09432 (D50804) phosphoinositide
                   specific phospholipase C [Arabidopsis thaliana]
Seq. No.
                   117525
                   778 1.R1010
Contig ID
5'-most EST
                   LIB3234-079-P1-K1-H8
Method
                   BLASTX
                   g1172704
NCBI GI
BLAST score
                   3056
E value
                   0.0e + 00
Match length
                   585
% identity
                   100
                  PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN)
NCBI Description
                  >gi 633940 (L39082) transport protein [Arabidopsis
                   thaliana] >gi_4406786_gb_AAD20096_ (AC006532) histidine
```

NCBI Description

transport protein PTR2-B [Arabidopsis thaliana]

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Seq. No.
                   117526
                   779 1.R1010
 Contig ID
 5'-most EST
                   PLN g217846
Method
                   BLASTX
                                                              4...
                   q3914370
NCBI GI
 BLAST score
                   2276
                   0.0e + 00
 E value
                   459
Match length
                   96
 % identity
                   GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
 NCBI Description
                   >gi 419754 pir S31083 glycerol-3-phosphate
                   O-acyltransferase (EC 2.3.1.15) precursor - Arabidopsis
                   thaliana >gi 217845 dbj BAA00575 (D00672)
                   glycerol-3-phosphate acyltransferase [Arabidopsis thaliana]
                   >gi 217847 dbj_BAA00576_ (D00673) glycerol-3-phosphate
                   acyltransferase precursor [Arabidopsis thaliana]
 Seq. No.
                   117527
                   780 1.R1010
 Contig ID
 5'-most EST
                   PLN g1109599
Method
                   BLASTX
                   g1109600
NCBI GI
BLAST score
                   1718
                   0.0e + 00
E value
Match length
                   321
 % identity
                   100
                   (D16628) ATSEH [Arabidopsis thaliana] >gi 2760840
NCBI Description
                   (AC003105) soluble epoxide hydrolase [Arabidopsis thaliana]
Seq. No.
                   117528
                   782 1.R1010
Contig ID
 5'-most EST
                   LIB3176-016-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g2493144
BLAST score
                   575
E value
                   4.0e-59
Match length
                   164
% identity
                   74
                   VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE
NCBI Description
                   16 KD PROTEOLIPID SUBUNIT) >gi 2118221 pir S60132
                   H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                   (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585)
                   vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                   thaliana]
                   117529
 Seq. No.
                   783 1.R1010
Contig ID
5'-most EST
                   LIB35-042-Q1-E1-G12
                   BLASTX
Method
NCBI GI
                   q2118222
BLAST score
                   585
                   2.0e-60
E value
                   166
Match length
                   75
% identity
```

H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain

```
thaliana]
                    117530
 Seq. No.
                    783 2.R1010
 Contig ID
 5'-most EST
                    LIB35-008-Q1-E1-B3
 Method
                    BLASTX
 NCBI GI
                    g2118222
 BLAST score
                    166
                    1.0e-11
 E value
 Match length
                    78
                    45
 % identity
 NCBI Description
                   H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                    (clone AVA-P4) - Arabidopsis thaliana >gi 926935 (L44584)
                    vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                    thaliana]
                    117531
 Seq. No.
 Contig ID
                    785 1.R1010
 5'-most EST
                    PLN g166633
                    BLASTX
 Method
                    q399091
 NCBI GI
* BLAST score
                    3603
 E value
                    0.0e + 00
                    770 -
 Match length
 % identity
                    93
 NCBI Description
                    PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP
                    (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)
                    (H+-PPASE) >gi 282878 pir A38230 inorganic pyrophosphatase
                    (EC 3.6.1.1), H+-translocating pyrophosphate-energized -
                    Arabidopsis thaliana >qi 166634 (M81892) vacuolar
                    H+-phosphatase [Arabidopsis thaliana]
                    117532
 Seq. No.
 Contig ID
                    785 2.R1010
                    jC-atXLIB327406P2f08b1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q3402487
 BLAST score
                    205
 E value
                    3.0e-64
 Match length
                    135
 % identity
                    96
                    (AB015138) Vacuolar proton pyrophosphatase [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    117533
                    785 4.R1010
 Contig ID
 5'-most EST
                    g2445875
 Method
                    BLASTX
                    q3402487
 NCBI GI
 BLAST score
                    50
 E value
                    3.0e-41
 Match length
                    91
                    99
 % identity
                    (AB015138) Vacuolar proton pyrophosphatase [Arabidopsis
 NCBI Description
```

(clone AVA-P4) - Arabidopsis thaliana >gi_926935 (L44584) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis

thalianal

```
117534
Seq. No.
                  785 14.R1010
Contig ID
5'-most EST
                  g2393454
Method
                  BLASTX
                  q399091
NCBI GI
BLAST score
                  51
                  3.0e-16
E value
                  64
Match length
                  71
% identity
                  PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP
NCBI Description
                   (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)
                   (H+-PPASE) >gi 282878_pir__A38230 inorganic pyrophosphatase
                   (EC 3.6.1.1), H+-translocating pyrophosphate-energized -
                  Arabidopsis thaliana >gi_166634 (M81892) vacuolar
                  H+-phosphatase [Arabidopsis thaliana]
                  117535
Seq. No.
                  786 1.R1010
Contig ID
                  jC-atXLIB327409P2g08b1
5'-most EST
Method
                  BLASTX
                  g399900
NCBI GI
BLAST score
                  1371 ·
                  1.0e-152
E value
Match length
                  272
% identity
                  96
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5)
NCBI Description
                   (HD-ZIP PROTEIN ATHB-1) >gi 99659 pir S16325 homeotic
                  protein Athb-1 - Arabidopsis thaliana
                  >qi 16329 emb CAA41625 (X58821) Athb-1 protein
                   [Arabidopsis thaliana]
                  117536
Seq. No.
Contig ID
                  786 3.R1010
                  jC-atXLIB327421P1c11b1
5'-most EST
Method
                  BLASTX
                  q399900
NCBI GI
BLAST score
                   424
                  1.0e-41
E value
Match length
                  84
% identity
                   98
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5)
NCBI Description
                   (HD-ZIP PROTEIN ATHB-1) >gi 99659 pir S16325 homeotic
                  protein Athb-1 - Arabidopsis thaliana
                  >qi 16329 emb CAA41625 (X58821) Athb-1 protein
                   [Arabidopsis thaliana]
                  117537
Seq. No.
Contig ID
                  786 5.R1010
                  LIB25-045-Q1-E1-F7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q399900
BLAST score
                   524
E value
                   3.0e-53
Match length
                   119
% identity
                   87
NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5)
```

NCBI GI

```
protein Athb-1 - Arabidopsis thaliana
                   >gi_16329_emb_CAA41625_ (X58821) Athb-1 protein
                   [Arabidopsis thaliana]
                   117538
Seq. No.
Contig ID
                   787 1.R1010
5'-most EST
                   jC-atXP69C217G11T7081d1
                   BLASTX
Method
NCBI GI
                   g1350720
BLAST score
                   572
                   9.0e~59
E value
                   111
Match length
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L32
                   117539
Seq. No.
                   787 2.R1010
Contig ID
                   jC-atXLIB327402P2h01a1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4584351
BLAST score
                   508
                   0.0e+00
E value
Match length
                   540
                   99
% identity
                   Arabidopsis thaliana chromosome II BAC T12H3 genomic
NCBI Description
                   sequence, complete sequence
                   117540
Seq. No.
                   787 3.R1010
Contig ID
5'-most EST
                   LIB3177-046-P1-K2-F9
                   BLASTN
Method
                   q527636
NCBI GI
BLAST score
                   71
                   1.0e-31
E value
Match length
                   75
                   99.
% identity
                   Arabidopsis thaliana clone HAT7 homeobox protein mRNA,
NCBI Description
                   complete cds
                   117541
Seq. No.
                   787 4.R1010
Contig ID
5'-most EST
                   g57\overline{2}572
Method
                   BLASTN
                   q3738275
NCBI GI
BLAST score
                   167
                   1.0e-88
E value
                   237
Match length
% identity
                   97
                   Arabidopsis thaliana chromosome II BAC F17A22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   117542
Seq. No.
                   787 5.R1010
Contig ID
                   jC-atXP102CE4D9T7b1
5'-most EST
Method
                   BLASTX
```

(HD-ZIP PROTEIN ATHB-1) >gi 99659 pir__S16325 homeotic

q1350720

NCBI GI

```
BLAST score
                  570
E value
                  1.0e-58
Match length
                  111
% identity
                  97
NCBI Description
                  60S RIBOSOMAL PROTEIN L32
Seq. No.
                  117543
Contig ID
                  787_6.R1010
5'-most EST
                  PLN g527636
                  BLASTX
Method
NCBI GI
                  g1170171
BLAST score
                  1089
E value
                  1.0e-119
Match length
                  251
% identity
                  84
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT7 (HD-ZIP PROTEIN 7)
NCBI Description
                  (HD-ZIP PROTEIN ATHB-3) >gi 549891 (U09340) homeobox
                  protein [Arabidopsis thaliana]
Seq. No.
                  117544
                  788 1.R1010
Contig ID
5'-most EST
                  LIB25-068-Q1-E1-G9
Method
                  BLASTX
NCBI GI
                 g1695719
BLAST score
                  3087
E value
                  0.0e + 00
Match length
                  645
% identity
                  95
NCBI Description
                  (D89342) luminal binding protein [Arabidopsis thaliana]
Seq. No.
                  117545
                  788 2.R1010
Contig ID
5'-most EST
                  g2748804
Method
                  BLASTX
NCBI GI
                  g1695719
BLAST score
                  144 .
                  1.0e-08
E value
Match length
                  65
% identity
                  52
NCBI Description
                  (D89342) luminal binding protein [Arabidopsis thaliana]
Seq. No.
                  117546
Contig ID
                  788 3.R1010
5'-most EST
                  jC-atXLIB327422P2e03b2
Method
                  BLASTX
NCBI GI
                  g1695719
BLAST score
                  852
                  2.0e-91
E value
Match length
                  198
% identity
                  (D89342) luminal binding protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117547
                  788 5.R1010
Contig ID
5'-most EST
                  LIB23-074-Q1-E1-H2
Method
                  BLASTX
```

g1695717

Seq. No.

117552

```
BLAST score
                  618
                  2.0e-64
E value
Match length
                  122 ...
% identity
                  100
                  (D89341) luminal binding protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117548
                  789 1.R1010
Contig ID
                  jC-atXLIB327424P1d01b2
5'-most EST
Method
                  BLASTX
                  q115385
NCBI GI
BLAST score
                  1329
                  1.0e-147
E value
Match length
                  251
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
                  117549
Seq. No.
Contig ID
                  789 2.R1010
                  jC-atXP115C247K14T7065d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g100197
BLAST score
                  149
E value
                  3.0e-89
Match length
                  176
% identity
                  chlorophyll a/b-binding protein (cab-12) - tomato
NCBI Description
                  117550
Seq. No.
Contig ID
                  789 4.R1010
                  jC-atXP53C183K19T7058d1
5'-most EST
Method
                  BLASTX
                  g115385
NCBI GI
BLAST score
                  552
E value
                  1.0e-105
Match length
                  337
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  117551
Contig ID
                  789 5.R1010
                  jC-atXP53C185B22T7086d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g115385
BLAST score
                  497
E value
                  4.0e-50
Match length
                  128
% identity
                  83
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
```

BLAST score

3002

```
Contig ID
                  789 6.R1010
5'-most EST
                  LIB23-015-01-E1-A12
Method
                  BLASTX
                  g115385
NCBI GI
BLAST score
                  447
E value
                  2.0e-44
Match length
                  105
                  87
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  117553
                  789 12.R1010
Contig ID
                  g2413927
5'-most EST
Method
                  BLASTX
                  g115385
NCBI GI
BLAST score
                  247
E value
                  1.0e-20
Match length
                  93
                  47
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
                  117554
Seq. No.
Contig ID
                  789 14.R1010
5'-most EST
                  LIB23-033-Q1-E1-E2
Method
                  BLASTX
NCBI GI
                  q115385
BLAST score
                  444
                  8.0e-44
E value
Match length
                  111
% identity
                  81
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
                  117555
Seq. No.
Contig ID
                  789 16.R1010
5'-most EST
                  g1053430
Method
                  BLASTX
NCBI GI
                  q115385
BLAST score
                  520
                  1.0e-52
E value
Match length
                  138
% identity
                  76
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  117556
Contiq ID
                  792 1.R1010
5'-most EST
                  LIB23-010-Q1-E2-E4
Method
                  BLASTX
NCBI GI
                  q729092
```

```
0.0e + 00
E value
Match length
                  601
                  97
% identity
                  CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK)
NCBI Description
                  >gi 477484_pir A49082 calcium-dependent protein kinase
                  isoform AK\overline{1} - \overline{Ar}abidopsis thaliana >gi_304105 (L14771)
                  calcium-dependent protein kinase [Arabidopsis thaliana]
                  117557
Seq. No.
Contig ID
                  793 1.R1010
                  jC-atXP107C116J3T7d1
5'-most EST
                  BLASTX
Method
                  g115486
NCBI GI
                  762
BLAST score
E value
                  9.0e-81
Match length
                  149
% identity
                  CALMODULIN-2/3/5 >qi 99671 pir S22503 calmodulin -
NCBI Description
                  Arabidopsis thaliana > gi 1076437 pir S53006 calmodulin -
                  leaf mustard >gi 2146726 pir S71513 calmodulin -
                  Arabidopsis thaliana >qi 166651 (M38380) calmodulin-2
                   [Arabidopsis thaliana] >gi 166653 (M73711) calmodulin-3
                   [Arabidopsis thaliana] >gi_474183_emb_CAA47690_ (X67273)
                  calmodulin [Arabidopsis thaliana] >gi_497992 (U10150)
                  calmodulin [Brassica napus] >gi_899058 (M88307) calmodulin
                   [Brassica juncea] >gi_1183005_dbj_BAA08283_ (D45848)
                  calmodulin [Arabidopsis thaliana] >gi 3402706 (AC004261)
                  unknown protein [Arabidopsis thaliana] >gi 3885333
                   (AC005623) calmodulin [Arabidopsis thaliana]
                  >qi 228407 prf 1803520A calmodulin 2 [Arabidopsis
                  thaliana]
                  117558
Seq. No.
                  793 2.R1010
Contig ID
                   q2763368
5'-most EST
                  BLASTX
Method
NCBI GI
                   q1168748
                   755
BLAST score
                   3.0e-80
E value
                   149
Match length
% identity
NCBI Description
                  CALMODULIN-4 >gi 479693 pir S35185 calmodulin 4 -
                  Arabidopsis thaliana >qi 16223 emb CAA78057 (Z12022)
                  calmodulin [Arabidopsis thaliana]
                   117559
Seq. No.
                   793 5.R1010
Contig ID
5'-most EST
                   g90<del>6</del>713
Method
                   BLASTX
                   q687677
NCBI GI
BLAST score
                   423
                   2.0e-41
E value
                   118
Match length
% identity
                   (U19925) unknown [Arabidopsis thaliana]
NCBI Description
```

117560

Seq. No.

```
Contig ID
                  793 6.R1010
5'-most EST
                  g905708
Method
                  BLASTX
NCBI GI
                  g2191138
BLAST score
                  576
                  2.0e-59
E value
Match length
                  130
                  90
% identity
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  117561
Seq. No.
                  796 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327424P4c03b1
Method
                  BLASTX
NCBI GI
                  q1708993
                  2231
BLAST score
                  0.0e+00
E value
                  453
Match length
% identity
                  97
                  CYSTATHIONINE BETA-LYASE PRECURSOR (CBL)
NCBI Description
                   (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
                  >gi 2129567 pir S61429 cystathionine beta-lyase (EC
                  4.4.1.8) - Arabidopsis thaliana >gi 704397 (L40511)
                  cystathionine beta-lyase [Arabidopsis thaliana]
                  117562
Seq. No.
Contig ID
                  796 2.R1010
5'-most EST
                  jC-atXP39C158P6T7d1
Method
                  BLASTX
NCBI GI
                  a1708993
BLAST score
                  483
E value
                  2.0e-79
Match length
                  169
% identity
                  92
NCBI Description
                  CYSTATHIONINE BETA-LYASE PRECURSOR (CBL)
                   (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
                  >gi_2129567_pir__S61429 cystathionine beta-lyase (EC
                  4.4.1.8) - Arabidopsis thaliana >gi 704397 (L40511)
                  cystathionine beta-lyase [Arabidopsis thaliana]
Seq. No.
                  117563
Contig ID
                  798 1.R1010
5'-most EST
                  PLN g1235716
Method
                  BLASTX
NCBI GI
                  q1084334
BLAST score
                  2399
E value
                  0.0e + 00
                  493
Match length
% identity
                  94
                  calcium-dependent protein kinase (EC 2.7.1.-) 1 -
NCBI Description
                  Arabidopsis thaliana >gi_604880_dbj_BAA04829_ (D21805)
                  calcium-dependent protein kinase [Arabidopsis thaliana].
                  117564
Seq. No.
                  799 1.R1010
Contig ID
                  jC-atXLIB327402P4h01b1
5'-most EST
```

5'-most EST

```
BLASTX
Method
                  g1084335
NCBI GI
BLAST score
                  2533
E value
                  0.0e + 00
                   495
Match length
% identity
                   98
                  calcium-dependent protein kinase (EC 2.7.1.-) 2 -
NCBI Description
                  Arabidopsis thaliana >qi 604881 dbj BAA04830 (D21806)
                  calcium-dependent protein kinase [Arabidopsis thaliana]
                  117565
Seq. No.
Contig ID
                  800 1.R1010
                  jC-atXLIB327420P4d07b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1209703
BLAST score
                  705
E value
                  0.0e + 00
                   619
Match length
                   96
% identity
                  (U40489) maize gl1 homolog [Arabidopsis thaliana]
NCBI Description
                  117566
Seq. No.
Contig ID
                  800 4.R1010
5'-most EST
                  jC-alXLIB327435P2e04b1
                  BLASTX
Method
NCBI GI
                  q1209703
BLAST score
                   367
                   8.0e-35
E value
Match length
                  71
% identity
                  (U40489) maize gl1 homolog [Arabidopsis thaliana]
NCBI Description
                  117567
Seq. No.
                  800 5.R1010
Contig ID
5'-most EST
                   q958004
                   BLASTX
Method
NCBI GI
                   g1209703
BLAST score
                   308
                   5.0e-52
E value
                   111
Match length
% identity
NCBI Description
                  (U40489) maize gll homolog [Arabidopsis thaliana]
                   117568
Seq. No.
                   801 1.R1010
Contig ID
                  LIB23-054-Q1-E1-B12
5'-most EST
                  BLASTX
Method
NCBI GI
                   g3559807
BLAST score
                   1837
                   0.0e + 00
E value
                   402
Match length
% identity
NCBI Description
                  (Y15628) HCF136 protein [Arabidopsis thaliana]
                   117569
Seq. No.
                   802 1.R1010
Contig ID
```

jC-atXP39C159O11T7d1

```
Method
                   BLASTX
 NCBI GI
                   g544018
 BLAST score
                   2846
 E value
                   0.0e + 00
Match length
                   590
% identity
NCBI Description
                   NITRATE/CHLORATE TRANSPORTER >gi 1076359 pir A45772
                   nitrate-inducible nitrate transporter - Arabidopsis
                   thaliana >gi 166668 (L10357) CHL1 [Arabidopsis thaliana]
                   >gi 3157921 (AC002131) Identical to nitrate/chlorate
                   transporter cDNA gb L10357 from A. thaliana. ESTs
                   gb H37533 and gb R2\overline{9}790, gb T46117, gb T46068, gb T75688,
                   gb R29817, gb R29862, gb Z34634 and gb Z34258 come from
                   this gene. [Arabidopsis thaliana]
                   117570
 Seq. No.
                   803 1.R1010
 Contig ID
                   jC-atX24031Q1E1E07b1
 5'-most EST
 Method
                   BLASTX
NCBI GI
                   g585349
BLAST score
                   1640
                   0.0e + 00
E value
 Match length
                   333
 % identity
                   94
 NCBI Description
                   CASEIN KINASE II, ALPHA CHAIN 1 (CK II)
                   >gi_419752_pir__S31098 casein kinase II (EC 2.7.1.-)
                   alpha-type chain (clone ATCKA1) - Arabidopsis thaliana
                   >gi 391603 dbj BAA01090 (D10246) casein kinase II
                   catalytic subunit [Arabidopsis thaliana]
 Seq. No.
                   117571
 Contig ID
                   804 1.R1010
 5'-most EST
                   jC-atXLIB327404P2a10b1
Method
                   BLASTX
NCBI GI
                   q585350
BLAST score
                   1636
E value
                   0.0e + 00
Match length
                   332
 % identity
                   93
NCBI Description
                   CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
                   >gi 419753 pir S31099 casein kinase II (EC 2.7.1.-)
                   alpha-type chain (clone ATCKA2) - Arabidopsis thaliana
                   >gi 391605 dbj BAA01091 (D10247) casein kinase II
                   catalytic subunit [Arabidopsis thaliana]
 Seq. No.
                   117572
 Contig ID
                   805 1.R1010
 5'-most EST
                   LIB25-030-Q1-E1-H9
Method
                   BLASTX
                   q729880
NCBI GI
BLAST score
                   1328
 E value
                   1.0e-147
Match length
                   287
 % identity
                   87
                   CASEIN KINASE II BETA CHAIN (CK II) >qi 1076299 pir S47967
 NCBI Description
                   casein kinase II (EC 2.7.1.-) beta chain CKB1 - Arabidopsis
```

thaliana >qi 468264 (L22563) casein kinase II beta subunit

CKB1 [Arabidopsis thaliana]

```
Seq. No.
                  117573
Contig ID
                  806 1.R1010
                  PLN_g1263313
5'-most EST
Method
                 BLASTX
NCBI GI
                  g2497953
BLAST score
                  3225
E value
                  0.0e + 00
Match length
                  658
% identity
                  97
                  MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM
NCBI Description
                  COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323)
                  molybdenum cofactor biosynthesis enzyme [Arabidopsis
                  thaliana] >gi 4469123 emb CAB38312 (AJ236870) molybdenum
                  cofactor biosynthesis enzyme [Arabidopsis thaliana]
                  117574
Seq. No.
Contig ID
                  806 2.R1010
5'-most EST
                  q2048532
Method
                  BLASTN
NCBI GI
                  g1263313
BLAST score
                  279
E value
                  1.0e-155
                  411
Match length
% identity
                  Arabidopsis thaliana molybdenum cofactor biosynthesis
NCBI Description
                  enzyme (cnx1) mRNA, complete cds
                  117575
Seq. No.
Contig ID
                  807 1.R1010
5'-most EST
                  PLN q530869
                  BLASTX
Method
NCBI GI
                  g1169013
BLAST score
                  814
E value
                  4.0e-87
Match length
                  165
% identity
                  COP9 PROTEIN (FUSCA PROTEIN FUS7) >gi_625971 pir A54842
NCBI Description
                  COP9 protein - Arabidopsis thaliana >gi_530870 (L32874)
                  COP9 [Arabidopsis thaliana] >gi 2244767 emb CAB10190_
                   (Z97335) COP9 protein [Arabidopsis thaliana]
                  117576
Seq. No.
                  810 1.R1010
Contig ID
                  jC-atXLIB327408P1a02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g336392
BLAST score
                  710
                   6.0e-75
E value
Match length
                  157
% identity
                   (J05215) ribosomal protein S17 [Arabidopsis thaliana]
NCBI Description
                  117577
Seq. No.
```

811 1.R1010

LIB25-098-Q1-E1-E3

Contig ID

5'-most EST

```
Method
                  BLASTX
NCBI GI
                  q1169128
BLAST score
                  3842
                  0.0e + 00
E value
Match length
                  821
% identity
                  89
                  SERINE/THREONINE-PROTEIN KINASE CTR1 >gi 166680 (L08789)
NCBI Description
                  protein kinase [Arabidopsis thaliana] >gi 166682 (L08790)
                  protein kinase [Arabidopsis thaliana]
                  117578
Seq. No.
                  812 1.R1010
Contig ID
                  jC-atXLIB327416P4h06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2146728
BLAST score
                  2165
                  0.0e + 00
E value
Match length
                  445
                  96
% identity
NCBI Description cyclin cyclb - Arabidopsis thaliana >gi 1360646 (L27223)
                  cyclin [Arabidopsis thaliana]
                  117579
Seq. No.
Contig ID
                  814 1.R1010
5'-most EST
                  LIB25-064-Q1=E1-B1
Method
                  BLASTX
NCBI GI
                  q1169598
BLAST score
                  2060
E value
                  0.0e+00
Match length
                  383
% identity
                  97
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   (DELTA-12 DESATURASE) >qi 438451 (L26296) delta-12
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  117580
Contig ID
                  814 2.R1010
5'-most EST
                  jC-atX24054Q1E1B06b1
Method
                  BLASTX
NCBI GI
                  q1169598
BLAST score
                  676
E value
                  5.0e-77
Match length
                  176
% identity
                  81
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  117581
Contig ID
                  815 1.R1010
                  LIB25-010-Q1-E1-C12
5'-most EST
Method
                  BLASTX
NCBI GI
                  g231562
BLAST score
                 · 2153
E value
                  0.0e + 00
Match length
                  525
% identity
                  94
```

```
NCBI Description PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 1 PRECURSOR
                   (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 1) (DAHP
                   SYNTHETASE 1) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE
                   SYNTHASE 1) >gi 166688 (M74819)
                   3-deoxy-D-arabino-heptulosonate y-phosphate synthase
                   [Arabidopsis thaliana]
Seq. No.
                   117582
                   815 3.R1010
Contig ID
5'-most EST
                   LIB3168-045-P1-K1-H11
Method
                   BLASTX
                   g99742
NCBI GI
BLAST score
                   548
                   3.0e-56
E value
                   125
Match length
                   86,
% identity
                   2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 1
NCBI Description
                   - Arabidopsis thaliana
                   117583
Seq. No.
Contig ID
                   816 1.R1010
5'-most EST
                   PLN_g166689
Method
                   BLASTX
NCBI GI
                   g231564
BLAST score
                   2634
E value
                   0.0e+00
Match length
                   507
% identity
                   100
                   PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 2 PRECURSOR
NCBI Description
                   (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 2) (DAHP
                   SYNTHETASE 2) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE
                   SYNTHASE 2) >gi 166690 (M74820)
                   3-deoxy-D-arabino-heptulosonate 7-phosphate synthase
                   [Arabidopsis thaliana]
                   117584
Seq. No.
Contig ID
                   817 1.R1010
5'-most EST
                   jC-atXLIB327412P3f02b1
Method
                   BLASTX
                   g2129579
NCBI GI
BLAST score
                   3007
                   0.0e + 00
E value
Match length
                   561
% identity
                   100
                   Dwarfl protein - Arabidopsis thaliana >gi 516043 (U12400)
NCBI Description
                   Dwarf1 [Arabidopsis thaliana]
                   117585
Seq. No.
                   817 3.R1010
Contig ID
5'-most EST
                   g2414029
Method
                   BLASTX
NCBI GI
                   g2129579
BLAST score
                   60
                   5.0e-37
E value
Match length
                   119
% identity
NCBI Description Dwarf1 protein - Arabidopsis thaliana >gi 516043 (U12400)
```

Contig ID 5'-most EST

Dwarf1 [Arabidopsis thaliana]

```
117586
Seq. No.
                  817 4.R1010
Contig ID
                  jC-atXLIB327437P4g05b2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2129579
BLAST score
                  815
                  2.0e-87
E value
                  158
Match length
% identity
                  99
                  Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400)
NCBI Description
                  Dwarf1 [Arabidopsis thaliana]
                  117587
Seq. No.
                  817 5.R1010
Contig ID
5'-most EST
                  jC-atXP101CE1D11T7089d1
Method
                  BLASTX
NCBI GI
                  g2129579
BLAST score
                  335
                  4.0e-60
E value
                  204
Match length
                  64
% identity
NCBI Description
                  Dwarfl protein - Arabidopsis thaliana >gi 516043 (U12400)
                  Dwarfl [Arabidopsis thaliana]
                  117588
Seq. No.
Contig ID
                  818 1.R1010
5'-most EST
                  jC-atXLIB327421P3g05b1
Method
                  BLASTX
NCBI GI
                  q1352316
BLAST score
                  699
                  2.0e-73
E value
Match length
                  159
% identity
                  86
                  DR1 PROTEIN HOMOLOG >gi 633026 dbj BAA07288 (D38110) Dr1
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  117589
                  819 1.R1010
Contig ID
5'-most EST
                  PLN g166693
Method
                  BLASTX
NCBI GI
                  q1169200
BLAST score
                  1594
                  1.0e-178
E value
Match length
                  383
% identity
                  82
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR
NCBI Description
                  >gi 421829 pir S33706 DNA-damage resistance protein -
                  Arabidopsis thaliana >gi 166694 (M98455) [Arabidopsis
                  thaliana recombination and DNA-damage resistance protein
                  (DRT111) mRNA, complete cds.], gene product [Arabidopsis
                  thaliana]
                                        25
Seq. No.
                  117590
                  820 1.R1010
```

LIB3177-049-P1-K1-G1

```
Method
                   BLASTX
NCBI GI
                   g1169201
BLAST score
                   727
E value
                   7.0e-77
Match length
                   167
                   87
% identity
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
NCBI Description
                   >qi 421830 pir S33707 DRT112 protein - Arabidopsis
                   thaliana >gi 166696 (M98456) DRT112 [Arabidopsis thaliana]
                   117591
Seq. No.
                   820 2.R1010
Contig ID
                   LIB35-039-Q1-E1-F8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1169201
BLAST score
                   327
                   1.0e-34
E value
Match length
                   118
                   66
% identity
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
NCBI Description
                   >gi 421830_pir__S33707 DRT112 protein - Arabidopsis
                   thaliana >qi 166696 (M98456) DRT112 [Arabidopsis thaliana]
                   117592
Seq. No.
                   820 4.R1010
Contig ID
5'-most EST
                   jC-atXLIB327427P2a12b1
Method
                   BLASTX
                   q1169201
NCBI GI
BLAST score
                   294
E value
                   3.0e-26
Match length
                   111
                   62
% identity
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
NCBI Description
                   >gi 421830 pir S33707 DRT112 protein - Arabidopsis
                   tha\overline{1}iana >\overline{g}i_1\overline{66}696 (M98456) DRT112 [Arabidopsis thaliana]
                   117593
Seq. No.
Contig ID
                   820 5.R1010
5'-most EST
                   LIB35-038-Q1-E1-B5
                   BLASTX
Method
NCBI GI
                   g1169201
BLAST score
                   48
E value
                   7.0e-26
Match length
                   165
% identity
                   54
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
NCBI Description
                   >gi 421830 pir S33707 DRT112 protein - Arabidopsis
                   thaliana >gi_1\overline{66}696 (M98456) DRT112 [Arabidopsis thaliana]
                   117594
Seq. No.
                   820 10.R1010
Contig ID
                   LIB3176-090-P1-K1-A2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1169201
BLAST score
                   232
E value
                   2.0e-19
                   88
Match length
```

NCBI GI

```
60
% identity
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                  >gi 421830 pir S33707 DRT112 protein - Arabidopsis
                  thaliana >gi 166696 (M98456) DRT112 [Arabidopsis thaliana]
                  117595
Seq. No.
                  821 2.R1010
Contig ID
5'-most EST
                  PLN g289194
Method
                  BLASTX
NCBI GI
                  q1169423
BLAST score
                  697
                  0.0e + 00
E value
Match length
                  659
% identity
                  77
                  DIHYDROFOLATE REDUCTASE 2 / THYMIDYLATE SYNTHASE 2
NCBI Description
                  (DHFR-TS) >gi 289195 (L08594) dihydrofolate
                  reductase-thymidylate synthase [Arabidopsis thaliana]
                  >gi 3096926 emb CAA18836.1 (AL023094) dihydrofolate
                  reductase-thymidylate synthase [Arabidopsis thaliana]
                  117596
Seq. No.
Contig ID
                  821 3.R1010
5'-most EST
                  jC-atXLIB327407P1c08b2
Method
                  BLASTX
NCBI GI
                  q1169423
BLAST score
                  1018
E value
                  1.0e-111
Match length
                  193
% identity
                  98
                  DIHYDROFOLATE REDUCTASE 2 / THYMIDYLATE SYNTHASE 2
NCBI Description
                  (DHFR-TS) >qi 289195 (L08594) dihydrofolate
                  reductase-thymidylate synthase [Arabidopsis thaliana]
                  >qi 3096926 emb CAA18836.1 (AL023094) dihydrofolate
                  reductase-thymidylate synthase [Arabidopsis thaliana]
Seq. No.
                  117597
                  823 1.R1010
Contig ID
5'-most EST
                  LIB3176-006-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1170237
BLAST score
                  2326
E value
                  0.0e + 00
Match length
                  466
% identity
                  FERROCHELATASE, CHLOROPLAST/MITOCHONDRIAL PRECURSOR
NCBI Description
                  (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE)
                  (FERROCHELATASE-I) >gi 1076325 pir A54125 ferrochelatase
                  (EC 4.99.1.1) precursor, chloroplast - Arabidopsis thaliana
                  >gi_511081_emb_CAA51819_ (X73417) ferrochelatase
                  [Arabidopsis thaliana] >gi 2597828 emb CAA73809 (Y13382)
                  ferrochelatase-I (Arabidopsis thaliana)
Seq. No.
                  117598
Contig ID
                  824 1.R1010
5'-most EST
                  PLN q443696
Method
                  BLASTX
```

q1169544

```
BLAST score
                    4373
E value
                   0.0e + 00
Match length
                   897
                   97
% identity
                   ERD1 PROTEIN PRECURSOR >gi 541859 pir JN0901 ERD1 protein
NCBI Description
                   - Arabidopsis thaliana >gi 497629 dbj BAA04506 (D17582)
                   ERD1 protein [Arabidopsis thaliana]
Seq. No.
                   117599
Contig ID
                   827 1.R1010
5'-most EST
                   jC-atXLIB327414P3a07a1
Method
                   BLASTX
NCBI GI
                    q1170089
BLAST score
                   1098
E value
                    1.0e-120
Match length
                   215
% identity
                   100
                   GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
NCBI Description
                   >qi 481822 pir S39542 probable qlutathione transferase (EC
                   2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase
                    [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione
                   S-transferase [Arabidopsis thaliana]
                   117600
Seq. No.
Contig ID
                   827 2.R1010
5'-most EST
                   jC-atXLIB327422P2h02b2
Method
                   BLASTX
NCBI GI
                    g2462929
BLAST score
                    431
E value
                    3.0e-53
Match length
                   136
% identity
                   76
NCBI Description
                   (Y12295) glutathione transferase [Arabidopsis thaliana]
Seq. No.
                   117601
Contig ID
                   827 3.R1010
5'-most EST
                   LIB23-039-Q1-E1-C6
Method
                   BLASTX
NCBI GI
                    g1170089
BLAST score
                    451
E value
                    1.0e-44
Match length
                   128
% identity
                   75
                   GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
NCBI Description
                   >qi 481822 pir S39542 probable glutathione transferase (EC
                   2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase
                    [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione
                   S-transferase [Arabidopsis thaliana]
Seq. No.
                   117602
Contig ID
                   828 1.R1010
5'-most EST
                   jC-atXLIB327432P3d12b1
Method
                   BLASTX
                   g1169278
NCBI GI
BLAST score
                   324
```

Seq. No.

117607

```
1.0e-29
E value
Match length
                  177
% identity
                  45
                  DEHYDRIN ERD14 >gi 556474 dbj BAA04569 (D17715) ERD14
NCBI Description
                  protein [Arabidopsis thaliana]
                  117603
Seq. No.
                  828 2.R1010
Contig ID
                  LIB23-024-Q1-E1-B9
5'-most EST
                  BLASTX
Method
                  g1169278
NCBI GI
                  158
BLAST score
                  1.0e-30
E value
Match length
                  175
                  50
% identity
                  DEHYDRIN ERD14 >gi 556474 dbj BAA04569 (D17715) ERD14
NCBI Description
                  protein [Arabidopsis thaliana]
                  117604
Seq. No.
Contig ID
                  828 3.R1010
                  LIB25-042-Q1-E1-B11
5'-most EST
Method
                  BLASTX
                  g3850579
NCBI GI
BLAST score
                  198
E value
                  8.0e-15
Match length
                  174
% identity
                  33
NCBI Description
                   (AC005278) Strong similarity to gb D14550 extracellular
                  dermal glycoprotein (EDGP) precursor from Daucus carota.
                  ESTs qb H37281, qb T44167, qb T21813, qb N38437, qb Z26470,
                  gb R65072, gb N76373, gb F15470, gb Z35182, gb H76373,
                  gb Z34678 an
                  117605
Seq. No.
Contig ID
                  828 5.R1010
5'-most EST
                  g1053747
Method
                  BLASTX
NCBI GI
                  g285741
BLAST score
                  284
E value
                  6.0e-25
Match length
                  155
% identity
                  47
                  (D14550) EDGP precursor [Daucus carota]
NCBI Description
Seq. No.
                  117606
Contig ID
                  828 6.R1010
5'-most EST
                  LIB3176-015-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g1169278
BLAST score
                  245
                  5.0e-25
E value
Match length
                  148
% identity
                  53
                  DEHYDRIN ERD14 >gi 556474 dbj BAA04569 (D17715) ERD14
NCBI Description
                  protein [Arabidopsis thaliana]
```

```
Contig ID
                   828 7.R1010
5'-most EST
                   jC-atXP78CF4F10T7b1
Method
                   BLASTX
                   q285741
NCBI GI
BLAST score
                   386
                   9.0e-37
E value
                   245
Match length
% identity
                   45
NCBI Description
                  (D14550) EDGP precursor [Daucus carota]
Seq. No.
                   117608
Contig ID
                   829 1.R1010
                   jC-atXLIB327420P4d10b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g710625
BLAST score
                   729
E value
                   0.0e + 00
                   750
Match length
                   99
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for ERD15 protein, complete cds
                   117609
Seq. No.
Contig ID
                   829 5.R1010
5'-most EST
                   jC-atXmonuni26Da06b1
Method
                   BLASTX
NCBI GI
                   q710626
BLAST score
                   645
E value
                   2.0e-67
Match length
                   164
% identity
                   77
NCBI Description
                   (D30719) ERD15 protein [Arabidopsis thaliana] >qi 3241941
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                   thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                   thaliana]
Seq. No.
                   117610
Contig ID
                   829 7.R1010
5'-most EST
                   LIB3234-071-P1-K1-B11
Method
                   BLASTN
NCBI GI
                   q710625
BLAST score
                   364
E value
                   0.0e + 00
Match length
                   404
                   99
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for ERD15 protein, complete cds
                   117611
Seq. No.
Contig ID
                   829 8.R1010
5'-most EST
                   g1328080
Method
                   BLASTN
NCBI GI
                   g3241939
BLAST score
                   307
E value
                   1.0e-172 .
Match length
                   377
% identity
                   97
                  Arabidopsis thaliana chromosome II BAC T26J13 genomic
NCBI Description
```

sequence, complete sequence [Arabidopsis thaliana]

5'-most EST

Method

```
117612.
Seq. No.
                  830 1.R1010
Contig ID
5'-most EST
                  LIB3175-033-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g1706772
BLAST score
                  2152
                  0.0e + 00
E value
Match length
                  410
                  100
% identity
                  FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE
NCBI Description
                  SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE)
                  >gi 1076324 pir S54251 farnesyl-diphosphate
                  farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana
                  >gi 798820 emb CAA60385 (X86692) farnesyl-diphosphate
                  farnesyltransferase [Arabidopsis thaliana]
                  >qi 806325 dbj BAA06103 (D29017) squalene synthase
                  [Arabidopsis thaliana] >gi 2232212 (AF004560) squalene
                  synthase 1 [Arabidopsis thaliana]
                  >gi 3096933 emb CAA18843.1 (AL023094) farnesyl-diphosphate
                  farnesyltransferase [Arabidopsis thaliana] >gi 4098519
                  (U79159) squalene synthase [Arabidopsis thaliana]
                  117613
Seq. No.
                  831 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327414P4g12b2
Method
                  BLASTX
NCBI GI
                  g544250
BLAST score
                  1120
E value
                  1.0e-123
Match length
                  215
                  100
% identity
                  ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR)
NCBI Description
                  >gi 541860 pir A49677 endoplasmic reticulum retention
                  receptor Erd2 - Arabidopsis thaliana
                  117614
Seq. No.
                  833 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327419P4e09b1
Method
                  BLASTX
NCBI GI
                  q1169599
BLAST score
                  2332
                  0.0e + 00
E value
                  474
Match length
                  93
% identity
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
                  >gi_541883 pir JQ2336 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CFD - Arabidopsis thaliana >gi 408481 (L22961)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi 468434 dbj BAA05040 (D26019) plastid fatty acid
                  desaturase [Arabidopsis thaliana] >gi 541653 dbj BAA03106
                  (D14007) omega-3-desaturase [Arabidopsis thaliana]
                  117615
Seq. No.
Contig ID
                  833 2.R1010
```

PLN g1030694

BLASTX

```
NCBI GI
                  g1345972
BLAST score
                  2267
E value
                  0.0e + 00
Match length
                  435
% identity
                  TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE,
NCBI Description
                  CHLOROPLAST PRECURSOR >gi 471093 dbj BAA04504 (D17578)
                  plastid fatty acid desaturase [Arabidopsis thaliana]
                  >qi 497219 (U08216) chloroplast linoleate desaturase
                  [Arabidopsis thaliana] >gi 516045 (L27158) omega-3 fatty
                  acid desaturase [Arabidopsis thaliana]
                  117616
Seq. No.
                  833 4.R1010
Contig ID
5'-most EST
                  jC-atXLIB327408P2c08b1
Method
                  BLASTX
NCBI GI
                  q1345969
BLAST score
                  351
                  4.0e-33
E value
                  118
Match length
% identity
                  OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 414732 (L25897) linoleoyl desaturase [Ricinus communis]
                  117617
Seq. No.
Contig ID
                  834 1.R1010
                  LIB3168-021-P1-K1-F6
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1345973
                  2025
BLAST score
                  0.0e + 00
E value
Match length
                  386
% identity
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi 541882 pir JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi 408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi 1197795 dbj BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
                  117618
Seq. No.
                  834 2.R1010
Contig ID
                  LIB3234-047-P1-K1-F1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1345973
BLAST score
                  157
                  8.0e-61
E value
                  136
Match length
% identity
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
```

>gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase

```
microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi 3420053.(AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
                  117619
Seq. No.
                  837 1.R1010
Contig ID
5'-most EST
                  PLN g166697
                  BLASTX
Method
                  g1931645
NCBI GI
                  765
BLAST score
                  6.0e-81
E value
                  164
Match length
% identity
                  93
                  (U95973) Fe(II) transporter isolog [Arabidopsis thaliana]
NCBI Description
                  117620
Seq. No.
                  837 2.R1010
Contig ID
                  q2580798
5'-most EST
Method
                  BLASTX
                  g119975
NCBI GI
BLAST score
                  452
                  9.0e-45
E value
                  120
Match length
% identity
                  78
                  FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin
NCBI Description
                  [2Fe-2S] precursor - Arabidopsis thaliana
                  >gi 16437 emb CAA35754 (X51370) ferredoxin precursor
                  [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
                   [Arabidopsis thaliana]
Seq. No.
                  117621
                  837 3.R1010
Contig ID
                  g2580714
5'-most EST
Method
                  BLASTX
NCBI GI
                  g119975
BLAST score
                  491
                  2.0e-49
E value
                  115
Match length
% identity
                  FERREDOXIN PRECURSOR >gi 99692_pir__S09979 ferredoxin
NCBI Description
                  [2Fe-2S] precursor - Arabidopsis thaliana
                  >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
                   [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
                   [Arabidopsis thaliana]
                  117622
Seq. No.
                  837 5.R1010
Contig ID
                  jC-atXLIB327408P4d10b1
5'-most EST
Method
                  BLASTX
                  q119975
NCBI GI
BLAST score
                   541
E value 👑
                  3.0e-55
```

[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)

[2Fe-2S] precursor - Arabidopsis thaliana

FERREDOXIN PRECURSOR >gi 99692 pir S09979 ferredoxin

143

79

Match length

NCBI Description

% identity

```
>gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
                   [Arabidopsis thaliana] >gi 166698 (M35868) ferrodoxin A
                  [Arabidopsis thaliana]
                  117623
Seq. No.
                  837 6.R1010
Contig ID
5'-most EST
                  g2047551
Method
                  BLASTX
                  g119975
NCBI GI
BLAST score
                  486
                  7.0e-49
E value
                  144
Match length
% identity
                  72
                  FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin
NCBI Description
                  [2Fe-2S] precursor - Arabidopsis thaliana
                  >gi 16437 emb CAA35754_ (X51370) ferredoxin precursor
                   [Arabidopsis thaliana] >gi 166698 (M35868) ferrodoxin A
                  [Arabidopsis thaliana]
Seq. No.
                  117624
                  837 7.R1010
Contig ID
5'-most EST
                  g2446123
Method :
                  BLASTX
                  g119975
NCBI GI
BLAST score
                  69
                  3.0e-17
E value
Match length
                  104
% identity
                  62
                  FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin
NCBI Description
                  [2Fe-2S] precursor - Arabidopsis thaliana
                  >gi 16437 emb CAA35754 (X51370) ferredoxin precursor
                   [Arabidopsis thaliana] >gi 166698 (M35868) ferrodoxin A
                   [Arabidopsis thaliana]
                  117625
Seq. No.
Contig ID
                  838 1.R1010
                  LIB3177-098-P1-K1-G1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4455253
BLAST score
                  931
E value
                  1.0e-101
                  220
Match length
% identity
                   (AL035523) superoxide dismutase (EC 1.15.1.1)
NCBI Description
                   (Fe)(fragment) [Arabidopsis thaliana]
Seq. No.
                  117626
                  838 3.R1010
Contig ID
5'-most EST
                  g906665
Method
                  BLASTX
                  g4455253
NCBI GI
BLAST score
                  640
                  7.0e-67
E value
                  191
Match length
                  57
% identity
                  (AL035523) superoxide dismutase (EC 1.15.1.1)
NCBI Description
                   (Fe)(fragment) [Arabidopsis thaliana]
```

```
117627
Seq. No.
                  839_1:R1010
Contig ID
5'-most EST
                  PLN g1146162
Method
                  BLASTX
NCBI GI
                  q2146730
BLAST score
                  1793
                  0.0e+00
E value
Match length
                  342
                  100
% identity
                  farnesyl diphosphate synthase (EC 2.5.1.10) FPS2 -
NCBI Description
                  Arabidopsis thaliana >gi_1146161 (L46350) farnesyl
                  diphosphate synthase [Arabidopsis thaliana] >gi_1146163
                  (L46349) farnesyl diphosphate synthase [Arabidopsis
                  thaliana] >gi 2245078 emb_CAB10500_ (Z97343) farnesyl
                  diphosphate synthase (FPS2) protein [Arabidopsis thaliana]
                  117628
Seq. No.
Contig ID
                  840 1.R1010
5'-most EST
                  LIB24-134-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                  g462174
BLAST score
                  1614
                  1.0e-180
E value
Match length
                  371
% identity
                  88
NCBI Description
                  GERANYLGERANYL PYROPHOSPHATE SYNTHETASE PRECURSOR (GGPP
                  SYNTHETASE) (DIMETHYLALLYLTRANSFERASE /
                  GERANYLTRANSTRANSFERASE / FARNESYLTRANSTRANSFERASE
                  >qi 413730 (L25813) geranylgeranyl pyrophosphate synthase
                  [Arabidopsis thaliana]
                  117629
Seq. No.
Contig ID
                  846 1.R1010
5'-most EST
                  jC-atXP31C145E2T7d2
Method
                  BLASTX
NCBI GI
                  g4467133
BLAST score
                  1495
                  1.0e-167
E value
Match length
                  326
% identity
                  89
NCBI Description
                  (AL035540) geranylgeranyl pyrophosphate synthase-related
                  protein [Arabidopsis thaliana]
                  117630
Seq. No.
                  847 1.R1010
Contig ID
5'-most EST
                  q634612
Method
                  BLASTX
                  q1170091
NCBI GI
BLAST score
                  1007
                  1.0e-109
E value
Match length
                  212
% identity
                  GLUTATHIONE S-TRANSFERASE PM24 (24 KD AUXIN-BINDING
NCBI Description
                  PROTEIN) (CLASS PHI) >gi 479736 pir S35268 glutathione
                  transferase (EC 2.5.1.18) gst2 - Arabidopsis thaliana
```

>gi 166723 (L07589) glutathione S-transferase [Arabidopsis

thaliana] >gi_347212 (L11601) glutathione S-transferase [Arabidopsis thaliana] >gi_407090_emb_CAA53051_ (X75303) glutathione S-transferase [Arabidopsis thaliana] >gi_2262152_gb_AAC78264.1_AAC78264 (AC002330) Atpm24.1 glutathione S transferase [Arabidopsis thaliana]

Seq. No. 117631 Contig ID 847_2.R1010

5'-most EST ARABL1-039-Q1-B1-E6

Method BLASTX
NCBI GI g1170091
BLAST score 541
E value 3.0e-55
Match length 151
% identity 76

NCBI Description

GLUTATHIONE S-TRANSFERASE PM24 (24 KD AUXIN-BINDING PROTEIN) (CLASS PHI) >gi_479736_pir__S35268 glutathione transferase (EC 2.5.1.18) gst2 - Arabidopsis thaliana >gi_166723 (L07589) glutathione S-transferase [Arabidopsis thaliana] >gi_347212 (L11601) glutathione S-transferase [Arabidopsis thaliana] >gi_407090_emb_CAA53051_ (X75303)

glutathione S-transferase [Arabidopsis thaliana]

>gi_2262152_gb_AAC78264.1_AAC78264 (AC002330) Atpm24.1

glutathione S transferase [Arabidopsis thaliana]

Seq. No. 117632 Contig ID 847 3.R1010

5'-most EST jC-atXP102CE2G3T7065d1

Method BLASTX
NCBI GI g1170091
BLAST score 441
E value 2.0e-44
Match length 132
% identity 78

NCBI Description GLUTATHIONE S-TRANSFERASE PM24 (24 KD AUXIN-BINDING PROTEIN) (CLASS PHI) >qi 479736 pir S35268 glutathi

PROTEIN) (CLASS PHI) >gi_479736_pir__S35268 glutathione transferase (EC 2.5.1.18) gst2 - Arabidopsis thaliana >gi_166723 (L07589) glutathione S-transferase [Arabidopsis thaliana] >gi_347212 (L11601) glutathione S-transferase [Arabidopsis thaliana] >gi_407090 emb CAA53051 (X75303)

glutathione S-transferase [Arabidopsis thaliana]

>gi 2262152 gb AAC78264.1 AAC78264 (AC002330) Atpm24.1

glutathione S transferase [Arabidopsis thaliana]

Seq. No. 117633 Contig ID 849 1.R1010 5'-most EST PLN g166726 Method BLASTX NCBI GI g120985 BLAST score 1894 E value 0.0e + 00Match length 383

% identity

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT

(GP-ALPHA-1) >gi_71923_pir__RGMUOA GTP-binding regulatory protein Go alpha chain - Arabidopsis thaliana >gi 166729

(M32887) G protein alpha subunit 1 (GP-alpha-1)

```
117634
Seq. No.
                  850 1.R1010
Contig ID
5'-most EST
                  jC-atXP82CG2C3T7b1
Method.
                  BLASTX
NCBI GI
                  g1170040
BLAST score
                  2736
E value
                  0.0e+00
Match length
                  565
% identity
                  94
NCBI Description
                  GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE)
                  >gi 451198_dbj_BAA03137_ (D14049) glutathione reductase
                  precursor [Arabidopsis thaliana] >gi_1944448_dbj_BAA19653_
                  (D89620) glutathione reductase precursor [Arabidopsis '
                  thaliana] >gi 740576 prf 2005376A glutathione reductase
                  [Arabidopsis thaliana]
Seq. No.
                  117635
                  852 1.R1010
Contig ID
5'-most EST
                  PLN_g598072
Method
                  BLASTX
                  g598073
NCBI GI
BLAST score
                  1991
E value
                  0.0e + 00
                  406
Match length
                  93
% identity
NCBI Description
                  (L36806) GT-1 [Arabidopsis thaliana]
                  117636
Seq. No.
                  853 1.R1010
Contig ID
5'-most EST
                  jC-alXLIB327435P3d03b1
Method
                  BLASTX
NCBI GI
                  q266989
BLAST score
                  833
                  3.0e-89
E value
                  193 🕝
Match length
% identity
                  84
                  GTP-BINDING PROTEIN SAR1B >gi 322517 pir S28603
NCBI Description
                  GTP-binding protein - Arabidopsis thaliana >gi 166734
                  (M95795) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                  117637
                  854 1.R1010
Contig ID
5'-most EST
                  LIB24-006-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  g3341681
BLAST score
                  1032
E value
                  1.0e-112
Match length
                  208
% identity
                  100
                  (AC003672) small GTP-binding protein [Arabidopsis thaliana]
NCBI Description
                  >gi 741994 prf 2008312A GTP-binding protein [Arabidopsis
                  thaliana]
```

[Arabidopsis thaliana] >gi_3075388 (AC004484) G protein

alpha subunit 1, GPA1 [Arabidopsis thaliana]

117638

Seq. No.

```
854 2.R1010
Contig ID
                  LIB25-085-Q1-E1-C5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3341681
BLAST score
                  429
E value
                  4.0e-42
Match length
                  103
% identity
                  85
NCBI Description
                  (AC003672) small GTP-binding protein [Arabidopsis thaliana]
                  >qi 741994 prf 2008312A GTP-binding protein [Arabidopsis
                  thaliana]
                  117639
Seq. No.
Contig ID
                  855 1.R1010
5'-most EST
                  LIB3168-018-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q2129608
BLAST score
                  3009
                  0.0e + 00
E value
Match length
                  610
% identity
                  98
                  GTP-binding protein, 68K - Arabidopsis thaliana >gi 807577
NCBI Description
                  (L38614) GTP-binding protein [Arabidopsis thaliana]
                  117640
Seq. No.
Contig ID
                  856 1.R1010
                  PLN q940382
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2462925
BLAST score
                  1333
                  1.0e-148
E value
Match length
                  259
% identity
                  (AJ000053) GTP cyclohydrolase II /
NCBI Description
                  3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                  thaliana]
                  117641
Seq. No.
                  857 1.R1010
Contig ID
5'-most EST
                  LIB24-094-Q1-E1-D9
Method
                  BLASTX
NCBI GI
                  a114330
BLAST score
                  2744
                  0.0e + 00
E value
                  949
Match length
                  89
% identity
                  PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
NCBI Description
                  >qi 67972 pir PXMUP1 H+-transporting ATPase (EC 3.6.1.35)
                  type 1, plasma membrane - Arabidopsis thaliana >gi 166746
                  (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis
                  thaliana]
Seq. No.
                  117642
Contig ID
                  857 2.R1010
5'-most EST
                  jC-atXLIB327421P3b12b1
Method
                  BLASTX
NCBI GI
                  q114335
```

Match length

321

```
BLAST score
                  1014
E value
                  1.0e-110
Match length
                  203
                  98
% identity
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
NCBI Description
                  >gi 67973 pir PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                  type 2, plasma membrane - Arabidopsis thaliana >gi 166629
                   (J05570) H+-ATPase [Arabidopsis thaliana]
                  117643
Seq. No.
                  857 5.R1010
Contig ID
5'-most EST
                  LIB22-059-Q1-E1-A9
                  BLASTX
Method
NCBI GI
                  g114335
                  403
BLAST score
                  1.0e-43
E value
                  135
Match length
                  72
% identity
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
NCBI Description
                  >gi 67973 pir PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                  type 2, plasma membrane - Arabidopsis thaliana >qi 166629
                   (J05570) H+-ATPase [Arabidopsis thaliana]
                  117644
Seq. No.
Contig ID
                  857 6.R1010
                  940\overline{4}171
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3004543
BLAST score
                  269
E value
                  1.0e-149
Match length
                  341
% identity
                  95
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F19F24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  117645
                  857 8.R1010
Contig ID
5'-most EST
                  g2749021
Method
                  BLASTX
NCBI GI
                  g114335
BLAST score
                  535
E value
                  1.0e-54
Match length
                  164
% identity
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
NCBI Description
                  >qi 67973 pir PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                  type 2, plasma membrane - Arabidopsis thaliana >qi 166629
                   (J05570) H+-ATPase [Arabidopsis thaliana]
Seq. No.
                  117646
Contig ID
                  857 11.R1010
5'-most EST
                  jC-atXLIB327427P1b11b1
Method
                  BLASTN
NCBI GI
                  q166745
BLAST score
                  281
E value
                  1.0e-157
```

```
88
% identity
NCBI Description
                  A.thaliana plasma membrane proton ATPase (PMA) mRNA,
                  complete cds
                  117647
Seq. No.
                  857 12.R1010
Contig ID
                  jC-\overline{a}1XLIB327435P3g06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g114335
BLAST score
                  408
                  2.0e-39
E value
Match length
                  82
% identity
                  99
NCBI Description
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
                  >gi 67973 pir PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                  type 2, plasma membrane - Arabidopsis thaliana >gi 166629
                   (J05570) H+-ATPase [Arabidopsis thaliana]
                  117648
Seq. No.
                  857 15.R1010
Contig ID
5'-most EST
                  g1054147
Method
                  BLASTX
                  g114335
NCBI GI
BLAST score
                  548
                  3.0e-56
E value
Match length
                  109
% identity
                  96
NCBI Description
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
                  >gi 67973 pir PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                  type 2, plasma membrane - Arabidopsis thaliana >gi 166629
                   (J05570) H+-ATPase [Arabidopsis thaliana]
                  117649
Seq. No.
                  857 17.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1e05b1
Method
                  BLASTX
                  g114335
NCBI GI
BLAST score
                  655
E value
                  2.0e-68
Match length
                  154
% identity
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
NCBI Description
                  >gi 67973 pir PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                  type 2, plasma membrane - Arabidopsis thaliana >gi 166629
                  (J05570) H+-ATPase [Arabidopsis thaliana]
Seq. No.
                  117650
                  857 20.R1010
Contig ID
5'-most EST
                  LIB3175-006-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g114335
BLAST score
                  815
E value
                  2.0e-87
Match length
                  176
                  92
% identity
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
NCBI Description
```

>gi 67973 pir PXMUP2 H+-transporting ATPase (EC 3.6.1.35)

Contig ID

```
(J05570) H+-ATPase [Arabidopsis thaliana]
                  117651
Seq. No.
Contig ID
                  859 1.R1010
5'-most EST
                  PLN_g217852
                  BLASTX
Method
NCBI GI
                   g729740
BLAST score
                   700
                   3.0e-73
E value
                   644
Match length
                  82
% identity
NCBI Description
                  STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 HOMOLOG (HMG
                  PROTEIN) >gi 217853 dbj BAA02719 (D13491) high mobility
                  group protein [Arabidopsis thaliana]
                  117652
Seq. No.
                  862 1.R1010
Contig ID
                  jC-atXLIB327408P2f01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1617013
BLAST score
                  397
                   6.0e-40
E value
Match length
                  92
% identity
                  100
                  (Y07745) histone H2B like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117653
                  863 1.R1010
Contig ID
5'-most EST
                  PLN g598074
Method
                  BLASTX
NCBI GI
                  q1345944
BLAST score
                  1935
                  0.0e + 00
E value
                   404
Match length
% identity
                  93
                  3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III PRECURSOR
NCBI Description
                   (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) >gi 598075
                   (L31891) 3-ketoacyl-acyl carrier protein synthase III (KAS
                  III) [Arabidopsis thaliana]
                  117654
Seq. No.
Contig ID
                  864 1.R1010
5'-most EST
                  PLN g1164999
Method
                  BLASTX
NCBI GI
                  g421842
BLAST score
                  3459
E value
                  0.0e + 00
Match length
                  677
                  97
% identity
                  potassium channel protein - Arabidopsis thaliana >gi 166774
NCBI Description
                  (M86990) potassium channel protein [Arabidopsis thalīana]
                  >gi_1065906 (U25088) potassium channel protein [Arabidopsis
                  thaliana]
                  117655
Seq. No.
```

type 2, plasma membrane - Arabidopsis thaliana >gi 166629

866 1.R1010

```
LIB22-032-Q1-E1-C9
5'-most EST
Method
                  BLASTX
                  g1170621
NCBI GI
BLAST score
                  3795
                  0.0e + 00
E value
                  754
Match length
% identity
                  100
                  KINESIN-LIKE PROTEIN C >gi 1084342_pir__S48020
NCBI Description
                  kinesin-related protein katC - Arabidopsis thaliana
                  >gi_1438844_dbj_BAA04674_ (D21138) heavy chain polypeptide
                  of kinesin-like protein [Arabidopsis thaliana]
                  117656
Seq. No.
Contig ID
                  866 2.R1010
5'-most EST
                  PLN_g1438841
Method
                  BLASTX
                  g1170620
NCBI GI
BLAST score
                  3687
                  0.0e + 00
E value
                  745
Match length
                  98
% identity
                  KINESIN-LIKE PROTEIN B >gi 1084341 pir S48019
NCBI Description
                  kinesin-related protein katB - Arabidopsis thaliana
                  >gi 1438842 dbj BAA04673 (D21137) heavy chain polypeptide
                  of kinesin-like protein [Arabidopsis thaliana]
Seq. No.
                  117657
Contig ID
                  868 1.R1010
5'-most EST
                  jC-atXLIB327433P1d02b1
Method
                  BLASTX
NCBI GI
                  q2494112
BLAST score
                  1722
                  0.0e + 00
E value
Match length
                  328
% identity
                  100
NCBI Description
                  (AC002376) Match to Arabidopsis ATHKCP (gb L40948). ESTs
                  gb ATTS0764, gb R90646, gb AA389809, gb ATTS2615 come from
                  this gene. [Arabidopsis thaliana] >gi 3126868 (AF061570)
                  potassium channel beta subunit homolog [Arabidopsis
                  thaliana]
Seq. No.
                  117658
                  868 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327409P4f03b1
Method
                  BLASTX
NCBI GI
                  g2494112
BLAST score
                  370
                  4.0e-35
E value
Match length
                  145
% identity
                  58
                  (ACO02376) Match to Arabidopsis ATHKCP (gb L40948). ESTs
NCBI Description
                  gb ATTS0764, gb R90646, gb AA389809, gb ATTS2615 come from
                  this gene. [Arabidopsis thaliana] >gi 3126868 (AF061570)
                  potassium channel beta subunit homolog [Arabidopsis
                  thaliana
```

12677

117659

Seq. No.

```
Contig ID
                  869_1.R1010
                  PLN_g289202
5'-most EST
                  BLASTX
Method
                  q547867
NCBI GI
                  4280
BLAST score
E value
                  0.0e + 00
Match length
                  859
% identity
                  95
                  LIPOXYGENASE 1 >gi_541878_pir__JQ2267 lipoxygenase (EC
NCBI Description
                  1.13.11.12) AtLox1 - Arabidopsis thaliana >gi_289203
                   (L04637) lipoxygenase [Arabidopsis thaliana] >gi_436920
                   (U01843) lipoxygenase 1 [Arabidopsis thaliana]
                  117660
Seq. No.
Contig ID
                  869 2.R1010
                  jC-atXLIB327410P1g10a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g289202
BLAST score
                  185
                  2.0e-99
E value
Match length
                  185
                  100
% identity
NCBI Description Arabidopsis thaliana lipoxygenase mRNA, complete cds
                  117661
Seq. No.
                  870_1..R1010
Contig ID
5'-most EST
                  PLN_g1399182
                  BLASTX
Method
NCBI GI
                  g1399183
BLAST score
                  2450
                  0.0e + 00
E value
Match length
                  501
                  94
% identity
                  (U50739) Lycopene beta cyclase [Arabidopsis thaliana]
NCBI Description
                  117662
Seq. No.
Contig ID
                  871_1.R1010
5'-most EST
                   jC-atXLIB327408P4a10b1
Method
                  BLASTX
NCBI GI
                  g1346724
                   977
BLAST score
                  1.0e-106
E value
Match length
                  208
% identity
                  93
                  FLORAL HOMEOTIC PROTEIN PISTILLATA >gi_625970_pir__A53839 B
NCBI Description
                  function floral homeotic protein PI - Arabidopsis thaliana
                  >gi_493620_dbj_BAA06465_ (D30807) PI protein [Arabidopsis
                  thaliana]
Seq. No.
                  117663
Contig ID
                   873 1.R1010
                   jC-atXP119C200M6T7038a1
5'-most EST
Method
                  BLASTN
                  q1209241
NCBI GI.
BLAST score
                  154
                  8.0e-81
E value
Match length
                  182
```

Match length

718.

```
98
% identity
NCBI Description Arabidopsis thaliana metallothionein mRNA sequence
                  117664
Seq. No.
Contig ID
                  873 2.R1010
5'-most EST
                  jC-atXLIB327422Pla09a1
Method
                  BLASTN
                  g2582640
NCBI GI
BLAST score
                  67
                  6.0e-29
E value
                  79
Match length
                  96
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
                  117665
Seq. No.
                  873 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327414P3c07a1
                  BLASTN
Method
NCBI GI
                  g1209241
BLAST score
                  399
                  0.0e + 00
E value
Match length
                 . 423
                  98
% identity
NCBI Description Arabidopsis thaliana metallothionein mRNA sequence
Seq. No.
                  117666
Contig ID
                  873 4.R1010
                  jC-atXP71C222N3T7092d1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1086460
BLAST score
                  188
E value
                  1.0e-101
Match length
                  313
% identity
                  57
NCBI Description Arabidopsis thaliana Columbia ecotype metallothionein
                  (MT1c) gene, complete cds
                  117667
Seq. No.
Contig ID
                  873 6.R1010
                  q3449671
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1209241
BLAST score
                  284
                  1.0e-158
E value
                  340
Match length
% identity
                  97
NCBI Description Arabidopsis thaliana metallothionein mRNA sequence
                  117668
Seq. No.
                  873 7.R1010
Contig ID
5'-most EST
                  g931992
Method
                  BLASTN
NCBI GI
                  g1086456
BLAST score
                  518
E value
                  0.0e + 00
```

```
76
% identity
NCBI Description
                   Arabidopsis thaliana Columbia ecotype metallothionein
                   (MT1a) gene, complete cds
                   117669
Seq. No.
                   873 8.R1010
Contig ID
5'-most EST
                   LIB35-056-Q1-E2-G2
Method
                   BLASTN
                   g1209241
NCBI GI
BLAST score
                   251
                   1.0e-139
E value
                   283
Match length
% identity
                   97
NCBI Description
                  Arabidopsis thaliana metallothionein mRNA sequence
                   117670
Seq. No.
                   874 1.R1010
Contig ID
5'-most EST
                   PLN g304106
                   BLASTX
Method
NCBI GI
                   g462650
BLAST score
                   7514
                   0.0e + 00
E value
                   1534
Match length
% identity
                   94
                   DNA (CYTOSINE-5)-METHYLTRANSFERASE (DNA METHYLTRANSFERASE)
NCBI Description
                   (DNA METASE) >gi 1363480 pir S59604 DNA
                   (cytosine-5-)-methyltransferase (EC 2.1.1.37) - Arabidopsis
                   thaliana >gi 304107 (L10692) cytosine-5 methyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                   117671
Contig ID
                   875 1.R1010
5'-most EST
                   jC-atXLIB327432P3d03b1
Method
                   BLASTX
                   g2832357
NCBI GI
BLAST score
                   443
                   2.0e-43
E value
                   140
Match length
% identity
NCBI Description
                   (Y14071) HMG protein [Arabidopsis thaliana] >gi 3068715
                   (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                   117672
Contig ID
                   876 1.R1010
5'-most EST
                   LIB23-031-Q1-E1-E2
Method
                   BLASTX
NCBI GI
                   g2832359
BLAST score
                   153
E value
                   2.0e-09
Match length
                   114
                   53
% identity
NCBI Description
                  (Y14072) HMG protein [Arabidopsis thaliana]
Seq. No.
                   117673 .
Contig ID
                 876 3.R1010
5'-most EST
                   LIB25-092-Q1-E1-F8
Method
                   BLASTX
```

¥.

Method

BLASTN

```
NCBI GI
                  q2832359
BLAST score
                  223
                  7.0e-18
E value
Match length
                  181
% identity
                  42
NCBI Description
                  (Y14072) HMG protein [Arabidopsis thaliana]
                  117674
Seq. No.
Contig ID
                  876_5.R1010
5'-most EST
                  jC-atXP91C247G19T7b1
                  BLASTX
Method
NCBI GI
                  g2832359
BLAST score
                  393
                  8.0e-38
E value
Match length
                  76
                  100
% identity
                  (Y14072) HMG protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117675
                  876 9.R1010
Contig ID
5'-most EST
                  jC-atXP111C126G16T7d1
                  BLASTX
Method
NCBI GI
                  g4503719
BLAST score
                  356
                  2.0e-33
E value
Match length
                  152
% identity
                  48
                  fragile histidine triad gene
NCBI Description
                  >gi 1706794 sp P49789 FHIT HUMAN
                  BIS (5'-ADENOSYL) - TRIPHOSPHATASE (DIADENOSINE
                  5',5'''-P1, P3-TRIPHOSPHATE HYDROLASE)
                  (DINUCLEOSIDETRIPHOSPHATASE) (AP3A HYDROLASE) (AP3AASE)
                  (FRAGILE HISTIDINE TRIAD PROTEIN) >gi 3114520 pdb 4FIT
                  Fhit-Apo >gi_3114524_pdb_6FIT_ Fhit-Transition State
                  Analog >gi_3318895_pdb_1FHI_ Substrate Analog (Ib2)
                  Complex With The Fragile Histidine Triad Protein, Fhit
                  >gi 1203836 (U46922) member of the histidine triad (HIT)
                  gene family; similar to the S. pombe diadenosine
                  5',5'''-P1,P4-tetraphosphate asymmetrical hydrolase [Homo
                  sapiens] >gi 1945066 (U76272) diadenosine triphosphate
                  (Ap3A) hydrolase [Homo sapiens]
                  117676
Seq. No.
                  876 10.R1010
Contig ID
5'-most EST
                  LIB35-017-Q1-E1-E4
Method
                  BLASTX
                  g2832359
NCBI GI
BLAST score
                  372
                  2.0e-35
E value
                  91
Match length
                  82
% identity
NCBI Description
                  (Y14072) HMG protein [Arabidopsis thaliana]
                  117677
Seq. No.
                  876 14.R1010
Contig ID
5'-most EST
                  jC-atXmonuni26Cd08a1
```

```
NCBI GI
                   g3869067
BLAST score
                   255
E value
                   1.0e-141
Match length
                   259
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCK7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   117678
                   877 1.R1010
Contig ID
5'-most EST
                   jC-atXP79C231J9T7d2
Method
                   BLASTX
                   q1694976
NCBI GI
BLAST score
                   459
E value
                   2.0e-45
Match length
                   111
% identity
                   84
                   (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                   >gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                   thaliana]
Seq. No.
                   117679
Contig ID
                   877 2.R1010
5'-most EST
                   jC-atXLIB327438P3g01a2
Method
                   BLASTX
NCBI GI
                   g1694976
BLAST score
                   459
E value
                   2.0e-45
Match length
                   111
% identity
NCBI Description
                   (Y09482) HMG1 [Arabidopsis thaliana]
                   >qi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                   thaliana]
                   117680
Seq. No.
Contig ID
                   877 3.R1010
5'-most EST
                   g936717
Method
                   BLASTX
NCBI GI
                   g1694976
BLAST score
                   389
E value
                   2.0e-37
Match length
                   107
% identity
                   74
                   (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                   >qi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                   thaliana]
Seq. No.
                   117681
Contig ID
                   879 1.R1010
5'-most EST
                   LIB3177-086-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   q2832363
BLAST score
                   599
E value
                   4.0e-62
Match length
                   114
% identity
                  (Y14075) HMG protein [Arabidopsis thaliana]
NCBI Description
```

```
[Arabidopsis thaliana]
                   117682
Seq. No.
Contig ID
                   880 1.R1010
5'-most EST
                   jC-atXLIB327413P1g12b1
                   BLASTX
Method
NCBI GI
                   g2832355
BLAST score
                   497
                   6.0e-50
E value
                   113
Match length
% identity
                   87
                   (Y14074) HMG protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117683
                   882 1.R1010
Contig ID
                   jC-atXLIB327423P3b04b1
5'-most EST
Method
                   BLASTX
                   q1708236
NCBI GI
BLAST score
                   2410
                   0.0e + 00
E value
                   461
Match length
                   100
% identity
                  HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
NCBI Description
                  -(3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
                   >qi 2129617 pir JC4567 hydroxymethylglutaryl-CoA synthase
                   (EC 4.1.3.5) - Arabidopsis thaliana
                   >gi_1143390_emb_CAA58763_ (X83882)
                   hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
                   >qi 1586548 prf 2204245A hydroxy methylglutaryl CoA
                   synthase [Arabidopsis thaliana]
Seq. No.
                   117684
Contig ID
                   882 2.R1010
5'-most EST
                   g2048592
Method
                   BLASTX
NCBI GI
                   g1708236
BLAST score
                   127
                   6.0e-26
E value
Match length
                   90
% identity
                   70
                   HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
NCBI Description
                   (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
                   >qi 2129617 pir JC4567 hydroxymethylglutaryl-CoA synthase
                   (EC 4.1.3.5) - Arabidopsis thaliana
                   >gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
                   >gi 1586548 prf 2204245A hydroxy methylglutaryl CoA
                   synthase [Arabidopsis thaliana]
                   117685
Seq. No.
Contig ID
                   883 1.R1010
                   LIB24-016-Q1-E1-B7
5'-most EST
Method
                   BLASTX
                   g1351987
NCBI GI
BLAST score
                   2955
                   0.0e + 00
E value
```

>gi_3367575_emb_CAA20027_ (AL031135) HMG delta protein

```
Match length
                   584
% identity
                   95
                  ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING)
NCBI Description
                  (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi 507946
                   (L29083) glutamine-dependent asparagine synthetase
                   [Arabidopsis thaliana]
Seq. No.
                   117686
                   884 1.R1010
Contig ID
                   jC-atXLIB327411P3h11b1
5'-most EST
                   BLASTX
Method
                   g128188
NCBI GI
BLAST score
                   4761
                   0.0e+00
E value
                   917
Match length
                   97
% identity
                  NITRATE REDUCTASE 2 (NR2) >gi_66202_pir__RDMUNH nitrate reductase (NADH) (EC 1.6.6.1) 2 - Arabidopsis thaliana
NCBI Description
                   >gi 166782 (J03240) nitrate reductase (EC 1.6.6.1)
                   [Arabidopsis thaliana]
                   117687
Seq. No.
                   884 2.R1010
Contig ID
5'-most EST
                   jC-atXP123C117N15T7071d1
Method
                   BLASTX
                   g930002
NCBI GI
BLAST score
                   578
                   2.0e-59
E value
                   115
Match length
% identity
                   (X13435) nitrate reductase NR2 (396 AA) [Arabidopsis
NCBI Description
                   thaliana]
                   117688
Seq. No.
                   884 3.R1010
Contig ID
                   g2446202
5'-most EST
                   BLASTX
Method
                                            q128188
NCBI GI
BLAST score
                   55
                   2.0e-40
E value
                   100
Match length
% identity
                   80
                   NITRATE REDUCTASE 2 (NR2) >gi_66202_pir__RDMUNH nitrate
NCBI Description
                   reductase (NADH) (EC 1.6.6.1) 2 - Arabidopsis thaliana
                  '>gi 166782 (J03240) nitrate reductase (EC 1.6.6.1)
                   [Arabidopsis thaliana]
                   117689
Seq. No.
                   885 1.R1010
Contig ID
5'-most EST
                   LIB146-003-Q1-E1-C6
Method
                   BLASTX
NCBI GI
                   g2129659
BLAST score
                   792
                   2.0e-84
E value
                   199
Match length
                   81
% identity
NCBI Description oleosin, isoform 21K - Arabidopsis thaliana >gi_725260
```

Match length

629

فرارز والمجاه عوما

(L40954) oleosin [Arabidopsis thaliana]

```
117690
Seq. No.
                  886 1.R1010
Contig ID
                  LIB24-120-Q1-E1-D5
5'-most EST
Method
                  BLASTX
                  g682728
NCBI GI
BLAST score
                  168
                  1.0e-110
E value
                  212
Match length
                  96
% identity
                  (L40031) S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A
NCBI Description
                  3-O-methyltransferase [Arabidopsis thaliana]
Seq. No.
                  117691
                  887 1.R1010
Contig ID
                  PLN g16337
5'-most EST
                  BLASTX
Method
                  q232274
NCBI GI
BLAST score
                  722
                  2.0e-76
E value
                  155
Match length
                  93
% identity
                  17.6 KD CLASS II HEAT SHOCK PROTEIN >gi_71499_pir__HHMU17
NCBI Description
                  heat shock protein 17.6-II - Arabidopsis thaliana
                  >gi 16338 emb CAA45039 (X63443) heat shock protein 17.6-II
                  [Arabidopsis thaliana]
                  117692
Seq. No.
                  888 1.R1010
Contig ID
                  iC-atXLIB327408P4c03b1
5'-most EST
                  BLASTX
Method
                  g115916
NCBI GI
BLAST score
                  1549
                  1.0e-173
E value
Match length
                  294
                  100
% identity
                  CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A
NCBI Description
                  >gi 282863 pir S23095 protein kinase (EC 2.7.1.37) cdc2 -
                  Arabidopsis thaliana >gi 251888 bbs 109461 p34cdc2 protein
                  kinase [Arabidopsis thaliana, flower, Peptide, 294 aa]
                  >gi 16219 emb CAA40971 (X57839) p34(cdc2) [Arabidopsis
                  thaliana] >gi_166784 (M59198) protein kinase [Arabidopsis
                  thaliana] >gi 217849 dbj BAA01623 (D10850) p32 protein
                  serine/threonine kinase [Arabidopsis thaliana]
                  >gi_257374_bbs_115411 (S45387) Aracdc2=p34cdc2 protein
                  kinase homolog [Arabidopsis thaliana, ecotype Columbia,
                  flowers, Peptide, 294 aa] [Arabidopsis thaliana]
                  117693
Seq. No.
                  889 1.R1010
Contig ID
5'-most EST
                  PLN g304108
Method
                  BLASTX
NCBI GI
                  q1171978
BLAST score
                  2771
                  0.0e + 00
E value
```

```
% identity
                  88
                  POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                   (PABP 2) >gi_304109 (L19414) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)
                  poly(A)-binding protein [Arabidopsis thaliana]
                  117694
Seq. No.
                  890_1.R1010
Contig ID
5'-most EST
                  PLN_g551166
                  BLASTX
Method
NCBI GI
                  g1483213
BLAST score
                  1372
E value
                  1.0e-152
                  313
Match length
% identity
                  (X96480) PAC [Arabidopsis thaliana]
NCBI Description
                  117695
Seq. No.
                  891 1.R1010
Contig ID
                  jC-atX24048Q1E2E02b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g585012.
BLAST score
                  2947
E value
                  0.0e + 00
                  566
Match length
% identity
                  100
                  PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE)
NCBI Description
                  >gi_289205 (L16237) phytoene desaturase [Arabidopsis
                  thaliana] >gi 2244777 emb CAB10200 (Z97335) unnamed
                  protein product [Arabidopsis thaliana]
                  117696
Seq. No.
                  892 1.R1010
Contig ID
5'-most EST
                   jC-atXP85C241D17T7b1
Method
                  BLASTX
                   g585748
NCBI GI
BLAST score
                   2073
E value
                  0.0e + 00
Match length
                   416
                   97
% identity
                  PHYTOENE SYNTHASE PRECURSOR >gi 413732 (L25812) phytoene
NCBI Description
                  synthase [Arabidopsis thaliana]
                  117697
Seq. No.
                  893 1.R1010
Contig ID
5'-most EST
                  PLN_g166794
                  BLASTX
Method
                  g112717
NCBI GI
BLAST score
                   450
                  1.0e-44
E value
Match length
                  165
% identity
                  52
                  21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi 82050 pir S10911
NCBI Description
                  hypothetical protein precursor - carrot
```

-22 to 171) [Daucus carota]

>gi 18312 emb CAA36642 (X52395) precursor polypeptide (AA

Method

NCBI GI

BLASTX g1352681

```
117698
Seq. No.
Contig ID
                  894 1.R1010
5'-most EST
                  PLN g642129
Method
                  BLASTX
                  g1703200
NCBI GI
BLAST score
                  2204
                  0.0e + 00
E value
Match length
                   427
% identity
                  96
                  PROTEIN KINASE AFC2 >gi 601789 (U16177) protein kinase
NCBI Description
                  [Arabidopsis thaliana] >gi 642130 dbj BAA08214 (D45353)
                  protein kinase [Arabidopsis thaliana]
                  >gi 4220516 emb CAA22989 (AL035356) protein kinase (AFC2)
                   [Arabidopsis thaliana]
Seq. No.
                  117699
Contig ID
                  895 1.R1010
5'-most EST
                  PLN g601786
                  BLASTX
Method
NCBI GI
                  q1703199
BLAST score
                  2369
E value
                  0.0e + 00
Match length
                   463
% identity
NCBI Description
                  PROTEIN KINASE AFC1 >gi 601787 (U16176) protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  117700
Contig ID
                  896 1.R1010
5'-most EST
                  jC-atXP92CH3H8T7047d1
Method
                  BLASTX
NCBI GI
                  q642134
BLAST score
                  2103
E value
                  0.0e + 00
Match length
                   396
% identity
                   100
NCBI Description
                   (D45355) protein kinase [Arabidopsis thaliana]
                  >gi 3063704_emb_CAA18595.1_ (AL022537) protein kinase AME3
                   [Arabidopsis thaliana]
Seq. No.
                   117701
Contig ID
                  896 2.R1010
5'-most EST
                  LIB23-036-Q1-E1-B1
Method
                  BLASTX
NCBI GI
                  q1703201
BLAST score
                  147
E value
                   2.0e-09
Match length
                  28
% identity
                  100
                  PROTEIN KINASE AFC3 >gi 601791 (U16178) protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  117702
Contig ID
                  897 1.R1010
                  jC-atXLIB327422P1g09b1
5'-most EST
```

```
BLAST score
                  1737
                   0.0e + 00
E value
                   397
Match length
                   85
% identity
NCBI Description
                  PROTEIN PHOSPHATASE 2C (PP2C) >gi 1076391 pir S55457
                  phosphoprotein phosphatase (EC 3.\overline{1}.3.16) \overline{2}C - Arabidopsis
                  thaliana >gi 633028 dbj BAA07287 (D38109) protein
                  phosphatase 2C [Arabidopsis thaliana]
                   117703
Seq. No.
                   897 4.R1010
Contig ID
                   g2733487
5'-most EST
                  BLASTX
Method
                  g1352681
NCBI GI
                   478
BLAST score
E value
                   5.0e-48
                   106
Match length
                   88
% identity
                   PROTEIN PHOSPHATASE 2C (PP2C) >gi 1076391 pir S55457
NCBI Description
                  phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis
                   thaliana >gi_633028_dbj_BAA07287 (D38109) protein
                  phosphatase 2C [Arabidopsis thaliana]
                   117704
Seq. No.
                   898 1.R1010
Contig ID
                   PLN g16432
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1346754
BLAST score
                   1668
                   0.0e + 00
E value
                   312
Match length
                   100
% identity
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 2
NCBI Description
                   >gi_421851_pir__S31086 phosphoprotein phosphatase (EC
                   3.1.3.16) \overline{1} catalytic chain (clone TOPP2) - Arabidopsis
                   thaliana >gi_166797 (M93409) catalytic subunit [Arabidopsis
                   thaliana]
                   117705
Seq. No.
                   898 2.R1010
Contig ID
                   jC-atXLIB327439P1e10b2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1346759
BLAST score
                   1665
                   0.0e + 00
E value
                   312
Match length
% identity
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 5
NCBI Description
                   >gi 421854 pir S31089 phosphoprotein phosphatase (EC
                   3.1.3.16) 1 catalytic chain (clone TOPP5) - Arabidopsis
                   thaliana >gi 166803 (M93412) phosphoprotein phosphatase 1
                   [Arabidopsis thaliana]
                   117706
Seq. No.
                   899 1.R1010
Contig ID
                   LIB35-016-Q1-E1-F1
5'-most EST
```

BLASTX

Method

5'-most EST

```
NCBI GI
                  g1346756
BLAST score
                  1599
E value
                  1.0e-179
                  298
Match length
                  100
% identity
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 3
NCBI Description
                  >gi 421852 pir S31087 phosphoprotein phosphatase (EC
                  3.1.3.16) \overline{1} catalytic chain (clone TOPP3) - Arabidopsis
                  thaliana >gi 166799 (M93410) phosphoprotein phosphatase 1
                   [Arabidopsis thaliana]
                  117707
Seq. No.
                  900 1.R1010
Contig ID
5'-most EST
                  LIB3177-036-P1-K2-E3
Method
                  BLASTX
                  q1346758
NCBI GI
BLAST score
                  1661
E value
                  0.0e + 00
Match length
                  321
% identity
                  97
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 4
NCBI Description
                  >gi 421853 pir S31088 phosphoprotein phosphatase (EC
                  3.1.3.16) 1 catalytic chain (clone TOPP4) - Arabidopsis
                  thaliana >gi 166801 (M93411) phosphoprotein phosphatase 1
                   [Arabidopsis thaliana] >gi 2642169 (AC003000)
                  serine/threonine protein phosphatase PP1 isozyme 4 (TOPP4)
                   [Arabidopsis thaliana]
Seq. No.
                  117708
Contig ID
                  902 1.R1010
5'-most EST
                  jC-atXLIB327414P2f07a1
Method
                  BLASTX
NCBI GI
                  g2495184
BLAST score
                  2614
E value
                  0.0e + 00
Match length
                  537
% identity
                  PROTOPORPHYRINOGEN OXIDASE, CHLOROPLAST PRECURSOR (PPO)
NCBI Description
                  >qi 1877018 dbj BAA11820 (D83139) protoporphyrinogen
                  oxidase [Arabidopsis thaliana]
Seq. No.
                  117709
Contig ID
                  903 1.R1010
5'-most EST
                  PLN g507219
Method
                  BLASTX
NCBI GI
                  q1346790
BLAST score
                  3320
E value
                  0.0e + 00
Match length
                  796
% identity
                  83
                  PATHOGENESIS-RELATED HOMEODOMAIN PROTEIN (PRHA) >gi 507220
NCBI Description
                  (L21991) homeodomain protein [Arabidopsis thaliana]
                  >gi 2501810 (U48864) PRHA [Arabidopsis thaliana]
                  117710
Seq. No.
                  903 2.R1010
Contig ID
```

jC-a1X24090Q1E1G01a1



```
Method
                  BLASTN
NCBI GI
                   q507219
BLAST score
                   397
                   0.0e + 00
E value
                   401
Match length
                   100
% identity
                  Arabidopsis thaliana homeodomain protein (PRHA) mRNA,
NCBI Description
                   complete cds
                   117711
Seq. No.
                   904 1.R1010
Contig ID
                   jC-atXmonuni25Ab06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1171642
BLAST score
                   2015
                   0.0e + 00
E value
                   389
Match length
                   100
% identity
                   PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK
NCBI Description
                   >gi_481206_pir__S38326 protein kinase - Arabidopsis
                   thaliana >gi_1 \overline{166}809 (L07248) protein kinase [Arabidopsis
                   thaliana]
                   117712
Seq. No.
Contig ID
                   904 2.R1010
                   g2762227
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1171642
BLAST score
                   266
                   6.0e-23
E value
Match length
                   133
% identity
                   56
                   PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK
NCBI Description
                   >gi 481206 pir S38326 protein kinase - Arabidopsis
                   thaliana >gi_166809 (L07248) protein kinase [Arabidopsis
                   thaliana]
                   117713
Seq. No.
                  *904_4.R1010
Contig ID
                   jC-alX25042Q1E1D02a1
5'-most EST
                   BLASTN
Method
                   q166808
NCBI GI
                   134
BLAST score
                   2.0e-69
E value
                   199
Match length
                   93
% identity
                   Arabidopsis thaliana Columbia protein kinase mRNA, complete
NCBI Description
                   117714
Seq. No.
                   905 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327410P2c04b1
Method
                   BLASTX
                   g1170949
NCBI GI
```

2313

434

0.0e + 00

BLAST score

E value Match length

```
100
% identity
                  SERINE/THREONINE-PROTEIN KINASE MHK >gi 481207 pir S38327
NCBI Description
                  protein kinase - Arabidopsis thaliana >gi 166811 (L07249)
                  protein kinase [Arabidopsis thaliana]
                  117715
Seq. No.
                  905 2.R1010
Contig ID
                  jC-atXmonuni10Bc04b1
5'-most EST
Method
                  BLASTX
                  g1170949
NCBI GI
BLAST score
                  225
                  3.0e-18
E value
                  52
Match length
% identity
                  87
NCBI Description
                  SERINE/THREONINE-PROTEIN KINASE MHK >gi 481207 pir S38327
                  protein kinase - Arabidopsis thaliana >gi 166811 (L07249)
                  protein kinase [Arabidopsis thaliana]
                  117716
Seq. No.
Contig ID
                  907 1.R1010
5'-most EST
                  LIB3176-109-P1-K1-E7
Method
                  BLASTX
                  q1362002
NCBI GI
BLAST score
                  1772
E value
                  0.0e + 00
Match length
                  362
% identity
                  95
                  protein kinase 1 - Arabidopsis thaliana >gi_166817 (L05561)
NCBI Description
                  protein kinase [Arabidopsis thaliana]
Seq. No.
                  117717
Contig ID
                  907 2.R1010
5'-most EST
                  PLN q166818
Method
                  BLASTX
NCBI GI
                  g2146746
BLAST score
                  1721
                  0.0e + 00
E value
Match length
                  361
                  92
% identity
                  protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                  >gi 166819 (L05562) protein kinase [Arabidopsis thaliana]
Seq. No.
                  117718
Contig ID
                  909 1.R1010
5'-most EST
                  PLN g166822
                  BLASTX
Method
NCBI GI
                  q585628
BLAST score
                  1663
                  0.0e + 00
E value
                  306
Match length
                  100
% identity
NCBI Description
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-1 CATALYTIC
                  SUBUNIT >gi 418779 pir S31162 phosphoprotein phosphatase
                  (EC 3.1.3.16) 2A-alpha catalytic chain (clone EP14a) -
                  Arabidopsis thaliana >gi 166823 (M96733) protein
```

phosphatase [Arabidopsis thaliana]

```
117719
Seq. No.
Contig ID
                  911 1.R1010
5'-most EST
                  jC-atXLIB327407P3a12b1
Method
                  BLASTX
                  q4204947
NCBI GI
                  1394
BLAST score
                  0.0e + 00
E value
Match length
                  351
% identity
                  (U60135) serine/threonine protein phosphatase 2A-3
NCBI Description
                  catalytic subunit [Arabidopsis thaliana]
                  117720
Seq. No.
Contig ID
                  911 2.R1010
5'-most EST
                  LIB3175-078-P1-K1-H2
                  BLASTX
Method
NCBI GI
                  g1352664
BLAST score
                  1703
E value
                  0.0e + 00
Match length
                  313
% identity
                  100
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC
NCBI Description
                  SUBUNIT >gi 2117984 pir S52660 phosphoprotein phosphatase
                  (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana
                  >gi 473259 (U08047) Ser/Thr protein phosphatase
                  [Arabidopsis thaliana] >qi 4204949 (U60136)
                  serine/threonine protein phosphatase 2A-4 catalytic subunit
                  [Arabidopsis thaliana]
                  117721
Seq. No.
Contia ID
                  911 3.R1010
5'-most EST
                  q906876
Method
                  BLASTX
NCBI GI
                  g1352664
BLAST score
                  271
E value
                  1.0e-23
Match length
                  88
                  73
% identity
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC
NCBI Description
                  SUBUNIT >gi 2117984 pir S52660 phosphoprotein phosphatase
                  (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana
                  >qi 473259 (U08047) Ser/Thr protein phosphatase
                  [Arabidopsis thaliana] >qi 4204949 (U60136)
                  serine/threonine protein phosphatase 2A-4 catalytic subunit
                  [Arabidopsis thaliana]
                  117722
Seq. No.
Contig ID
                  911 4.R1010
5'-most EST
                  jC-atX24110Q1E1D06b1
Method
                  BLASTX
NCBI GI
                  g1352664
BLAST score
                  199
E value
                  3.0e-15
Match length
                  53
% identity
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC
NCBI Description
```

SUBUNIT >qi 2117984 pir S52660 phosphoprotein phosphatase

```
[Arabidopsis thaliana] >gi 4204949 (U60136)
                  serine/threonine protein phosphatase 2A-4 catalytic subunit
                  [Arabidopsis thaliana]
                  117723
Seq. No.
                  912 1.R1010
Contig ID
5'-most EST
                  jC-atXP75C226K23T7d1
Method
                  BLASTX
NCBI GI
                  g117687
BLAST score
                  1412
E value
                  1.0e-157
Match length
                  270
% identity
                  100
                  GAP JUNCTION CX32 PROTEIN (CONNEXIN 32) >gi 166832 (M63234)
NCBI Description
                  plant-type connexin 32 [Arabidopsis thaliana]
                  117724
Seq. No.
Contig ID
                  914 1.R1010
5'-most EST
                  LIB24-093-Q1-E1-H11
Method
                  BLASTX
NCBI GI
                  g2507281
BLAST score
                  1094
E value
                  1.0e-120
Match length
                  201
% identity
                  100
NCBI Description
                  GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi 1668706 emb CAA66048
                  (X97380) atran2 [Arabidopsis thaliana]
Seq. No.
                  117725
Contig ID
                  914 2.R1010
5'-most EST
                  jC-atXP96C248K4T7b1
Method
                  BLASTX
NCBI GI
                  g1172833
BLAST score
                  1090
                  1.0e-119
E value
Match length
                  200
                  100
% identity
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-1 >gi 495729 (L16789) small
                  ras-related protein [Arabidopsis thaliana]
                  >gi 2058278 emb CAA66047 (X97379) atran1 [Arabidopsis
                  thaliana]
                  117726
Seq. No.
                  914 3.R1010
Contig ID
5'-most EST
                  LIB3177-016-P1-K2-G10
Method
                  BLASTX
NCBI GI
                  g1172833
BLAST score
                  724
E value
                  1.0e-114
Match length
                  200
% identity
                  95
                  GTP-BINDING NUCLEAR PROTEIN RAN-1 >gi 495729 (L16789) small
NCBI Description
                  ras-related protein [Arabidopsis thaliana]
                  >gi_2058278_emb_CAA66047_ (X97379) atran1 [Arabidopsis
```

(EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana >gi 473259 (U08047) Ser/Thr protein phosphatase

thaliana]

Match length

287

```
117727
Seq. No.
                  914 4.R1010
Contig ID
5'-most EST
                  g473298
                  BLASTX
Method
                  g1172833
NCBI GI
                  185
BLAST score
                  3.0e-13
E value
Match length
                  36
                  97
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-1 >gi 495729 (L16789) small
NCBI Description
                  ras-related protein [Arabidopsis thaliana]
                  >gi 2058278_emb_CAA66047_ (X97379) atran1 [Arabidopsis
                  thaliana]
Seq. No.
                  117728
                  916 1.R1010
Contig ID
5'-most EST
                  PLN g4165447
                  BLASTX
Method
                  g516118
NCBI GI
BLAST score
                  311
                  3.0e-27
E value
                  1084
Match length
% identity
                  86
                  (L08469) envelope Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117729
Contig ID
                  916 2.R1010
                  PLN g509809
5'-most EST
                  BLASTX
Method
NCBI GI
                  q509810
BLAST score
                  5113
                  0.0e+00
E value
                  1020
Match length
                  99
% identity
                  (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
                  117730
Seq. No.
                  917 1.R1010
Contig ID
5'-most EST
                  jC-atXP78CF4G6T7b1
Method
                  BLASTX
                  g2924520
NCBI GI
BLAST score
                  1466
                  1.0e-163
E value
                  280
Match length
% identity
                  100
                  (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                  [Arabidopsis thaliana]
                  117731
Seq. No.
                  917 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327420P4g08b1
Method
                  BLASTX
                  g1175013
NCBI GI
                  1416
BLAST score
                  1.0e-157
E value
```

BLAST score

587

```
% identity
NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi 629542 pir S44084
                  plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                  >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic
                  protein 2a [Arabidopsis thaliana]
                  117732
Seq. No.
Contig ID
                  917 3.R1010
5'-most EST
                  LIB35-036-Q1-E2-D3
Method
                  BLASTX
NCBI GI
                  q1175014
BLAST score
                  1409
E value
                  1.0e-156
Match length
                  285
% identity
                  95
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2B >gi 629543 pir $44085
NCBI Description
                  plasma membrane intrinsic protein 2b - Arabidopsis thaliana
                  >gi_472879_emb_CAA53478_ (X75884) plasma membrane intrinsic
                  protein 2b [Arabidopsis thaliana]
Seq. No.
                  117733
                  917 4.R1010
Contig ID
                  LIB3168-010-P1-K1-D4
5'-most EST
                  BLASTX
Method
NCBI GI
                  q267136
BLAST score
                  1339
                  1.0e-148
E value
Match length
                  285
% identity
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2C (WATER-STRESS INDUCED
NCBI Description
                  TONOPLAST INTRINSIC PROTEIN) (WSI-TIP)
                  >gi 217869 dbj BAA02520 (D13254) transmembrane channel
                  protein [Arabidopsis thaliana] >qi 4371283 qb AAD18141
                  (AC006260) putative plasma membrane intrinsic protein 2C
                  [Arabidopsis thaliana] >qi 384324 prf 1905411A
                  transmembrane channel [Arabidopsis thaliana]
Seq. No.
                  117734
Contig ID
                  917 5.R1010
5'-most EST
                  jC-atXP86CG9D9T7d2
Method
                  BLASTX
NCBI GI
                  g1175013
BLAST score
                  1061
E value
                  1.0e-116
Match length
                  281
% identity
NCBI Description
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi 629542 pir S44084
                  plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                  >gi 472877 emb CAA53477_ (X75883) plasma membrane intrinsic
                  protein 2a [Arabidopsis thaliana]
                  117735
Seq. No.
Contig ID
                  917 6.R1010
5'-most EST
                  q906723
Method
                  BLASTX
NCBI GI
                  q2924520
```

```
E value
                  1.0e-60
Match length
                  150
% identity
                  81
                  (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                  117736
Seq. No.
                  917 8.R1010
Contig ID
                  g2759539
5'-most EST
                  BLASTX
Method
                  g1175013
NCBI GI
                  384
BLAST score
E value
                  9.0e-38
Match length
                  85
% identity
                  98
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi 629542 pir S44084
NCBI Description
                  plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                  >gi 472877 emb CAA53477 (X75883) plasma membrane intrinsic
                  protein 2a [Arabidopsis thaliana]
                  117737
Seq. No.
                  917 12.R1010
Contig ID
                  jC-atXP50C179J16T7079d1
5'-most EST
                  BLASTX
Method
                  g2924520
NCBI GI
BLAST score
                  669
E value
                  8.0e-86
Match length
                  189
                  87
% identity
                  (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                  117738
Seq. No.
                  917 14.R1010
Contig ID
5'-most EST
                  g11\overline{5}8978
Method
                  BLASTX
                  g1175013
NCBI GI
BLAST score
                  408
                  1.0e-39
E value
                  170
Match length
% identity
                  59
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi 629542 pir S44084
NCBI Description
                  plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                  >gi 472877 emb CAA53477 (X75883) plasma membrane intrinsic
                  protein 2a [Arabidopsis thaliana]
                  117739
Seq. No.
                  917 15.R1010
Contig ID
5'-most EST
                  g2748161
Method
                  BLASTN
                  g4455339
NCBI GI
BLAST score
                  333
                  0.0e + 00
E value
Match length
                  382
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5
NCBI Description
```

(ESSAII project)

```
Seq. No.
                   117740
Contig ID
                   918 1.R1010
                   jC-alXLIB327435P4f01b1
5'-most EST
                   BLASTX
Method
                   g2500098
NCBI GI.
                   1929
BLAST score
                   0.0e + 00
E value
                   439
Match length
                   89
% identity
                  DNA REPAIR PROTEIN RECA PRECURSOR >gi_289208 (L15229) DNA
NCBI Description
                   repair protein [Arabidopsis thaliana] >gi 3152570
                   (AC002986) Match to nuclear-encoded chloroplast DNA repair
                  protein (E. coli recA homolog) gb L15229. [Arabidopsis
                   thaliana]
                   117741
Seq. No.
                  919_1.R1010
Contig ID
                  jC-atXLIB327406P4a07b2
5'-most EST
Method
                   BLASTX
                   q2129717
NCBI GI
BLAST score
                   902
E value
                   3.0e-97
                   303
Match length
% identity
                   61
NCBI Description
                  ribonucleoprotein - Arabidopsis thaliana >gi 166844
                   (M98340) ribonucleoprotein [Arabidopsis thaliana]
                   >gi 1582992 prf 2119375A Ser/Arg-rich protein [Arabidopsis
                   thaliana]
Seq. No.
                   117742
Contig ID
                   920 1.R1010
5'-most EST
                   PLN q166845
Method
                   BLASTX
NCBI GI
                   g282881
BLAST score
                  4213
                   0.0e + 00
E value
                   819
Match length
% identity
                   97
NCBI Description
                  receptor-like protein kinase precursor - Arabidopsis
                   thaliana >gi 166846 (M84658) receptor-like protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   117743
Contig ID
                   921 1.R1010
5'-most EST
                   PLN g166847
Method
                   BLASTX
NCBI GI
                   g282882
BLAST score
                  3873
                   0.0e + 00
E value
                  783
Match length
% identity
                   93
NCBI Description
                  receptor-like protein kinase precursor - Arabidopsis
                   thaliana >gi 166848 (M84659) receptor-like protein kinase
                   [Arabidopsis thaliana]
```

Seq. No.

```
922 1.R1010
Contig ID
5'-most EST
                  LIB25-108-Q1-E1-D5
                  BLASTN
Method
                  g4220510
NCBI GI
                  231
BLAST score
                  1.0e-127
E value
                  437
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
NCBI Description
                  (ESSAII project)
                  117745
Seq. No.
Contig ID
                  922 4.R1010
5'-most EST
                  jC-atX35004Q1E1G03a1
                  BLASTN
Method
                  g2842474
NCBI GI
                  158
BLAST score
                  1.0e-83
E value
Match length
                  162
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                  (ESSAII project)
                  117746
Seq. No.
                  924 2.R1010
Contig ID
5'-most EST
                  LIB25-103-Q1-E1-B1
                  BLASTX
Method
                  q585917
NCBI GI
BLAST score
                  731
E value
                  1.0e-77
                  141
Match length
                  99
% identity
                  DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (RNA
NCBI Description
                  POLYMERASE II SUBUNIT 5) >gi_322592_pir__A44457
                  DNA-directed RNA polymerase (EC 2.7.7.6) II fifth largest
                  chain - Arabidopsis thaliana >gi_166854 (M90505) RNA
                  polymerase II [Arabidopsis thaliana]
                  117747
Seq. No.
                  925 1.R1010
Contig ID
5'-most EST
                  LIB25-026-Q1-E1-H11
Method
                  BLASTX
                  q1173104
NCBI GI
BLAST score
                  1368
                  1.0e-152
E value
Match length
                  259
                  95
% identity
                  RIBONUCLEASE 2 PRECURSOR >gi 289210 (M98336) ribonuclease
NCBI Description
                  [Arabidopsis thaliana] >gi 2642160 (AC003000) ribonuclease,
                  RNS2 [Arabidopsis thaliana]
                  117748
Seq. No.
                  925 3.R1010
Contig ID
                  g957919
5'-most EST
                  BLASTX
Method
                  g1173104
NCBI GI
BLAST score
```

```
E value
                  9.0e-54
Match length
                  120
% identity
                  RIBONUCLEASE 2 PRECURSOR >gi 289210 (M98336) ribonuclease
NCBI Description
                  [Arabidopsis thaliana] >gi 2642160 (AC003000) ribonuclease,
                  RNS2 [Arabidopsis thaliana]
                  117749
Seq. No.
                  926_1.R1010
Contig ID
                  jC-\overline{a}tXLIB327428P4g09b2
5'-most EST
Method
                  BLASTX
                  g461903
NCBI GI
BLAST score
                  844
                  1.0e-90
E value
                  172
Match length
                  93
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_405129
                   (L14844) cyclophilin [Arabidopsis thaliana]
                  >gi 4490326_emb_CAB38608.1_ (AL035656) peptidylprolyl
                  isomerase ROC1 [Arabidopsis thaliana]
                  117750
Seq. No.
Contig ID
                  927 1.R1010
                  jC-atXLIB327404P2h03b1
5'-most EST
                  BLASTX
Method
                  g461899
NCBI GI
                   1240
BLAST score
E value
                   1.0e-137
                  255
Match length
                   95
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING
                   PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase
                   (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131
                   (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278
                   (U42724) cyclophilin [Arabidopsis thaliana]
                   117751
Seq. No.
Contig ID
                   927 2.R1010
5'-most EST
                   jC-atXLIB327420P1a06a1
                   BLASTN
Method
NCBI GI
                   g405130
BLAST score
                   132
E value
                   1.0e-67
Match length
                  228
                   93
% identity
                  Arabidopsis thaliana nuclear-encoded chloroplast stromal
NCBI Description
                   cyclophilin (ROC4) mRNA, complete cds
Seq. No.
                   117752
Contig ID
                   928 1.R1010
                   jC-atXLIB327420P3c03b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3201608
BLAST score
                   447
```

0.0e + 00

E value

```
Match length
                  859
                  96
% identity
                  Arabidopsis thaliana chromosome II BAC F7F1 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  117753
Seq. No.
Contig ID
                  928 2.R1010
5'-most EST
                  PLN q409183
Method
                  BLASTX
NCBI GI
                  g464720
BLAST score
                  251
E value
                  2.0e-21
Match length
                  50
                  100
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S28 >qi 409184 (L09755) ribosomal
                  protein S28 [Arabidopsis thaliana]
                  117754
Seq. No.
Contiq ID
                  929 1.R1010
                  q550281
5'-most EST
Method
                  BLASTX
                  q3617741
NCBI GI
BLAST score
                  1999
                  0.0e+00 ~
E value
                  389
Match length
% identity
NCBI Description (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis
                  thaliana]
                  117755
Seq. No.
Contiq ID
                  929 3.R1010
5'-most EST
                  g1053309
                  BLASTX
Method
NCBI GI
                  q132939
BLAST score
                  447
                  1.0e-72
E value
Match length
                  200
                  78
% identity
                  60S RIBOSOMAL PROTEIN L3 >qi 81657 pir JQ0771 ribosomal
NCBI Description
                  protein L3 (ARP1) - Arabidopsis thaliana >gi 166858
                  (M32654) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                  117756
                  929 4.R1010
Contig ID
5'-most EST
                  LIB3177-072-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g3047082
BLAST score
                  465
E value
                  1.0e-53
Match length
                  114
% identity
NCBI Description
                  (AF058914) similar to Vigna radiata pectinacetylesterase
                  precursor (GB:X99348) [Arabidopsis thaliana]
                  117757
Seq. No.
                  931 1.R1010
Contig ID
```

LIB23-061-Q1-E1-D8

Contig ID

```
Method
                  BLASTX
NCBI GI
                  q416923
BLAST score
                  124
                  1.0e-162
E value
                  301
Match length
                  96
% identity
                  GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, ACIDIC ISOFORM PRECURSOR
NCBI Description
                  ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                  (BETA-1, 3-ENDOGLUCANASE) (PATHOGENESIS-RELATED PROTEIN 2)
                  (PR-2) (BETA-1,3-GLUCANASE 2) >gi 322558_pir__JQ1694
                  pathogenesis-related protein 2 precursor - Arabidopsis
                  thaliana >gi 166637 (M58462) beta-1,3-glucanase 2
                  [Arabidopsis thaliana] >gi 166863 (M90509)
                 beta-1,3-glucanase [Arabidopsis thaliana]
Seq. No.
                  117758
Contig ID
                  932 1.R1010
5'-most EST
                  PLN g166864
Method
                  BLASTX
NCBI GI
                  q135915
BLAST score
                  1238
E value
                  1.0e-137
                  239
Match length
% identity
                  95
NCBI Description
                  PATHOGENESIS-RELATED PROTEIN 5 PRECURSOR (PR-5)
                  >gi 322559_pir__JQ1695 pathogenesis-related protein 5
                  precursor - Arabidopsis thaliana >gi 166865 (M90510)
                  thaumatin-like protein [Arabidopsis thaliana] >gi_1448919
                  (L78079) thaumatin-like protein [Arabidopsis thaliana]
Seq. No.
                  117759
Contig ID
                  933 1.R1010
                  LIB3176-040-P1-K1-C6
5'-most EST
Method
                  BLASTX
                  q514322
NCBI GI
BLAST score
                  1888
                  0.0e + 00
E value
                  375-
Match length
                  97
% identity
NCBI Description
                  (L34772) RNA polymerase subunit [Arabidopsis thaliana]
                  >gi 1586549 prf 2204246A RNA polymerase [Arabidopsis
                  thaliana]
                  117760
Seq. No.
                  934 1.R1010
Contig ID
5'-most EST
                  LIB25-001-Q1-E2-C10
Method
                  BLASTX
                  q166867
NCBI GI
BLAST score
                  848
                  4.0e-91
E value
                  180
Match length
% identity
                  92
NCBI Description
                  (J05216) ribosomal protein S11 (probable start codon at bp
                  67) [Arabidopsis thaliana]
Seq. No.
                  117761
```

934 2.R1010

```
5'-most EST
                   PLN g166868
                   BLASTX
Method
                   g1173221
NCBI GI
                   726
BLAST score
                   7.0e-77
E value
                   159
Match length
                   88
% identity
                   40S RIBOSOMAL PROTEIN S11-BETA >gi 166869 (L07877)
NCBI Description
                   ribosomal protein S11 [Arabidopsis thaliana]
                   117762
Seq. No.
                   934 3.R1010
Contig ID
5'-most EST
                   jC-atXP92CH4B5T7072d1
Method
                   BLASTX
                   g166867
NCBI GI
BLAST score
                   553
                   1.0e-56
E value
                   135
Match length
                   87
% identity
                   (J05216) ribosomal protein S11 (probable start codon at bp
NCBI Description
                   67) [Arabidopsis thaliana]
                   117763.
Seq. No.
                   937 1.R1010
Contig ID
                   jC-\overline{a}lXLIB327436P1b04b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2924792
BLAST score
                   1030
                   1.0e-112
E value
Match length
                   221
% identity
                   90
                   (AC002334) similar to synaptobrevin [Arabidopsis thaliana]
NCBI Description
                   117764
Seq. No.
                   937 2.R1010
Contig ID
5'-most EST
                   LIB22-069-Q1-E1-H9
                   BLASTX
Method
                   q4090884
NCBI GI
BLAST score
                   1027
E value
                   1.0e-112
Match length
                   219
% identity
                   91
NCBI Description
                   (AF025333) vesicle-associated membrane protein 7B;
                   synaptobrevin 7B [Arabidopsis thaliana]
                   117765
Seq. No.
                   937 3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327409P1d09b1
                   BLASTX
Method
NCBI GI
                   g2914706
BLAST score
                   477
E value
                   2.0e-94
Match length
                   199
% identity
                   (AC003974) putative homeobox protein [Arabidopsis thaliana]
NCBI Description
                   117766
Seq. No.
```

BLAST score

```
Contig ID
                   937 6.R1010
5'-most EST
                   q2048376
                   BLASTN
Method
NCBI GI
                   q600709
BLAST score
                   135
E value
                   2.0e-69
                   328
Match length
                   97
% identity
                   Arabidopsis thaliana synaptobrevin-related protein (SAR1)
NCBI Description
                   mRNA, complete cds
                   117767
Seq. No ...
                   940 1.R1010
Contig ID
                   LIB22-006-Q1-E1-H8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1705463
BLAST score
                   1758
E value
                   0.0e + 00
                   378
Match length
                   90
% identity
                   BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >qi 2129547 pir S71201
NCBI Description
                   biotin sythase - Arabidopsis thaliana >gi 10453\overline{16} (\overline{U2}4147)
                   biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806)
                   BIO2 protein [Arabidopsis thaliana] >gi 1\overline{7}69457 (L34413)
                   biotin synthase [Arabidopsis thaliana] >gi_2288983
                   (ACO02335) biotin synthase (Bio B) [Arabidopsis thaliana]
                   >gi_1589016_prf__2209438A biotin synthase [Arabidopsis
                   thaliana]
                   117768
Seq. No.
Contig ID
                   941 1.R1010
5'-most EST
                   PLN g166877
Method
                   BLASTX
NCBI GI
                   q166878
BLAST score
                   1779
E value
                   0.0e + 00
Match length
                   393
% identity
                   (M95796) St12p protein [Arabidopsis thaliana]
NCBI Description
                   117769
Seq. No.
                   941 2.R1010
Contig ID
5'-most EST
                   LIB3234-085-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   g3785976
BLAST score
                   49
                   2.0e-20
E value
Match length
                   92
% identity
                  (AC005560) Sec12p-like protein [Arabidopsis thaliana]
NCBI Description
                   117770
Seq. No.
                   942 1.R1010
Contig ID
                   LIB25-037-Q1-E1-A12
5'-most EST
Method
                   BLASTX
                   q1168529
NCBI GI
```

```
E value
                  0.0e + 00
                  363
Match length
% identity
                  90
                  SERINE/THREONINE-PROTEIN KINASE ASK1 >qi 541890 pir S36944
NCBI Description
                  probable serine/threonine-specific protein kinase (EC
                  2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi 166882
                  (M91548) serine/threonine kinase [Arabidopsis thaliana]
                  >gi 1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana]
                  117771
Seq. No.
                  944 1.R1010
Contig ID
5'-most EST
                  q934868
Method
                  BLASTX
NCBI GI
                  q2464881
BLAST score
                  1037
                  1.0e-113
E value
Match length
                  284
% identity
                  74
                  (Z99707) heat shock transcription factor HSF4 [Arabidopsis
NCBI Description
                  thaliana] >gi 3256070 emb CAA74398 (Y14069) Heat Shock
                  Factor 4 [Arabidopsis thaliana]
                  117772
Seq. No.
                  945 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327401P3c10b2
Method
                  BLASTX
                  g3024526
NCBI GI
BLAST score
                  1100
E value
                  1.0e-120
Match length
                  216
% identity
                  100
                  RAS-RELATED PROTEIN RAB11 >qi 2118459 pir S59942 small
NCBI Description
                  GTP-binding protein Rabl1 - Arabidopsis thaliana >qi 451860
                  (L18883) small GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                  117773
                  949 1.R1010
Contig ID
5'-most EST
                  PLN g1495250
Method
                  BLASTX
NCBI GI
                  q1495251
                  3909
BLAST score
E value
                  0.0e + 00
Match length
                  831
% identity
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                  117774
Seq. No.
Contig ID
                  949 3.R1010
                  jC-atXLIB327415P3e01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1495251
BLAST score
                  482
E value
                  2.0e-48
Match length
                  99
% identity
                  94
NCBI Description (270314) heat-shock protein [Arabidopsis thaliana]
```

E value

0.0e+00

```
117775
Seq. No.
Contig ID
                  949 5.R1010
5'-most EST
                  g1328091
Method
                  BLASTN
                  q1495250
NCBI GI
                  154
BLAST score
                  5.0e-81
E value
                  338
Match length
                  90
% identity
                  A.thaliana mRNA for heat-shock protein
NCBI Description
                  117776
Seq. No.
                  949 6.R1010
Contig ID
5'-most EST
                  jC-atXP65C208K19T7095d1
Method
                  BLASTX
                  q1495251
NCBI GI
                  814
BLAST score
                  7.0e-87
E value
                  211
Match length
% identity
                  79
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117777
                  950_1.R1010
Contig ID
5'-most EST
                  PLN g899121
Method
                  BLASTX
NCBI GI
                  g2501101
BLAST score
                  1013
                  1.0e-110
E value
                  260
Match length
% identity
                  82
                  SYNTAXIN HOMOLOG (PEP12 HOMOLOG) >gi 899122 (L41651)
NCBI Description
                  syntaxin [Arabidopsis thaliana]
                  117778
Seq. No.
Contig ID
                  952 1.R1010
5'-most EST
                  LIB25-109-Q1-E1-D5
                  BLASTX
Method
NCBI GI
                  g135535
BLAST score
                  2684
                  0.0e + 00
E value
Match length
                  545
                  100
% identity
                  T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
NCBI Description
                  (CCT-ALPHA) >gi 322602 pir JN0448 t-complex polypeptide
                  Tcp-1 - Arabidopsis thaliana >gi 217871 dbj BAA01955
                  (D11351) t-complex polypeptide 1 homologue [Arabidopsis
                  thaliana] >gi 2326265_dbj_BAA21772_ (D11352) CCT
                  alpha/TCP-1 [Arabidopsis thaliana]
                  117779
Seq. No.
Contig ID
                  953 1.R1010
5'-most EST
                  jC-atXP92CH4A9T7024d1
Method
                  BLASTX
                  g1076385
NCBI GI
BLAST score
                  3115
```

```
Match length
                  688
                  89
% identity
                  protein kinase (EC 2.7.1.37) tousled - Arabidopsis thaliana
NCBI Description
                  >gi 433052 (L23985) protein kinase [Arabidopsis thaliana]
                  117780
Seq. No.
Contig ID
                  954 1.R1010
                  LIB3168-018-P1-K1-B5
5'-most EST
                  BLASTX
Method
                  g2129753
NCBI GI
BLAST score
                  2677
                  0.0e + 00
E value
Match length
                  525
% identity
                  98
                  threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
NCBI Description
                  thaliana (fragment) >gi 1448917 (L41666) threonine synthase
                  [Arabidopsis thaliana]
                  117781
Seq. No.
Contig ID
                  955 1.R1010
                  PLN g536824
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1729980
BLAST score
                  1230
E value
                  1.0e-136
Match length
                  239
% identity
                  93
NCBI Description
                  THAUMATIN-LIKE PROTEIN PRECURSOR >gi 2129751 pir S71175
                  thaumatin-like protein - Arabidopsis thaliana >gi 536825
                  (L34693) thaumatin-like protein [Arabidopsis thaliana]
                  >gi 1094863 prf 2106421A thaumatin-like protein
                  [Arabidopsis thaliana]
                  117782
Seq. No.
Contig ID
                  956 1.R1010
5'-most EST
                  jC-alXLIB327436P1c03b1
Method
                  BLASTX
NCBI GI
                  g535780
BLAST score
                  1476
E value
                  1.0e-164
Match length
                  281
% identity
NCBI Description
                  (D26609) transmembrane protein [Arabidopsis thaliana]
                  117783
Seq. No.
                  956 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327416P3d05b1
Method
                  BLASTX
                  q535780
NCBI GI
BLAST score
                  418
                  6.0e-41
E value
Match length
                  114
% identity
                  77
                  (D26609) transmembrane protein [Arabidopsis thaliana]
NCBI Description
                  117784
Seq. No.
```

956 4.R1010

Contig ID

```
jC-atX35002Q1E1E04b1
5'-most EST
                  BLASTX
Method
                  q2252825
NCBI GI
BLAST score
                  256
E value
                  6.0e-22 ·
Match length
                  64
% identity
                  (AF013293) Similar to transmembrane protein; coded for by
NCBI Description
                  A. thaliana cDNA H37637; coded for by A. thaliana cDNA
                  T41850; coded for by A. thaliana cDNA T13717; coded for by
                  A. thaliana cDNA T04371; coded for by A. thaliana cDNA
                  T43789; coded
                  117785
Seq. No.
                  958 1.R1010
Contig ID
                  PLN_g349212
5'-most EST
                  BLASTX
Method
NCBI GI
                  q464987
                  799
BLAST score
                  2.0e-85
E value
Match length
                  148
% identity
                  100
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                  >gi 421858 pir S32672 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC10 - Arabidopsis thaliana
                  >gi 297878 emb CAA78715 (Z14991) ubiquitin conjugating
                  enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin
                  conjugating enzyme [Arabidopsis thaliana]
                  117786
Seq. No.
                  958 2.R1010
Contig ID
5'-most EST
                  jC-atXP79CF4H3T7b1
                  BLASTX
Method
                  a464987
NCBI GI
BLAST score
                  755
                  3.0e-80
E value
Match length
                  141
                  98
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                  >gi 421858_pir__S32672 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC10 - Arabidopsis thaliana
                  >gi 297878_emb_CAA78715 (Z14991) ubiquitin conjugating
                  enzyme [Arabidopsis thaliana] >gi 349213 (L00640) ubiquitin
                  conjugating enzyme [Arabidopsis thaliana]
                  117787
Seq. No.
Contig ID
                  958 3.R1010
                  LIB3177-041-P1-K2-A3
5'-most EST
                  BLASTX
Method
                  g464986
NCBI GI
BLAST score
                  801
E value
                  1.0e-85
Match length
                  148
% identity
                  100
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
```

Seq. No. Contig ID

Method

NCBI GI BLAST score

E value Match length

Seq. No.

NCBI GI BLAST score

E value

Seq. No.

Method NCBI GI

E value

Contig ID 5'-most EST .

BLAST score

Match length

NCBI Description

66

% identity

Contig ID

5'-most EST Method

Match length

% identity

% identity

5'-most EST

```
LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                  enzyme E2 [Arabidopsis thaliana]
                  >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                  ligase UBC9 [Arabidopsis thaliana]
                  117788
                  958 5.R1010
                  jC-alX35030Q1E1C01b1
                  BLASTX
                  q464987
                  391
                  1.0e-56
                  118
                  100
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                  >gi 421858 pir S32672 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC10 - Arabidopsis thaliana
                  >gi 297878 emb CAA78715 (Z14991) ubiquitin conjugating
                  enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin
                  conjugating enzyme [Arabidopsis thaliana]
                  117789
                  958 6.R1010
                  q27\overline{3}3346
                  BLASTX
                  g464987
                  70
                  3.0e-40
                  93
                  94
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                  >gi 421858 pir S32672 ubiquitin--protein ligase (EC
                  6.3.2.19) \overline{UBC10} - Arabidopsis thaliana
                  >gi 297878 emb CAA78715 (Z14991) ubiquitin conjugating
                  enzyme [Arabidopsis thaliana] >qi 349213 (L00640) ubiquitin
                  conjugating enzyme [Arabidopsis thaliana]
                  117790
                  958 9.R1010
                  ARABLI-06-Q1-B1-F9
                  BLASTX
                  g464986
                  412
                  3.0e-40
                  115
```

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

Seq. No. Contig ID

NCBI GI

E value

Seq. No.

Method

NCBI GI BLAST score

E value

Seq. No.

NCBI GI

E value

Seq. No. Contig ID

NCBI GI

5'-most EST Method

BLAST score

BLASTX q3789942

591

·Contig ID

5'-most EST Method

BLAST score

Match length % identity

Match length

% identity

Contig ID 5'-most EST

5'-most EST Method

BLAST score

Match length

% identity

```
>gi 297884 emb CAA78714 (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >qi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                  enzyme E2 [Arabidopsis thaliana]
                  >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                  ligase UBC9 [Arabidopsis thaliana]
                  117791
                  958 11.R1010
                  LIB25-015-Q1-E1-H7
                  BLASTX
                  g464987
                  296
                  1.0e-33
                  85
                  78
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                  >qi 421858 pir S32672 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC10 - Arabidopsis thaliana
                  >qi 297878 emb CAA78715 (Z14991) ubiquitin conjugating
                  enzyme [Arabidopsis thaliana] >qi 349213 (L00640) ubiquitin
                  conjugating enzyme [Arabidopsis thaliana]
                  117792
                  960 1.R1010
                  q937337
                  BLASTX
                  q2668744
                  766
                  1.0e-81
                  148
                  94
                  (AF034946) ubiquitin conjugating enzyme [Zea mays]
NCBI Description
                  117793
                  961 1.R1010
                  jC-atXLIB327412P3f03b1
                  BLASTX
                  q170352
                  2280
                  0.0e + 00
                  457
                  (M74101) hexameric polyubiquitin [Nicotiana sylvestris]
NCBI Description
                  >gi 870792 (L05361) polyubiquitin [Arabidopsis thaliana]
                  >gi 4115333 (L81139) ubiquitin [Pisum sativum] >gi 4115335
                  (L81140) ubiquitin [Pisum sativum]
                  117794
                  961 2.R1010
                  jC-atXP71C222O20T7077d1
```

6.3.2.19) UBC9 - Arabidopsis thaliana

```
E value
                   4.0e-61
Match length
                  144
                  17
% identity
NCBI Description
                  (AF093505) polyubiquitin [Saccharum hybrid cultivar
                  H32-8560]
                   117795
Seq. No.
                  961_3.R1010
Contig ID
                   jC-atXP85CG7F8T7b1
5'-most EST
                  BLASTX
Method
                   q170352
NCBI GI
BLAST score
                   1137
E value
                   1.0e-125
                   229
Match length
                   25
% identity
                   (M74101) hexameric polyubiquitin [Nicotiana sylvestris]
NCBI Description
                  >gi_870792 (L05361) polyubiquitin [Arabidopsis thaliana]
                  >gi 4115333 (L81139) ubiquitin [Pisum sativum] >gi 4115335
                   (L81140) ubiquitin [Pisum sativum]
                   117796
Seq. No.
                  961 4.R1010
Contig ID
5'-most EST
                   jC-atXLIB327423P3e11b1
Method
                  BLASTX
                  g870794
NCBI GI
                   391
BLAST score
                   1.0e-75
E value
                  578
Match length
                  13
% identity
                  (L05917) polyubiquitin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117797
                  961 6.R1010
Contig ID
5'-most EST
                  LIB3168-024-P1-K1-B3
Method
                   BLASTX
                  g421929
NCBI GI
BLAST score
                   403
                   2.0e-46
E value
Match length
                   136
% identity
                   12
                  ubiquitin - tomato >gi 312160 emb CAA51679 (X73156)
NCBI Description
                  ubiquitin [Lycopersicon esculentum]
                   117798
Seq. No.
Contig ID
                  961 8.R1010
5'-most EST
                   g1216567
Method
                   BLASTX
                   g170352
NCBI GI
BLAST score
                   427
E value
                   2.0e-57
Match length
                   147
% identity
                   15
                   (M74101) hexameric polyubiquitin [Nicotiana sylvestris]
NCBI Description
                   >gi_8,70792 (L05361) polyubiquitin [Arabidopsis thaliana]
                   >gi 4115333 (L81139) ubiquitin [Pisum sativum] >gi 4115335
```

(L81140) ubiquitin [Pisum sativum]

```
Seq. No.
                  117799
Contig ID
                  961 9.R1010
5'-most EST
                  g1158339
                  BLASTX
Method
NCBI GI
                  g82426
BLAST score
                  437
E value
                  2.0e-43
                  92
Match length
                  44
% identity
                  ubiquitin precursor - barley (fragment)
NCBI Description
                  >gi 755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor
                  (171 aa) [Hordeum vulgare]
                  117800
Seq. No.
                  963_1.R1010
Contig ID
                  PLN_g166925
5'-most EST
Method
                  BLASTX
                  g1169198
NCBI GI
BLAST score
                  316
                  1.0e-125
E value
Match length
                  270
                  87
% identity
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR
                  >gi 479738 pir S35270 hypothetical protein - Arabidopsis
                  thaliana >gi_166926 (L11367) [Arabidopsis thaliana
                  unidentified mRNA sequence, complete cds.], gene product
                  [Arabidopsis thaliana]
                  117801
Seq. No.
                  964 1.R1010
Contig ID
5'-most EST
                  LIB3176-008-P1-K2-A1
Method
                  BLASTX
                  g1169199
NCBI GI
BLAST score
                  1150
E value
                  1.0e-126
                  216
Match length
% identity
                  100
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT102
                  >gi 479739 pir S35271 hypothetical protein - Arabidopsis
                  thaliana >gi_166928 (L11368) [Arabidopsis thaliana
                  unidentified mRNA sequence, complete cds.], gene product
                  [Arabidopsis thaliana]
                  117802
Seq. No.
Contig ID
                  965_1.R1010
5'-most EST
                  PLN_g498706
                  BLASTX
Method
NCBI GI
                  g498707
BLAST score
                  2223
E value
                  0.0e + 00
Match length
                  468
                  93
% identity
```

Seq. No. 117803 Contig ID 969 1.R1010

NCBI Description

5'-most EST jC-atXP69C219E3T7061d1

(X78422) HYP1 [Arabidopsis thaliana]

```
BLASTX
Method
NCBI GI
                  g1362017
BLAST score
                  373
                  3.0e - 35
E value
                  261
Match length
                  50
% identity
                  zinc finger protein 4 - Arabidopsis thaliana >gi 790679
NCBI Description
                   (L39647) zinc finger protein [Arabidopsis thaliana]
                  117804
Seq. No.
                  970 1.R1010
Contig ID
                  LIB23-032-Q1-E1-G7
5'-most EST
                  BLASTN
Method
NCBI GI
                  q4558521
BLAST score
                  812
                  0.0e + 00
E value
                  812
Match length
                  100
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T10024,
NCBI Description
                  complete sequence
                  117805
Seq. No.
                   971 1.R1010
Contig ID
5'-most EST
                  g502120
Method
                  BLASTX
NCBI GI
                  g1362019
BLAST score
                   719
E value
                   6.0e-76
                   197
Match length
                   74
% identity
                   zinc finger protein 6 - Arabidopsis thaliana >gi_790683
NCBI Description
                   (L39649) zinc finger protein [Arabidopsis thaliana]
                   117806
Seq. No.
                   973 1.R1010
Contig ID
                   jC-atXP41C163F20T7d1
5'-most EST
Method
                   BLASTX
                   g790687
NCBI GI
                  1067
BLAST score
E value
                   1.0e-116
                   239
Match length
% identity
                   (L39651) zinc finger protein [Arabidopsis thaliana]
NCBI Description
                   117807
Seq. No.
                   974 1.R1010
Contig ID
                   LIB3168-086-P1-K1-G11
5'-most EST
Method
                   BLASTX
                   g3660465
NCBI GI
BLAST score
                   1647
                   0.0e + 00
E value
Match length
                   319
% identity
                   100
                   (AJ001753) Inositol 1,3,4-Trisphosphate 5/6 kinase
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No.

```
975 1.R1010
Contig ID
                   jC-atXLIB327416P4g08b1
5'-most EST
Method
                   BLASTX
                   q1903021
NCBI GI
                   2029
BLAST score
                   0.0e + 00
E value
                   405
                                                                            .....
Match length
                   100
% identity
                   (Y10216) hypothetical 3-isopropylmalate dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
                   117809
Seq. No.
                   975 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327421P1e09b1
Method
                   BLASTX
NCBI GI
                   g4512615
BLAST score
                   336
                   1.0e-116
E value
Match length
                   232
% identity
                   92
                   (AC004793) Strong similarity to gb X59970 3-isopropylmalate
NCBI Description
                   dehydrogenase (IMDH) from Brassica napus. EST gb_F14478
                   comes from this gene. [Arabidopsis thaliana]
Seq. No.
                   117810
                   976_1.R1010
Contig ID
5'-most EST
                  LIB22-036-Q1-E1-H6
Method
                  BLASTX
                   g3122288
NCBI GI
BLAST score
                   2706
E value
                   0.0e + 00
                   595
Match length
% identity
                   91
                  IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT) (KAP
NCBI Description
                   ALPHA) >gi 1568635 (U69533) AtKAP alpha [Arabidopsis
                   thaliana]
                   117811
Seq. No.
                   977 1.R1010
Contig ID
5'-most EST
                  LIB3168-026-P1-K1-B4
                  BLASTX
Method
                   q2950210
NCBI GI
BLAST score
                   2761
                   0.0e + 00
E value
                   535
Match length
% identity
                   (Y14615) Importin alpha-like protein [Arabidopsis thaliana]
NCBI Description
                   117812
Seq. No.
                   977 4.R1010
Contig ID
5'-most EST
                  ARABLI-10-Q1-B1-G1
Method
                  BLASTX
                   g2950210
NCBI GI
                  90
BLAST score
                  1.1e-02
E value
                  129
Match length
% identity
                   30
```

BLAST score

```
(Y14615) Importin alpha-like protein [Arabidopsis thaliana]
NCBI Description
                   117813
Seq. No.
                   977_5.R1010
Contig ID
                   LIB3177-072-P1-K1-D5
5'-most EST
                   BLASTN
Method
                   g2244950
NCBI GI
BLAST score
                   179
                   5.0e-96
E value
                   316
Match length
                   99
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contiq
NCBI Description
                   fragment No
                   117814
Seq. No.
                   978 1.R1010
Contig ID
                   PLN_g2154716
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3122271
                   2533
BLAST score
                   0.0e+00
E value
                   531
Match length
                   95
% identity
                   IMPORTIN ALPHA-2 SUBUNIT (KARYOPHERIN ALPHA-2 SUBUNIT) (KAP
NCBI Description
                   ALPHA) >gi_2154717_emb_CAA70703_ (Y09511) Kap alpha protein
                   [Arabidopsis thaliana]
Seq. No.
                   117815
                   978 2.R1010
Contig ID
5'-most EST
                   jC-atXP83CG3D8T7069d1
Method
                   BLASTX
                   g2949588
NCBI GI
BLAST score
                   2562
                   0.0e + 00
E value
Match length
                   531
% identity
                   95
                   (Y15225) Importin alpha-like protein [Arabidopsis thaliana]
NCBI Description
                   117816
Seq. No.
                   978_5.R1010 ·
Contig ID
5'-most EST
                   LIB23-049-Q1-E1-C2
                   BLASTX
Method
                   g3122271
NCBI GI
BLAST score
                   732
                   1.0e-77
E value
Match length
                   202
                   42
% identity
                   IMPORTIN ALPHA-2 SUBUNIT (KARYOPHERIN ALPHA-2 SUBUNIT) (KAP
NCBI Description
                   ALPHA) >gi 2154717 emb CAA70703 (Y09511) Kap alpha protein
                   [Arabidopsis thaliana]
Seq. No.
                   117817
                   979 1.R1010
Contig ID
5'-most EST
                   g1159274
                   BLASTX
Method
                   g124868
NCBI GI
```

```
1.0e-148
E value
Match length
                  263
                  99
% identity
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                  PHOSPHO-HYDROLASE) (PPASE) >gi_81645_pir__S13379 inorganic
                  pyrophosphatase (EC 3.6.1.1) - Arabidopsis thaliana
                  >gi_16348_emb_CAA40764_ (X57545) inorganic pyrophosphatase
                   [Arabidopsis thaliana]
                  117818
Seq. No.
                  980 1.R1010
Contig ID
5'-most EST
                  LIB3176-073-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g2760172
BLAST score
                  649
                  0.0e + 00
E value
                  649
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUB3, complete sequence [Arabidopsis thaliana]
                  117819
Seq. No.
                  982 1.R1010
Contig ID
5'-most EST
                  j.C-atXLIB327423P4h11b1
Method
                  BLASTX
NCBI GI
                  g4454056
BLAST score
                  1041
                  1.0e-113
E value
                  228
Match length
% identity
                  93
                  (AJ000930) ClpP [Arabidopsis thaliana]
NCBI Description
                  117820
Seq. No.
Contig ID
                  983 1.R1010
5'-most EST
                  PLN_g3087736
Method
                  BLASTX
NCBI GI
                  g3087737
BLAST score
                  2987
E value
                  0.0e+00
Match length
                  617
% identity
                  96
                  (AJ001158) ABC1 protein [Arabidopsis thaliana]
NCBI Description
                  117821
Seq. No.
                  984 1.R1010
Contig ID
5'-most EST
                  PLN g4138854
Method
                  BLASTX
NCBI GI
                  g4138855
BLAST score
                  1566
                  1.0e-175
E value
Match length
                  345
% identity
                  87
                  (AF098072) IMMUTANS [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117822
                  985 1.R1010
Contig ID
```

LIB3234-086-Q1-K1-B12

```
Method
                  BLASTX
                  q2181184
NCBI GI
                  2124
BLAST score
                  0.0e + 00
E value
                  444
Match length
% identity
                  94
NCBI Description
                  (Y13577) JR3 protein [Arabidopsis thaliana]
                  117823
Seq. No.
                  987_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327405P1e07b2
Method
                  BLASTX
                  q480450
NCBI GI
                  2703
BLAST score
                  0.0e + 00
E value
Match length
                  564
                  95
% identity
NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
                  thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                  reductoisomerase [Arabidopsis thaliana]
                  117824
Seq. No.
Contig ID
                  987 4.R1010
5'-most EST
                  g3450279
Method
                  BLASTX
NCBI GI
                  q480450
                  106
BLAST score
                  2.0e-35
E value
Match length
                  91
                  92
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                  thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                  reductoisomerase [Arabidopsis thaliana]
                  117825
Seq. No.
                  987 6.R1010
Contig ID
5'-most EST
                  jC-atXLIB327438P2g10a1
Method
                  BLASTX
                  g480450 .
NCBI GI
BLAST score
                  423
                  2.0e-41
E value
                  105
Match length
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                  thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                  reductoisomerase [Arabidopsis thaliana]
                  117826
Seq. No.
                  989 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327438P2b12a1
Method
                  BLASTX
                  g2129628
NCBI GI
BLAST score
                  571
                  2.0e-61
E value
Match length
                  128
% identity
                  91
NCBI Description ketoconazole resistent protein - Arabidopsis thaliana
```

Method

```
>gi 928938 emb CAA61433 (X89036) ketoconazole resistent
                    protein [Arabidopsis thaliana]
                    117827
 Seq. No.
                    990 1.R1010
 Contig ID
 5'-most EST
                    PLN g1045041
                    BLASTX
 Method
 NCBI GI
                    g1346387
                    1630
 BLAST score
                    0.0e + 00
 E value
                    431
 Match length
 % identity
 NCBI Description
                    KNOTTED-LIKE HOMEOBOX PROTEIN 3 >gi_1045042_emb_CAA63130_
                    (X92392) KNAT3 homeobox protein [Arabidopsis thaliana]
                    >gi_4063731 (AC006259) KNAT3 homeodomain protein
                    [Arabidopsis thaliana]
                    117828
 Seq. No.
                    991 1.R1010
 Contig ID
 5'-most EST
                    PLN g1045043
                    BLASTX
 Method
                    g1346388
NCBI GI
 BLAST score
                    1744
                    0.0e + 00
 E value
 Match length
                    393
 % identity
                    86
                    KNOTTED-LIKE HOMEOBOX PROTEIN 4 >qi 1045044 emb CAA63131
 NCBI Description
                    (X92393) KNAT4 homeobox protein [Arabidopsis thaliana]
                    117829
 Seq. No.
                    991 3.R1010
 Contig ID
                    jC-atXLIB327406P4e02a2
 5'-most EST
 Method
                    BLASTN
                    g1045043
 NCBI GI
 BLAST score
                    166
                    3.0e-88
 E value
                    166
 Match length
                    100
 % identity
                    A.thaliana mRNA for KNAT4 homeobox protein
 NCBI Description
                    117830
 Seq. No.
                    992 1.R1010
 Contig ID
 5'-most EST
                    q2756966
 Method
                    BLASTX
                    g2506031
 NCBI GI
 BLAST score
                    1885
                    0.0e + 00
 E value
 Match length
                    357
                    100
 % identity
                    (D43962) homeodomein containing protein 1 [Arabidopsis
 NCBI Description
                    thaliana] >gi 3858938 emb CAA16585.1 (AL021636)
                    homeodomain containing protein 1 [Arabidopsis thaliana]
                    117831
 Seq. No.
                    994 1.R1010
 Contig ID
```

PLN g3395759

BLASTX

```
g2129630
NCBI GI
                  937
BLAST score
E value
                   1.0e-101
                   172
Match length
                   100
% identity
                  lamin - Arabidopsis thaliana >gi 1262754 emb CAA65750
NCBI Description
                   (X97023) lamin [Arabidopsis thaliana] >gi 3395760 (U77721)
                   unknown [Arabidopsis thaliana]
                   117832
Seq. No.
                   994 2.R1010
Contig ID
5'-most EST
                   g2414106
Method
                   BLASTX
NCBI GI
                   g2129630
BLAST score
                   545
                   9.0e-56
E value
                   161
Match length
                   70
% identity
                   lamin - Arabidopsis thaliana >gi 1262754 emb CAA65750
NCBI Description
                   (X97023) lamin [Arabidopsis thaliana] >gi 3395760 (U77721)
                   unknown [Arabidopsis thaliana]
                   117833
Seq. No.
Contig ID
                   995 1.R1010
5'-most EST
                  LIB3234-025-P1-K1-D4
Method
                  BLASTX
NCBI GI
                   q2129641
BLAST score
                  844
                   1.0e-90
E value
                   155
Match length
% identity
                   100
                  major latex protein type 1 - Arabidopsis thaliana
NCBI Description
                  >gi 1107493 emb CAA63026 (X91960) major latex protein
                   typel [Arabidopsis thaliana]
Seq. No.
                   117834
                   995 2.R1010
Contig ID
5'-most EST
                  LIB3168-061-P1-K1-F11
Method
                  BLASTX
NCBI GI
                   g2129641
BLAST score
                   651
E value
                   3.0e-68
Match length
                  133
                   91
% identity
NCBI Description
                  major latex protein type 1 - Arabidopsis thaliana
                  >gi 1107493 emb CAA63026 (X91960) major latex protein
                  typel [Arabidopsis thaliana]
                  117835
Seq. No.
                   996 1.R1010
Contig ID
5'-most EST
                  LIB3168-040-P1-K1-F6
Method
                  BLASTX
                  g2129642
NCBI GI
BLAST score
                  849
                  3.0e-91
E value
                  155
Match length
% identity
                  100
```

```
NCBI Description major latex protein type 3 - Arabidopsis thaliana
                   >gi 1107495 emb CAA63027 (X91961) major latex protein
                   type3 [Arabidopsis thaliana]
                   117836
 Seq. No.
                   996 2.R1010
 Contig ID
 5'-most EST
                   PLN g1592682
 Method
                   BLASTX
                   g1592683
 NCBI GI
 BLAST score
                   840
                   3.0e-90
 E value
                   155
 Match length
 % identity
                   100
                   (X91914) major latex homologue type2 [Arabidopsis thaliana]
 NCBI Description
                   117837
 Şeq. No.
                   997 1.R1010
 Contig ID
 5'-most EST
                   PLN_g3970651
 Method
                   BLASTX
                   g3970652
 NCBI GI
 BLAST score
                   2384
                   0.0e + 00
 E value
                   476
 Match length
                   96
 % identity
                   (X77499) amino acid permease [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   117838
                   998 1.R1010
 Contig ID
                   jC-atXLIB327420P3e11b1
 5'-most EST
 Method
                   BLASTX
                   q1076290
 NCBI GI
                   2427
 BLAST score
                   0.0e+00
 E value
                   466
 Match length
 % identity
                   100
                   amino acid transporter AAP4 - Arabidopsis thaliana
 NCBI Description
                   >gi_608671_emb_CAA54631_ (X77500) amino acid transporter
                   [Arabidopsis thaliana]
                   117839
 Seq. No.
 Contig ID
                   999 1.R1010
 5'-most EST
                   LIB22-079-Q1-E1-G1
 Method
                   BLASTX
 NCBI GI
                   g1076289
 BLAST score
                   2258
                   0.0e + 00
E value
 Match length
                   480
                   90
 % identity
                   amino acid permease AAP5 - Arabidopsis thaliana
 NCBI Description
                   >gi_608673_emb_CAA54632_ (X77501) amino acid permease
                   [Arabidopsis thaliana]
                   117840
 Seq. No.
                 · 1001_1.R1010
 Contig ID
 5'-most EST
                   jC-atXP88C244I18T7d1
 Method
                   BLASTX
                   g1592675
 NCBI GI
```

```
BLAST score
                   735
                   6.0e-78
E value
                   169
Match length
                   87
% identity
                  (X91919) LEA76 homologue typel [Arabidopsis thaliana]
NCBI Description
                   117841
Seq. No.
Contig ID
                  1002 1.R1010
5'-most EST
                  LIB3234-046-P1-K1-B2
                  BLASTX
Method
NCBI GI
                   g1592677
BLAST score
                   692
E value
                   9.0e-73
Match length
                   225
% identity
                   64
NCBI Description
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
                  117842
Seq. No.
Contiq ID
                  1003 1.R1010
5'-most EST
                   LIB3234-076-P1-K1-D7
                   BLASTX
Method
NCBI GI
                   g1592679
BLAST score
                   421
                  5.0e-41
E value
Match length
                  134
% identity
                   66
NCBI Description
                   (X91915) LEA D113 homologue typel [Arabidopsis thaliana]
                  117843
Seq. No.
                   1004 1.R1010
Contig ID
5'-most EST
                  LIB3177-096-P1-K1-F9
Method
                  BLASTX
                   g1592681
NCBI GI
BLAST score
                   499
E value
                   2.0e-50
Match length
                   97
% identity
                  100
                  (X91917) LEA D113 homologue type2 [Arabidopsis thaliana]
NCBI Description
                  >gi 3668076 (AC004667) LEA D113 type2 protein [Arabidopsis
                   thaliana]
Seq. No.
                   117844
                   1005 1.R1010
Contig ID
5'-most EST
                   PLN = \frac{1}{9}
Method
                  BLASTX
NCBI GI
                   g2129632
BLAST score
                   996
                   1.0e-108
E value
Match length
                  262
% identity
                  80
NCBI Description
                  LEA D34 protein homolog type 1 - Arabidopsis thaliana
                  >gi 1113094 emb CAA63085 (X92115) LEA D34 protein
                  homologue type 1 [Arabidopsis thaliana]
                  117845
Seq. No.
Contig ID
                  1006 1.R1010
```

LIB146-017-Q1-E1-F5

```
BLASTX
Method
                   g2129633
NCBI GI
                   448
BLAST score
                   2.0e-44
E value
                   114
Match length
                   82
% identity
                   LEA protein Le25 homolog - Arabidopsis thaliana
NCBI Description
                   >gi 984050_emb CAA61676_ (X89505) LEA protein Le25 homolog
                   [Arabidopsis thaliana]
                   117846
Seq. No.
                   1007 1.R1010
Contig ID
5'-most EST
                   LIB2\overline{2}-074-Q1-E1-A12
Method
                   BLASTX
                   g1418331
NCBI GI
                   3034
BLAST score
                   0.0e + 00
E value
Match length
                   635
% identity
                   92
                   (X95909) receptor like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   117847
Seq. No.
                   1010 1.R1010
Contig ID
                   LIB35-020-Q1-E1-G9
5'-most EST
                   BLASTX
Method
                   g1169341
NCBI GI
                   707
BLAST score
                   1.0e-74
E value
Match length
                   193
                   70
% identity
                   DEHYDRIN XERO 2 (LOW-TEMPERATURE-INDUCED PROTEIN LTI30)
NCBI Description
                   >gi 2129571 pir S63689 dehydrin - Arabidopsis thaliana
                   >gi 633763 (U19536) dehydrin [Arabidopsis thaliana]
                   117848
Seq. No.
                   1013 1.R1010
Contig ID
5'-most -EST
                   jC-atXLIB327410P3h10b1
Method
                   BLASTX
                   q231536
NCBI GI
BLAST score
                   2538
E value
                   0.0e + 00
Match length
                   520
% identity
                   97
                   CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)
NCBI Description
                   (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL
                   AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase
                   (EC 3.4.11.1) - Arabidopsis thaliana
                   >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase
[Arabidopsis thaliana] >gi_4115380 (AC005967) putative
                   leucine aminopeptidase [Arabidopsis thaliana]
                   117849
Seq. No.
                   1018 1.R1010
Contig ID
                   PLN g2330563
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3914826
```

```
BLAST score
                   5049
                   0.0e+00
E value
Match length
                   978
                   98
% identity
                   DNA-DIRECTED RNA POLYMERASE CHLOROPLAST PRECURSOR
NCBI Description
                   >gi 2330560 emb CAA69972 (Y08722) chloroplast
                   single-subunit DNA-dependent RNA polymerase [Arabidopsis
                   thaliana] >gi_2330564_emb_CAA69717_ (Y08463) chloroplast
                   single-subunit DNA-dependent RNA polymerase [Arabidopsis
                   thaliana] >gi_4115372 (AC005967) chloroplast single subunit
                   DNA-dependent RNA polymerase [Arabidopsis thaliana]
                   117850
Seq. No.
Contig ID
                   1019 1.R1010
                   jC-atXLIB327431P2h04a1
 5'-most EST
                   BLASTX
Method
                   q3256066
NCBI GI
                   1732
BLAST score
                   0.0e + 00
E value
Match length
                   365
 % identity
                   95
                   (Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]
NCBI Description
                   117851
Seq. No.
Contig ID
                   1019 2.R1010
                   LIB22-055-Q1-E1-E5
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3256065
BLAST score
                   343
E value
                   0.0e + 00
Match length
                   363
                   99
 % identity
                   Arabidopsis thaliana mRNA for chloroplast NAD-dependent
NCBI Description
                   malate dehydrogenase
 Seq. No.
                   117852
 Contig ID
                   1019 3.R1010
                   jC-atXLIB327431P2h04b1
 5'-most EST
Method
                   BLASTX
NCBI GI
                   g3256066
 BLAST score
                   289
 E value
                   9.0e-26
 Match length
                   75
 % identity
                   (Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]
 NCBI Description
                   117853
Seq. No.
 Contig ID
                   1020 1.R1010
                   LIB3177-087-P1-K1-D1
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   q629562
 BLAST score
                   2410
 E value
                   0.0e+00
 Match length
                   476
                   97
 % identity
                   sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis
 NCBI Description
                   thaliana >qi 2129743 pir S68024 sulfate
```

```
>gi 1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana]
                   >qi 1378028 (U40715) ATP sulfurylase precursor [Arabidopsis
                   thaliana] >gi 1575324 (U59737) ATP sulfurylase [Arabidopsis
                   thaliana]
                   117854
Seq. No.
                   1021 1.R1010
Contig ID
                   PLN \overline{g}456613
 5'-most EST
                   BLASTX
Method
                   g1170660
NCBI GI
BLAST score
                   1818
E value
                   0.0e + 00
Match length
                   378
 % identity
                   96
                   MEVALONATE KINASE (MK) >gi 541880_pir_ S42088 mevalonate
NCBI Description
                   kinase (EC 2.7.1.36) - Arabidopsis thaliana
                   >qi 456614 emb CAA54820 (X77793) mevalonate kinase
                   [Arabidopsis thaliana]
                   117855
 Seq. No.
 Contig ID
                   1022 1.R1010
 5'-most EST
                 .. jC-atXLIB327403P3c09b2
 Method
                   BLASTX
 NCBI GI
                   g3367638
 BLAST score
                   2275
 E value
                   0.0e + 00
 Match length
                   468
                    94
 % identity
                    (AJ000331) monogalactosyldiacylglycerol synthase
 NCBI Description
                    [Arabidopsis thaliana]
                   117856
 Seq. No.
                   1023 1.R1010
 Contig ID
 5'-most EST
                   PLN g1514441
 Method
                   BLASTX
 NCBI GI
                    g282964
 BLAST score
                    843
                    3.0e-90
 E value
 Match length
                    326
 % identity
                    62
                   transforming protein (myb) homolog (clone myb.Ph3) - garden
 NCBI Description
                   petunia >qi 20563 emb CAA78386 (Z13996) protein 1 [Petunia
                   x hybrida]
 Seq. No.
                    117857
 Contig ID
                    1025 1.R1010
 5'-most EST
                    PLN g2980640
 Method
                    BLASTX
 NCBI GI
                    g2980641
 BLAST score
                    7152
                    0.0e + 00
 E value
                    1514
 Match length
 % identity
                    93
                   (Y11250) multi resistance protein [Arabidopsis thaliana]
 NCBI Description
```

adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) - Arabidopsis thaliana >gi_487404_emb_CAA55799_ (X79210) sùlfate adenylyltransferase [Arabidopsis thaliana]

```
Seq. No.
                    117858
 Contig ID
                    1026 1.R1010
                    jC-atXLIB327403P3b11b2
 5'-most EST
                    BLASTX
 Method
                    g1491615
 NCBI GI
                    2383
 BLAST score
                    0.0e+00
 E value
 Match length
                    491
 % identity
                    (X99923) male sterility 2-like protein [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    117859
                    1027_1.R1010
 Contig ID
                    LIB24-004-Q1-E1-A5
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g1171027
 BLAST score
                    3025
 E value
                    0.0e + 00
 Match length
                    616
 % identity
                    MALE STERILITY PROTEIN 2 >gi 421835 pir S33804 gene MS2
 NCBI Description
                    protein - Arabidopsis thaliana >gi 396835 emb CAA52019
                    (X73652) male sterility 2 (MS2) protein [Arabidopsis
                    thaliana] >gi 448297 prf 1916413A male sterility 2 gene
                    [Arabidopsis thaliana]
 Seq. No.
                    117860
, Contig ID
                    1028 1.R1010
 5'-most EST
                    jC-atXLIB327432P3f10b1
 Method
                    BLASTX
                    q116464
 NCBI GI
 BLAST score
                    458
 E value
                    0.0e + 00
 Match length
                    469
 % identity
                    CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR
 NCBI Description
                    >gi 68230_pir__YKMUM citrate (si)-synthase (EC 4.1.3.7)
                    precursor, mitochondrial - Arabidopsis thaliana
                    >gi 2652924 emb CAA35570 (X17528) citrate synthetase
                    [Arabidopsis thaliana]
 Seq. No.
                    117861
 Contig ID
                    1031 1.R1010
 5'-most EST
                    LIB23-019-Q1-E1-D7
 Method
                    BLASTX
 NCBI GI
                    g3451392
 BLAST score
                    1568
 E value
                    1.0e-175
 Match length
                    306
 % identity
                    100
 NCBI Description
                    (AJ001264) mitochondrial uncoupling protein [Arabidopsis
                    thaliana].>gi 4127446 emb CAA77109 (Y18291) uncoupling
                    protein [Arabidopsis thaliana]
```

Seq. No.

BLAST score

```
Contig ID
                  1032 1.R1010
5'-most EST
                  jC-atXLIB327414P3g12b1
Method
                  BLASTX
                  g2129648
NCBI GI
                  1308
BLAST score
                  1.0e-145
E value
                  305
Match length
% identity
                  83
                  MYB-related protein 33,3K - Arabidopsis thaliana
NCBI Description
                  >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein
                  [Arabidopsis thaliana]
                  117863
Seq. No.
Contig ID
                  1033 1.R1010
5'-most EST
                  PLN g2832405
                  BLASTX
Method
                  q2129647
NCBI GI
BLAST score
                  1214
                  1.0e-134
E value
                  304
Match length
                  78
% identity
                  MYB-related protein 33,2K - Arabidopsis thaliana
NCBI Description
                  >gi_1263097_emb_CAA90810_ (Z54137) MYB-related protein
                  [Arabidopsis thaliana]
                  117864
Seq. No.
                  1034 1.R1010
Contig ID :
5'-most EST
                  PLN g1197189
                  BLASTX
Method
                  q2129650
NCBI GI
                  1087
BLAST score
                  1.0e-119
E value
                  213
Match length
                  95
% identity
                  myb-related transcription factor 24,7K - Arabidopsis
NCBI Description
                  thaliana >gi 1197190 emb CAA92280 (Z68157) myb-related
                  transcription factor [Arabidopsis thaliana]
                  117865
Seq. No.
Contig ID
                  1037 1.R1010
5'-most EST
                  PLN g499046
Method
                  BLASTX
NCBI GI
                  q2129653
BLAST score
                  7499
                  0.0e+00
E value
Match length
                  1515
% identity
                  myosin heavy chain MYA2 - Arabidopsis thaliana
NCBI Description
                  >gi 499047 emb CAA84066 (Z34293) myosin [Arabidopsis
                  thaliana]
Seq. No.
                  117866
Contig ID
                  1039 1.R1010
5'-most EST
                  LIB23-043-Q1-E1-H11
                  BLASTX
Method
                  q1076348
NCBI GI
```

```
0.0e + 00
E value
                  1520
Match length
% identity
                  myosin MYA1, class V - Arabidopsis thaliana
NCBI Description
                  >qi 433663 emb CAA82234 (Z28389) myosin [Arabidopsis
                  thaliana]
                  117867
Seq. No.
                  1041_1.R1010
Contig ID
                   jC-atXLIB327406P3b10b2
5'-most EST
                   BLASTX
Method
                   q2499327
NCBI GI
BLAST score
                   828
                   1.0e-88
E value
                   218
Match length
% identity
                  NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX:I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH
                   dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana
                   >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase
                   [Arabidopsis thaliana]
                   117868
Seq. No.
                   1041 3.R1010
Contig ID
                   jC-a\overline{t}XLIB327432P2d06b1
5'-most EST
                   BLASTN
Method
                   g643089
NCBI GI ·
                   240
BLAST score
                   1.0e-132
E value
Match length
                   329
                   95
% identity
NCBI Description A.thaliana mRNA for NADH:ubiquinone oxidoreductase (complex
                   117869
Seq. No.
                   1042 1.R1010
Contig ID
                   jC-atXP69C218L14T7050d1
5'-most EST
                   BLASTX
Method
                   g2765837
NCBI GI
BLAST score
                   433
                   2.0e-52
E value
                   145
Match length
                   78
% identity
                  (Z96936) NAP16kDa protein [Arabidopsis thaliana]
NCBI Description
                   117870
Seq. No.
                   1043 1.R1010
Contig ID
                   g937<del>5</del>90
5'-most EST
                   BLASTX
Method
                   g730129
NCBI GI
BLAST score
                   779
                   3.0e-83
E value
                   149
Match length
                   100
% identity
                   NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                   >gi_3169310 (AF017641) nucleoside diphosphate kinase type 1
```

[Arabidopsis thaliana]

```
117871
Seq. No.
 Contig ID
                    1043 2.R1010
 5'-most EST
                    g2747425
                   BLASTX
 Method
                    g322551
 NCBI GI
 BLAST score
                    468
                    1.0e-46
 E value
                    98
 Match length
                    93
 % identity
                   nucleoside-diphosphate kinase (EC 2.7.4.6) - Arabidopsis
 NCBI Description
                    thaliana >gi_16398 emb_CAA49173_ (X69376) nucleoside
                    diphosphate kinase [Arabidopsis thaliana]
                    117872
 Seq. No.
                    1044 1.R1010
 Contig ID
                   LIB22-004-Q1-E1-E7
 5'-most EST
 Method
                    BLASTX
                    g1389699
 NCBI GI
 BLAST score
                    1780
                    0.0e + 00
 E value
 Match length
                    346
                    97
 % identity
 NCBI Description
                   (U38845) nitrilase 1 [Arabidopsis thaliana]
 Seq. No.
                    117873
 Contig ID
                    1044 2.R1010
 5'-most EST
                    PLN g508732
 Method
                    BLASTX
 NCBI GI
                    g417383
 BLAST score
                    1737
 E value
                    0.0e + 00
 Match length
                    339
 % identity
                   NITRILASE 2 >gi 322548 pir S31969 nitrilase (EC 3.5.5.1) -
 NCBI Description
                   Arabidopsis thaliana >gi 22656 emb CAA48377 (X68305)
                   nitrilase II [Arabidopsis thaliana] >gi_508733 (U09958)
                   nitrilase [Arabidopsis thaliana]
 Seq. No.
                    117874
 Contig ID
                    1044 3.R1010
 5'-most EST
                    PLN g508734
 Method
                   BLASTX
 NCBI GI
                    q1171770
 BLAST score
                    1825
 E value
                    0.0e + 00
 Match length
                    346
 % identity
                   NITRILASE 3 >gi 508735 (U09959) nitrilase [Arabidopsis
 NCBI Description
                   thaliana]
 Seq. No.
                    117875
 Contig ID
                    1044 5.R1010
 5'-most EST
                    g2446080
 Method
                   BLASTX
 NCBI GI
                    g1171770
 BLAST score
                    62
```

BLAST score

```
E value
                  6.0e-16
Match length
                  61
% identity
                  79
                  NITRILASE 3 >gi 508735 (U09959) nitrilase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  117876
                  1044_7.R1010
Contig ID
                  jC-atX22089Q1E1F02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1171770
BLAST score
                  954
                  1.0e-103
E value
Match length
                  197
% identity
                  88
                  NITRILASE 3 >gi 508735 (U09959) nitrilase [Arabidopsis
NCBI Description
                  thaliana]
                  117877
Seq. No.
                  1046 1.R1010
Contig ID
5'-most EST
                  LIB3176-004-P1-K1-F6
                  BLASTX
Method
NCBI GI
                  g2677614
BLAST score
                  1419
E value
                  1.0e-158
Match length
                  279
                  100
% identity
NCBI Description (Y07625) NLM1 protein (NodLikeMip1) [Arabidopsis thaliana]
                  117878
Seq. No.
                  1047 1.R1010
Contig ID
5'-most EST
                  LIB24-134-Q1-E1-A8
                  BLASTX
Method
                  g3075395
NCBI GI
BLAST score
                  1611
                  1.0e-180
E value
Match length
                  309
                  100
% identity
NCBI Description (AC004484) nodulin-35 homologue [Arabidopsis thaliana]
                  117879
Seq. No.
                  1048 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327423P1h05b1
                  BLASTX
Method
NCBI GI
                  g1729444
BLAST score
                  2698
                  0.0e + 00
E value
Match length
                  512
% identity
                  100
NCBI Description (X99279) AKin11 [Arabidopsis thaliana]
                  117880
Seq. No.
Contig ID
                  1049 1.R1010
5'-most EST
                  LIB3176-073-P1-K1-C12
               BLASTX
Method
NCBI GI
                  g548355
```

NCBI GI

```
E value
                    0.0e + 00
Match length
                    431
                    100
% identity
                   NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__S35228 nitrate reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana
NCBI Description
                    >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase
                    [Arabidopsis thaliana] >gi 448286 prf 1916406A nitrate
                    reductase [Arabidopsis thaliana]
                    117881
Seq. No.
Contig ID
                    1049_2.R1010
5'-most EST
                    LIB35-045-Q1-E1-B2
                    BLASTX
Method
                    q548355
NCBI GI
BLAST score
                    375
                    5.0e-36
E value
Match length
                    73
% identity
                    97
NCBI Description
                   NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__S35228 nitrate
                    reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana
                    >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase
[Arabidopsis thaliana] >gi_448286_prf__1916406A nitrate
                    reductase [Arabidopsis thaliana]
Seq. No.
                    117882
Contig ID
                    1051_1.R1010
5'-most EST
                    jC-atXLIB327411P1a06b1
Method
                    BLASTX
NCBI GI
                    q3242062
BLAST score
                    2713
                    0.0e + 00
E value
Match length
                    530
% identity
                    98
NCBI Description
                    (Z97058) NRT2;1p [Arabidopsis thaliana] >gi_3608362
                    (AF019748) high-affinity nitrate transporter ACH1
                    [Arabidopsis thaliana] >gi_3747058 (AF093754)
                    trans-membrane nitrate transporter protein AtNRT2:1
                    [Arabidopsis thaliana]
                    117883
Seq. No.
                    1054_1.R1010
Contig ID
5'-most EST
                    jC-atXLIB327410P4g01b1
Method
                    BLASTX
NCBI GI
                    q1076422
BLAST score
                    1860
                    0.0e + 00
E value
Match length
                    358
% identity
                   transcription factor OBF4 - Arabidopsis thaliana
NCBI Description
                    >gi_414613_emb_CAA49524_ (X69899) ocs-element binding
                    factor 4 [Arabidopsis thaliana]
                    117884
Seq. No.
Contig ID .
                    1058 1.R1010
5'-most EST
                   LIB3168-043-P1-K1-A4
Method
                   BLASTX
```

g2129657

```
727
BLAST score
                   7.0e-77
E value
                   172
Match length
                   85
% identity
                   oleosin isoform - Arabidopsis thaliana
NCBI Description
                   >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
                  thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin
                   [Arabidopsis thaliana]
                   117885
Seq. No.
                   1058 2.R1010
Contig ID
                   jC-alXLIB327436P2f09b1
5'-most EST
                   BLASTX
Method
                   g4567303
NCBI GI
BLAST score
                   604
                   2.0e-62
E value
Match length
                   114
                   100
% identity
                   (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117886
                   1058 4.R1010
Contig ID
                   LIB3177-044-P1-K2-G5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2129657
BLAST score
                   540
E value
                   3.0e-55
Match length
                   155
                   73
% identity
NCBI Description
                   oleosin isoform - Arabidopsis thaliana
                   >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
                   thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin
                   [Arabidopsis thaliana]
                   117887
Seq. No.
                   1059 1.R1010
Contig ID
                   LIB3168-032-P1-K1-D10
5'-most EST
Method
                   BLASTX
                   g266693
NCBI GI
BLAST score
                   278
                   2.0e-24
E value
Match length
                   139
% identity
                   50
                   OLEOSIN >gi 282875 pir S22538 oleosin - Arabidopsis
NCBI Description
                   thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_
                   (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
Seq. No.
                   117888
                   1061 1.R1010
Contig ID
                   LIB3175-035-P1-K1-H4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1107501
BLAST score
                   366
E value
                   1.0e-34
Match length
                   91
```

% identity

% identity

NCBI Description

29

```
NCBI Description
                  (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
                  Match to gb X91954 orf gene product from A. thaliana. ESTs
                  gb Z17604, gb H76594, gb AA597972 and gb AA394824 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  117889
                  1061 2.R1010 ---
Contig ID
5'-most EST
                  jC-atXP60C19806T7032d1
                  BLASTN
Method
NCBI GI
                  q4027862
BLAST score
                  286
E value
                  1.0e-160
Match length
                  290
                  50
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T7A14 sequence,
                  complete sequence [Arabidopsis thaliana]
                  117890
Seq. No.
                  1061_3.R1010
Contig ID
                  q931\overline{9}86
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1107501
BLAST score
                  252
                  5.0e-44
E value
                  118
Match length
% identity
                  85
                   (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
NCBI Description
                  Match to gb X91954 orf gene product from A. thaliana. ESTs
                  gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from
                  this gene. [Arabidopsis thaliana]
                  117891
Seq. No.
                  1061_6.R1010
Contig ID
5'-most EST
                  LIB3234-047-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q2160133
BLAST score
                  287 -
E value
                  1.0e-25
Match length
                  98
% identity
                   (ACO00375) Strong similarity to Arabidopsis
NCBI Description
                  gb X91953, F19K23.3, F19K23.15. ESTs
                  gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this
                  gene. [Arabidopsis thaliana]
                  117892
Seq. No.
                  1061_7.R1010
g3449689
Contig ID
5'-most EST'
Method
                  BLASTN
NCBI GI
                  q2160132
BLAST score
                  208
E value
                  1.0e-113
Match length
                  397
```

1, complete sequence [Arabidopsis thaliana]

Sequence of BAC F19K23 from Arabidopsis thaliana chromosome

```
117893
Seq. No.
Contig ID
                   1062 1.R1010
                  LIB3234-090-P1-K1-G3
5'-most EST
Method
                  BLASTX
                   g1402876
NCBI GI
BLAST score
                   2799
E value
                   0.0e+00
Match length
                   582
                   95
% identity
                   (X98130) putative phosphate permease [Arabidopsis thaliana]
NCBI Description
                  >gi_1495255_emb_CAA66116_ (X97484) orf01 [Arabidopsis
                   thaliana]
                   117894
Seq. No.
Contig ID
                  1063 1.R1010
                  g2581733
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2995384
BLAST score
                  109
                  3.0e-84
E value
Match length
                  339
                   57
% identity
NCBI Description
                  (AJ004810) cytochrome P450 monooxygenase [Zea mays]
Seq. No.
                  117895
Contig ID
                  1063 2.R1010
5'-most EST
                   jC-atXP92C249B11T7091d1
                  BLASTX
Method
NCBI GI
                   q2062157
BLAST score
                   1095
E value
                   1.0e-120
Match length
                   209
                   31
% identity
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                   117896
Seq. No.
                  1063_3.R1010
Contig ID
5'-most EST
                  PLN g1495256
Method
                  BLASTX
NCBI GI
                   q1402877
                   1654
BLAST score
                   0.0e + 00
E value
Match length
                   350
% identity
                   (X98130) unknown [Arabidopsis thaliana]
NCBI Description
                  >gi_1495257_emb_CAA66117_ (X97485) orf03 [Arabidopsis
                   thaliana)
Seq. No.
                   117897
                  1063 4.R1010
Contig ID
5'-most EST
                  q244\overline{6}130
Method
                  BLASTX
                  q2995384
NCBI GI
BLAST score
                  226
E value
                  2.0e-18
Match length
                  119
```

```
% identity
NCBI Description
                    (AJ004810) cytochrome P450 monooxygenase [Zea mays]
                    117898
Seq. No.
                    1063 5.R1010
Contig ID
 5'-most EST
                    q244\overline{6}111
                    BLASTX
Method
NCBI GI
                    q2995384
BLAST score
                    276
E value
                    7.0e-27
Match length
                    123
% identity
                    67
                    (AJ004810) cytochrome P450 monooxygenase [Zea mays]
NCBI Description
                    117899
Seq. No.
                    1063 6.R1010
Contig ID
5'-most EST
                    LIB22-086-Q1-E1-F4
                    BLASTX
Method
NCBI GI
                    g2062157
BLAST score
                    1908
                    0.0e + 00
E value
Match length
                    438
% identity
                    42
                    (ACO01645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                    thaliana]
                    117900
Seq. No.
Contig ID
                    1063_8.R1010
                    q906\overline{5}22
5'-most EST
                    BLASTN
Method
                    g2244788
NCBI GI
BLAST score
                    262
E value
                    1.0e-145
Match length
                    266
% identity
                    100
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                    fragment No
                                                                             ٠,٠
Seq. No.
                    117901
                    1063 11.R1010
Contig ID
5'-most EST
                    LIB35-018-Q1-E1-D1
Method
                    BLASTX
NCBI GI
                    q4262232
BLAST score
                    1136
                    1.0e-125
E value
Match length.
                    242
                    93
% identity
NCBI Description
                    (AC006200) putative ribosomal protein L7 [Arabidopsis
                    thaliana]
                    117902
Seq. No.
                    1063 12.R1010
Contig ID
5'-most EST
                    jC-atXLIB327430P3b07b1
Method
                    BLASTX
NCBI GI
                    q4586109
BLAST score
                    936
E value
                    1.0e-101
```

BLAST score

50

```
175
Match length
% identity
                   99
                  (AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  117903
                  1063 13.R1010
Contig ID
5'-most EST
                  LIB3168-082-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g132863
BLAST score
                  716
E value
                  2.0e-75
Match length
                  141
% identity
                   95
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L2
NCBI Description
                  >gi 12214 emb CAA46568 (X65615) ribosomal protein L2
                   [Sinapis alba]
                  117904
Seq. No.
                  1063_14.R1010
Contig ID
5'-most EST
                  q1517289
                  BLASTN
Method
NCBI GI
                  q2687432
BLAST score
                  810
E value
                  0.0e + 00
Match length
                  971
                  96
% identity
NCBI Description
                  Plumbago auriculata large subunit 26S ribosomal RNA gene,
                  partial sequence
                  117905
Seq. No.
                  1063 16.R1010
Contig ID
5'-most EST
                  g1216825
Method
                  BLASTN
NCBI GI
                  q16472
BLAST score
                  593
E value
                  0.0e + 00
Match length
                  701
% identity
NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type
                  117906
Seq. No.
                  1063 17.R1010
Contig ID
5'-most EST
                  g2748357
Method
                  BLASTN
NCBI GI
                  g16473
BLAST score
                  451
                  0.0e+00
E value
Match length
                  557
% identity
                  95
NCBI Description Arabidopsis thaliana 25S-18S ribosomal DNA spacer
Seq. No.
                  117907
                  1063 20.R1010
Contig ID
5'-most EST
                  jC-atXLIB327427P2c05b1
Method
                  BLASTX
                  g4539447
NCBI GI
```

```
E value
                   2.0e-80
Match length
                   157
                   97
% identity
                   (AL049523) retrotransposon like protein [Arabidopsis
NCBI Description
                   thaliana]
                   117908
Seq. No.
Contig ID
                   1063 23.R1010
                   g2580786
5'-most EST
Method
                   BLASTN
NCBI GI
                   g16472
BLAST score
                   223
E value
                   1.0e-122
Match length
                   443
% identity
                   91
NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type
                   117909
Seq. No.
                   1063_24.R1010
Contig ID
                   g493347
5'-most EST
Method
                   BLASTX
NCBI GI
                   g132866
BLAST score
                   564
E value
                   2.0e-87
                 . 199
Match length
                   84
% identity
                   CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_71086_pir__R5NT2
NCBI Description
                   ribosomal protein L2 - common tobacco chloroplast
                   >gi_435269_emb_CAA77384_ (Z00044) ribosomal protein L2
[Nicotiana tabacum] >gi_1223691_emb_CAA77409_ (Z00044)
                   ribosomal protein L2 [Nicotiana tabacum]
                   >gi 225238 prf 1211235BW ribosomal protein L2 [Nicotiana
                   tabacum]
                   117910
Seq. No.
                   1063_30.R1010
Contig ID
5'-most EST
                   jC-atXLIB327426P4d10a1
Method
                   BLASTN
NCBI GI
                   q4586098
                   203
BLAST score
                   1.0e-110
E value
Match length
                   215
% identity
                   99
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
NCBI Description
                   (ESSA project)
                   117911
Seq. No.
Contig ID
                   1063_36.R1010
                   LIB25-111-Q1-E1-G9
5'-most EST
Method
                   BLASTN
                   a1877523
NCBI GI
BLAST score
                   208
                   1.0e-113
E value
Match length
                   391
% identity
NCBI Description
                   Arabidopsis thaliana BAC T7I23, complete sequence
                   [Arabidopsis thaliana]
```

```
Seq. No.
                   117912
                   1063 37.R1010
Contig ID
5'-most EST
                   jC-atX24067Q1E1C07b1
Method
                   BLASTX
                   g549741
NCBI GI
BLAST score
                   283
                   3.0e-25
E value
Match length
                   126
% identity
NCBI Description
                   PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT SDS22
                   >gi_539368_pir__S38030 suppressor protein SDS22 - yeast
                   (Saccharomyces cerevisiae) >gi_1042084_bbs_168782
                   Egp1=Sds22 homolog [Saccharomyces cerevisiae=baker's yeast,
                   NH102-2C-M5, Peptide, 338 aa] >gi_486343_emb_CAA82037_(Z28193) ORF YKL193c [Saccharomyces cerevisiae]
                   >gi 619516 emb CAA58588 (X83609) Sds22p [Saccharomyces
                   cerevisiae]
                   117913
Seq. No.
Contig ID
                   1063_38.R1010
5'-most EST
                   LIB35-028-Q1-E1-C12
Method
                   BLASTN
NCBI GI
                   q1877523
BLAST score
                   1.31
                   2.0e-67
E value
Match length
                   393
% identity
                   95
                   Arabidopsis thaliana BAC T7I23, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
                   117914
Seq. No.
Contig ID
                   1063 40.R1010
5'-most EST
                   LIB3175-046-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   q2132502
BLAST score
                   226
E value
                   3.0e-18
Match length
                   106
% identity
                   probable membrane protein YDR326c - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi 915002 (U32517) Ydr326cp [Saccharomyces
                   cerevisiae]
                   117915
Seq. No.
                   1065 1.R1010
Contig ID
5'-most EST
                   PLN_g1495258
Method
                   BLASTX
NCBI GI
                   q1402878
BLAST score
                   2404
E value
                   0.0e + 00
Match length
                   500
% identity
                   (X98130) unknown [Arabidopsis thaliana]
NCBI Description
                   117916
Seq. No.
```

1065_2.R1010

NCBI Description

```
5'-most EST
                   g1053531
                   BLASTX
Method
NCBI GI
                   q1402878
BLAST score
                   477
                   2.0e-47
E value
Match length
                   149
                   74
% identity
                   (X98130) unknown [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117917
Contig ID
                   1065 4.R1010
5'-most EST
                   jC-atXP66C210G13T7020a1
                   BLASTX
Method
NCBI GI
                   q1495259
BLAST score
                   356
E value
                   2.0e-33
Match length
                   137
% identity
                   43
                   (X97826) orf04 [Arabidopsis thaliana]
NCBI Description
                   117918
Seq. No.
Contig ID
                   1067_1.R1010
                   jC-atXLIB327409P1a08b1
5'-most EST
Method
                   BLASTX
                   q1402883
NCBI GI
                   1786
BLAST score
                   0.0e + 00
E value
Match length
                   434
% identity
                   96
NCBI Description
                   (X98130) unknown [Arabidopsis thaliana]
                   >gi 1495263 emb CAA66119 (X97487) orf09 [Arabidopsis
                   thaliana]
                   117919
Seq. No.
Contig ID
                   1068_1.R1010
                  LIB3234-087-Q1-K1-F6
5'-most EST
Method
                   BLASTX
                   q1402884
NCBI GI
BLAST score
                   1814
                   0.0e + 00
E value
                   346
Match length
                   100
% identity
NCBI Description
                   (X98130) unknown [Arabidopsis thaliana]
                  >gi 1495265 emb CAA66120 (X97488) beta-transducin like
                  protein [Arabidopsis thaliana]
                   117920
Seq. No.
Contig ID
                   1070_1.R1010
5'-most EST
                   PLN_g1495266
Method
                  BLASTX
NCBI GI
                  g1495267
BLAST score
                  2345
                  0.0e + 00
E value
Match length
                   484
% identity
                  (X97827) orf12 [Arabidopsis thaliana]
```

NCBI GI

```
Seq. No.
                   117921
                   1071 1.R1010
Contig ID
5'-most EST
                   jC-atXP79C230N13T7b1
                   BLASTX
Method
                   g1495269
NCBI GI
BLAST score
                   551
E value
                   3.0e-56
Match length
                   141
                   77
% identity
NCBI Description
                   (X97829) product similar to ccr protein, Citrus paradisi;
                   PIR: S52663 [Arabidopsis thaliana]
                   >gi 1550735 emb CAA66824 (X98130) unknown [Arabidopsis
                   thalianal
                   117922
Seq. No.
                   1071 2.R1010
Contig ID
5'-most EST
                   g2048089
                   BLASTN
Method
NCBI GI
                   q3449321
BLAST score
                   200
                   1.0e-108
E value
Match length
                   236
% identity
                   97
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTG10, complete sequence [Arabidopsis thaliana]
                   117923
Seq. No.
                   1071 3.R1010
Contig ID
                   jC-aTXP100C251014T7b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q112717
BLAST score
                   421
E value
                   6.0e-41
Match length
                   176
% identity
                   51
NCBI Description
                   21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi 82050 pir S10911
                   hypothetical protein precursor - carrot
                   >gi_18312_emb_CAA36642_ (X52395) precursor polypeptide (AA
                   -22 to 171) [Daucus carota]
                   117924
Seq. No.
                   1071 4.R1010
Contiq ID
5'-most EST
                   LIB3177-093-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q2275217
BLAST score
                   531
E value
                   4.0e-54
Match length
                   124
                   85
% identity
NCBI Description
                   (AC002337) chloroplast protein CP12 isolog [Arabidopsis
                   thaliana
                   117925
Seq. No.
Contig ID
                   1071 5.R1010
5'-most EST
                   jC-atXLIB327426P2g07b1
Method
                   BLASTN
```

g1495268

```
45
BLAST score
E value
                   8.0e-16
Match length
                   334
                   94
% identity
NCBI Description
                  A.thaliana mRNA (orf19) from chromosome III
                   117926
Seq. No.
                   1071_6.R1010
Contig ID
                   g2047402
5'-most EST
                   BLASTX
Method
                   q1495269
NCBI GI
BLAST score
                   403
                   7.0e-39
E value
Match length
                   145
% identity
                   61
NCBI Description
                   (X97829) product similar to ccr protein, Citrus paradisi;
                   PIR: S52663 [Arabidopsis thaliana]
                   >gi_1550735_emb_CAA66824_ (X98130) unknown [Arabidopsis
                   thaliana]
Seq. No.
                   117927
                   1071_7.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P4c10b1
Method
                   BLASTX
NCBI GI
                   q3212610
BLAST score
                   287
E value
                   1.0e-26
Match length
                   136
% identity
                   49
NCBI Description
                   Chain A, Sulfite Oxidase From Chicken Liver
                   >gi 3212611 pdb 1SOX B Chain B, Sulfite Oxidase From
                   Chicken Liver
Seq. No.
                   117928
                   1071 9.R1010
Contig ID
                   q105\overline{4}488
5'-most EST
Method
                   BLASTN
NCBI GI .
                   q1495268
BLAST score
                   124
E value
                   4.0e-63
Match length
                   270
% identity
                   98
NCBI Description A.thaliana mRNA (orf19) from chromosome III
                   117929
Seq. No.
                   1071_10.R1010
Contig ID
5'-most EST
                   q931\overline{2}73
Method
                   BLASTN
NCBI GI
                   q1402874
BLAST score
                   204
E value
                   1.0e-111
Match length
                   535
% identity
                   99
NCBI Description A.thaliana 81kb genomic sequence
Seq. No.
                   117930
```

1071_13.R1010

```
g2047596
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1871577
BLAST score
                   155
                   6.0e-10
E value
Match length
                   72
                   50
% identity
                   (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
                   117931
Seq. No.
Contig ID
                   1071 14.R1010
5'-most EST
                   ARABL1-05-Q1-B1-E5
                   BLASTX
Method
NCBI GI
                   a2275217
                   379
BLAST score'
                   3.0e-41
E value
Match length
                   112
% identity
                   83
                   (ACO02337) chloroplast protein CP12 isolog [Arabidopsis
NCBI Description
                   thaliana]
                   117932
Seq. No.
Contig ID
                   1072_1.R1010
                   jC-atXLIB327405P1f04b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1175011
BLAST score
                   1442
E value
                   1.0e-160
Match length
                   274
% identity
                   100
                   PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN
NCBI Description
                   A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665)
                   plasma membrane intrinsic protein 1B [Arabidopsis thaliana]
                   117933
Seq. No.
                   1072_2.R1010
Contig ID
                   LIB35-038-Q1-E1-E3
5'-most EST
Method
                   BLASTX
                   q1175010
NCBI GI
BLAST score
                   874
                   1.0e-153
E value
Match length
                   286
% identity
                   95
NCBI Description
                   PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082
                   plasma membrane intrinsic protein la - Arabidopsis thaliana
                   >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic
                   protein la [Arabidopsis thaliana]
Seq. No.
                   117934
                   1072 3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327416P1g09b1
Method
                   BLASTN
NCBI GI
                   q2264303
BLAST score
                   287
E value
                   1.0e-160
Match length
```

```
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBB18, complete sequence [Arabidopsis thaliana]
Seq. No.
                   117935
                   1072 4.R1010
Contig ID
                   LIB3176-118-P2-K1-G2
5'-most EST
Method
                   BLASTN
NCBI GI
                   q2351065
BLAST score
                   173
E value
                   3.0e-92
Match length
                   635
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MHF15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   117936
                   1072 6.R1010
Contig ID
                   jC-atXLIB327423P4e12b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1175010
BLAST score
                   180
E value
                   8.0e-13
                   39
Match length
                   90
% identity
                   PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi 629540 pir S44082
NCBI Description
                   plasma membrane intrinsic protein 1a - Arabidopsis thaliana
                   >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic
                   protein la [Arabidopsis thaliana]
                   117937
Seq. No.
                   1072_7.R1010
Contig ID
5'-most EST
                   jC-atXLIB327416P3f03b1
                   BLASTX
Method
NCBI GI
                   q1175010
BLAST score
                   580
E value
                   6.0e-60
Match length
                   123
% identity
                   92
                   PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi 629540 pir S44082
NCBI Description
                   plasma membrane intrinsic protein 1a - Arabidopsis thaliana
                   >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic
                   protein la [Arabidopsis thaliana]
                   117938
Seq. No.
                   1072 8.R1010
Contig ID
                   jC-atXLIB327418P4a05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1175011
BLAST score
                   322
E value
                   1.0e-29
Match length
                   126
                   59
% identity
NCBI Description
                   PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN
                   A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665)
```

plasma membrane intrinsic protein $\overline{1}B$ [Arabidopsis thaliana]

```
117939
Seq. No.
                    1072 9.R1010
Contig ID
                     jC-aTXLIB327421P2f03b1
5'-most EST
                     BLASTX
Method
                    g1199503
NCBI GI
                     431
BLAST score
                     2.0e-42
E value
Match length
                     117
                     79
% identity
                     (X95640) transmembrane channel protein [Brassica oleracea]
NCBI Description
                    117940
Seq. No.
                     1072 10.R1010
Contig ID
                    LIB22-006-Q1-E1-E5
5'-most EST
Method
                    BLASTX
                     g1175010
NCBI GI
BLAST score
                     245
                     1.0e-20
E value
Match length
                     62
% identity
                    79
                    PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi 629540 pir $44082
NCBI Description
                    plasma membrane intrinsic protein la - Arabidopsis Thaliana
                    >gi_472873_emb_CAA53475 (X75881) plasma membrane intrinsic protein la [Arabidopsis thaliana]
Seq. No.
                     117941
                     1072 11.R1010
Contig ID
5'-most EST
                     g2581623
Method
                     BLASTX
                     q2199574
NCBI GI
BLAST score
                     318
                     5.0e-29
E value
Match length
                     145
                     54
% identity
                     (AF004293) aquaporin [Brassica rapa]
NCBI Description
Seq. No.
                     117942
                     1072 12.R1010
Contig ID
                    LIB3176-021-P1-K1-A9
5'-most EST
                     BLASTX
Method
                     q1175011
NCBI GI
BLAST score
                     440
                     1.0e-100
E value
                     266
Match length
% identity
                     80
                    PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN
NCBI Description
                    A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]
Seq. No.
                     117943
                     1075 1.R1010
Contig ID
5'-most EST
                     PLN g2462076
                    BLASTX
Method
                     g2462077
NCBI GI
```

1997

BLAST score

```
E value
                  0.0e + 00
                  418
Match length
% identity
                  (Y.11871) Oxal protein [Arabidopsis thaliana]
NCBI Description
                  117944
Seq. No.
Contig ID
                  1076_1.R1010
                  PLN_{g}886427
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2498731
BLAST score
                  1790
E value
                  0.0e + 00
                  345
Match length
                  99
% identity
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                  >gi 1362013 pir S57611 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)
                  zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
                  117945
                  1076_2.R1010
Contig ID
5'-most EST
                  LIB3175-038-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q2498732
BLAST score
                  1759
                  0.0e + 00
E value
Match length
                  341
% identity
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2
NCBI Description
                  >gi 1362014 pir S57612 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi_886430_emb_CAA89262_ (Z49268)
                   zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
                  117946
Contig ID
                  1076_3.R1010
5'-most EST
                  LIB3176-102-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g2498731
BLAST score
                  157
                   2.0e-37
E value
Match length
                  101
                   73
% identity
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                  >gi_1362013_pir__S57611 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)
                   zeta-crystallin homologue [Arabidopsis thaliana]
                  117947
Seq. No.
                  1077 1.R1010
Contig ID
5'-most EST
                  g1216872
Method
                  BLASTX
                  q3004558
NCBI GI
BLAST score
                  1661
                  0.0e+00
E value
Match length
                   323
% identity
                  (AC003673) peroxidase ATP22a [Arabidopsis thaliana]
NCBI Description
```

NCBI GI

```
117948
Seq. No.
Contig ID
                   1078 1.R1010
5'-most EST
                   g671799
Method
                  BLASTX
NCBI GI
                   g1620371
BLAST score
                   1745
E value
                  0.0e + 00
Match length
                   336
% identity
                   100
NCBI Description
                   (Y08782) peroxidase ATP23a [Arabidopsis thaliana]
                   117949
Seq. No.
                   1080 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P3h09b1
                  BLASTX
Method
NCBI GI
                  q1708420
BLAST score
                   1560
                   1.0e-174
E value
Match length
                   310
                   100
% identity
NCBI Description
                  ISOFLAVONE REDUCTASE HOMOLOG P3 >gi 1361992 pir S57613
                   isoflavonoid reductase homolog - Arabidopsis thaliana
                  >gi 886432 emb CAA89859 (Z49777) isoflavonoid reductase
                  homologue [Arabidopsis thaliana]
                   117950
Seq. No.
Contig ID
                  1080 3.R1010
5'-most EST
                   jC-atXLIB327432P3h09a1
                  BLASTX
Method
NCBI GI
                  q1708420
BLAST score
                   558
E value
                  2.0e-57
Match length
                  115
% identity
                   97
NCBI Description
                  ISOFLAVONE REDUCTASE HOMOLOG P3 >gi 1361992 pir S57613
                   isoflavonoid reductase homolog - Arabidopsis thaliana
                  >gi 886432 emb CAA89859 (Z49777) isoflavonoid reductase
                  homologue [Arabidopsis thaliana]
                  117951
Seq. No.
                  1081 1.R1010
Contig ID
5'-most EST
                  LIB25-052-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  q1361983
BLAST score
                   3204
E value
                  0.0e + 00
Match length
                  629
                  100
% identity
NCBI Description
                  ARP protein - Arabidopsis thaliana >gi 886434 emb CAA89858_
                   (Z49776) ARP protein [Arabidopsis thaliana]
Seq. No.
                  117952
Contig ID
                  1086 1.R1010
5'-most EST
                  jC-atXLIB327412P4a07b1
Method
                  BLASTX
```

g1491617

```
BLAST score
                   1450
E value
                   1.0e-161
Match length
                   327
% identity
                   87
                   (X99952) peroxidase [Arabidopsis thaliana]
NCBI Description
                   117953
Seq. No.
                   1087 1.R1010
Contig ID
5'-most EST
                   LIB3176-040-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g1402902
BLAST score
                   1618
E value
                   0.0e + 00
Match length
                   329
                   95
% identity
                   (X98323) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >gi 1419386_emb_CAA67428_ (X98928) peroxidase ATP10a
                   [Arabidopsis thaliana]
                   117954
Seq. No.
                   1088_1.R1010
Contig ID
5'-most EST
                   LIB22-085-Q1-E2-B6
Method
                   BLASTX
                   q1402920
NCBI GI
                   1541
BLAST score
                   1.0e-172
E value
                   326
Match length
% identity
                   93
NCBI Description
                   (X98321) peroxidase [Arabidopsis thaliana]
                   117955
Seq. No.
                   1089 1.R1010
Contig ID
5'-most EST
                   PLN g1546705
                   BLASTX
Method
                   g1546706
NCBI GI
BLAST score
                   555
E value
                   1.0e-175
Match length
                   325
% identity
                   93
NCBI Description
                  (X98855) peroxidase ATP8a [Arabidopsis thaliana]
                   117956
Seq. No.
                   1090 1.R1010
Contig ID
5'-most EST
                   PLN g2108251
                   BLASTX
Method
NCBI GI
                   g2108252
BLAST score
                   6126
E value
                   0.0e + 00
Match length
                   1233
% identity
                   100
NCBI Description (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
                   >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
[Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_
                   (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
                   117957
Seq. No.
```

1091 1.R1010

Contig ID 5'-most EST

Method

```
jC-atXLIB327422P4b11b1
5'-most EST
                  BLASTX
Method
                  g2833379
NCBI GI
BLAST score
                  1640
                  0.0e+00
E value
                  341
Match length
                  93
% identity
                  RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL
NCBI Description
                  PYROPHOSPHATE SYNTHETASE 1) (PRS I) >gi 1076397 pir S51270
                  ribose-phosphate pyrophosphokinase (EC 2.7.6.1) -
                  Arabidopsis thaliana >gi 633140 emb CAA58717 (X83764)
                  phosphoribosyl diphosphate synthetase [Arabidopsis
                  thaliana] >gi 3608149 (AC005314) phosphoribosyl diphosphate
                  synthetase [Arabidopsis thaliana]
Seq. No.
                  117958
                  1091 2.R1010
Contig ID
                  jC-atXP34C150P10T7d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2833379
BLAST score
                  1789
E value
                  0.0e + 00
Match length
                  352
                  100
% identity
                  RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL
NCBI Description
                  PYROPHOSPHATE SYNTHETASE 1) (PRS I) >gi 1076397 pir S51270
                  ribose-phosphate pyrophosphokinase (EC 2.7.6.1) -
                  Arabidopsis thaliana >gi 633140 emb CAA58717 (X83764)
                  phosphoribosyl diphosphate synthetase [Arabidopsis
                  thaliana] >gi 3608149 (AC005314) phosphoribosyl diphosphate
                  synthetase [Arabidopsis thaliana]
                  117959
Seq. No.
                  1091 4.R1010
Contig ID
                  jC-atXLIB327415P1g11b1
5'-most EST
                  117960
Seq. No.
                  1091 5.R1010
Contig ID
                  LIB146-004-Q1-E1-B8
5'-most EST
Method
                  BLASTX
                  g2833379
NCBI GI
BLAST score
                  256
                  2.0e-43
E value
                  103
Match length
                  93
% identity
                  RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL
NCBI Description
                  PYROPHOSPHATE SYNTHETASE 1) (PRS I) >gi 1076397_pir_ S51270
                  ribose-phosphate pyrophosphokinase (EC 2.7.6.1) -
                  Arabidopsis thaliana >gi 633140 emb CAA58717 (X83764)
                  phosphoribosyl diphosphate synthetase [Arabidopsis
                  thaliana] >gi 3608149 (AC005314) phosphoribosyl diphosphate
                  synthetase [Arabidopsis thaliana]
Seq. No.
                  117961
```

1093 1.R1010

PLN_g16422 BLASTX

```
NCBI GI
                    g130189
BLAST score
                    5892
                    0.0e + 00
E value
Match length
                    1147
% identity
                    100
                    PHYTOCHROME B >gi_65879_pir__FKMUB phytochrome B -
NCBI Description
                    Arabidopsis thaliana >gi 16423 emb CAA35222 (X17342) phyB
                    photoreceptor [Arabidopsis thaliana] >gi 4185145 (AC005724)
                    phytochrome B [Arabidopsis thaliana]
                    117962
Seq. No.
                    1095 1.R1010
Contig ID
                    PLN q4467358
5'-most EST
                    BLASTX
Method
                    q4467359
NCBI GI
BLAST score
                    5261
                    0.0e+00
E value
Match length
                    1121
% identity
                    91
                    (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis
NCBI Description
                    117963
Seq. No.
                    1096 1.R1010
Contig ID
5'-most EST
                    LIB35-004-Q1-E1-H1
Method
                    BLASTX
NCBI GI
                    q322571
BLAST score
                    303
E value
                    2.0e-27
Match length
                    77
% identity
                    79
                    proteinase inhibitor II - Arabidopsis thaliana
>gi_16427_emb_CAA48892_ (X69139) protease inhibitor II
[Arabidopsis thaliana] >gi_4038041 (AC005936) proteinase
NCBI Description
                    inhibitor II [Arabidopsis thaliana]
                    117964
Seq. No.
Contig ID
                    1096 2.R1010
5'-most EST
                    jC-atXP40C162J14T7d1
Method
                    BLASTX
                    g4038040
NCBI GI
BLAST score
                    301
E value
                    3.0e-27
Match length
                    77
% identity
                    79
NCBI Description
                    (AC005936) proteinase inhibitor II [Arabidopsis thaliana]
Seq. No.
                    117965
Contig ID
                    1098 1.R1010
5'-most EST
                    jC-atXLIB327437P4e07a2
Method
                    BLASTX
NCBI GI
                    q1175012
BLAST score
                    1430
E value
                    1.0e-159
Match length
                    286
% identity
                    97
                    PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN
NCBI Description
```

```
B) (TMP-B) >qi 396218 emb CAA49155 (X69294) transmembrane
                   protein TMP-B [Arabidopsis thaliana]
                   117966
Seq. No.
                   1098 2.R1010
Contig ID
                   LIB2\overline{2} - 084 - Q1 - E1 - C1
5'-most EST
                   BLASTX
Method
                   q1361155
NCBI GI
BLAST score
                   247
                   2.0e-20
E value
Match length
                   199
                   36
% identity
                   hypothetical protein o215b - Escherichia coli >gi 537235
NCBI Description
                   (U14003) Kenn Rudd identifies as gpmB [Escherichia coli]
                   >qi 1790856 (AE000509) phosphoglyceromutase 2 [Escherichia
                   coli]
                   117967
Seq. No.
                   1098 3.R1010
Contig ID
                   jC-atXLIB327423P1d11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2373401
BLAST score
                   852
E value
                   1.0e-142
                   286
Match length
                   87
% identity
NCBI Description
                   (D85192) transmembrane protein [Arabidopsis thaliana]
                   117968
Seq. No.
                   1098 6.R1010
Contig ID
5'-most EST
                   g16918
Method
                   BLASTX
NCBI GI
                   g2440042
BLAST score
                   310
E value
                   3.0e-41
Match length
                   137
% identity
                   70
NCBI Description
                   (AJ001292) major intrinsic protein PIPa2 [Craterostigma
                   plantagineum]
                   117969
Seq. No.
                   1098 7.R1010
Contig ID
5'-most EST
                   g498689
Method
                   BLASTN
                   q396217
NCBI GI
BLAST score
                   146
E value
                   2.0e-76
                   178
Match length
% identity
                   96
NCBI Description A.thaliana mRNA for transmembrane protein TMP-B
Seq. No.
                   117970
                   1098 8.R1010
Contig ID
                   ARAB\overline{L}1-042-Q1-B1-C7
5'-most EST
                   BLASTX
Method
                   g1175012
NCBI GI
                   78
BLAST score
```

```
E value
                   2.0e-37
Match length
                   113
% identity
                   78
                   PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN
NCBI Description
                   B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]
                   117971
Seq. No.
                   1098 9.R1010
Contig ID
                   jC-atXP75C226H22T7d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1175012
BLAST score
                   492
E value
                   1.0e-49
Match length
                   166
                   73
% identity
                   PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN
NCBI Description
                   B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane
                   protein TMP-B [Arabidopsis thaliana]
                   117972
Seq. No.
Contig ID
                   1101_1.R1010
5'-most EST
                   LIB3175-079-P1-K1-A10
                   BLASTX
Method
NCBI GI
                   q3367632
BLAST score
                   1176
                   1.0e-129
E value
Match length
                   227
                   100
% identity
                   (AJ000539) phosphatidylinositol synthase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   117973
                   1102_1.R1010
Contig ID
5'-most EST
                   PLN g769742
Method
                   BLASTX
NCBI GI
                   q1076281
BLAST score
                   2827
E value
                   0.0e + 00
Match length
                   531
                   99
% identity
                   1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
NCBI Description
                   (EC 3.1.4.11) - Arabidopsis thaliana
                   >gi_769743_emb_CAA59962_ (X85973)
                   1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
                   [Arabidopsis thaliana]
Seq. No.
                   117974
Contig ID
                   1103 1.R1010
5'-most EST
                   jC-atXLIB327426P3f11b1
                   BLASTX
Method
NCBI GI
                   q3914658
BLAST score
                   897
E value
                   8.0e-97
Match length
                   198
                   89
% identity
                   50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
NCBI Description
```

NCBI Description

Seq. No.

117979

```
>gi 1694974 emb CAA70851 (Y09635) plastid ribosomal
                   protein [Arabidopsis thaliana]
                   117975
Seq. No.
                   1103 2.R1010
Contig ID
5'-most EST
                   q937\overline{3}95
                   BLASTX
Method
                   q3914658
NCBI GI
BLAST score
                   495
E value
                   7.0e-50
Match length
                   178
% identity
                   61
                   50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi 1694974 emb CAA70851 (Y09635) plastid ribosomal
                   protein [Arabidopsis thaliana]
                   117976
Seq. No.
                   1103 4.R1010
Contig ID
5'-most EST
                   jC-atXLIB327426P4f11a1
Method
                   BLASTX
NCBI GI
                   q3914658
BLAST score
                   209
E value
                   3.0e-38
Match length
                   87
% identity
                   100
                   50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi 1694974 emb CAA70851 (Y09635) plastid ribosomal
                   protein [Arabidopsis thaliana]
                   117977
Seq. No.
                   1106_1.R1010
Contig ID
5'-most EST
                   PLN g1708776
Method
                   BLASTX
                   q1708777
NCBI GI
BLAST score
                   3151
E value
                   0.0e + 00
Match length
                   628
% identity
NCBI Description
                   (Z83202) potassium channel [Arabidopsis thaliana]
                   >gi_3063705_emb_CAA18596.1_ (AL022537) potassium channel
                   protein [Arabidopsis thaliana] >gi_4090537 (U73325) K+ inward rectifying channel protein [Arabidopsis thaliana]
                   >gi 4098949 (U81239) K+ inward rectifying channel
                   [Arabidopsis thaliana]
                   117978
Seq. No.
Contig ID
                   1107 1.R1010
5'-most EST
                   LIB22-067-Q1-E1-D8
                   BLASTX
Method
NCBI GI
                   q1817544
BLAST score
                   2468
E value
                   0.0e + 00
Match length
                   499
% identity
```

(D83025) proline oxidase precursor [Arabidopsis thaliana]

```
1107 2.R1010
Contig ID
                     jC-atXLIB327417P2e06b1
5'-most EST
                     BLASTX
Method
                     g1531760
NCBI GI
                     646
BLAST score
                     1.0e-67
E value
                     138
Match length
                     91
% identity
                     (X97075) proline oxidase [Arabidopsis thaliana]
NCBI Description
                     117980
Seq. No.
                     1110 1.R1010
Contig ID
                     PLN g1905774
5'-most EST
                     BLASTX
Method
NCBI GI
                     g1905775
BLAST score
                     2657
                     0.0e+00
E value
                     519
Match length
                     100
% identity
                     (Y11930) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                     117981
                     1112 1.R1010
Contig ID
                     LIB24-111-Q1-E1-F9
5'-most EST
                     BLASTX
Method
                     q1488521
NCBI GI
BLAST score
                     2741
                     0.0e + 00
E value
                     550
Match length
                     100
% identity
NCBI Description
                     (X99938) RNA helicase [Arabidopsis thaliana]
                     117982
Seq. No.
                     1113 1.R1010
Contig ID
                     PLN g577734
5'-most EST
                     BLASTX
Method
NCBI GI
                     q3122638
                     2519
BLAST score
                     0.0e + 00
E value
Match length
                     486
                     97
% identity
                     PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1
NCBI Description
                     >gi_1076381_pir__S49820 PRL1 protein - Arabidopsis thaliana
>gi_577733 emb_CAA58031_ (X82824) PRL1 [Arabidopsis thaliana] >gi_577735_emb_CAA58032_ (X82825) PRL1 [Arabidopsis thaliana] >gi_2244947_emb_CAB10369.1_ (Z97339)
                     PRL1 protein - Arabidopsis thaliana
                     117983
Seq. No.
                     1115 1.R1010
Contig ID
                     LIB24-022-Q1-E1-C9
5'-most EST
                     BLASTX
Method
NCBI GI
                     g1168530
                     1708
BLAST score
                     0.0e+00
E value
Match length
                     353
                     93
% identity
```

Method NCBI GI

```
NCBI Description SERINE/THREONINE-PROTEIN KINASE ASK2 >gi 99748 pir S24586
                   probable serine/threonine-specific protein kinase (EC
                   2.7.1.-) (clone ASK2) - Arabidopsis thaliana >gi_16443_emb_CAA78106_ (Z12120) protein kinase
                   [Arabidopsis thaliana]
                   117984
Seq. No.
                   1116 1.R1010
Contig ID
                   LIB23-004-Q1-E1-D1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1346780
BLAST score
                   1635
                   0.0e + 00
E value
Match length
                   305
                   100
% identity
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP-X ISOZYME 2
NCBI Description
                   >gi_629550_pir__S42559 phosphoprotein phosphatase (EC
                   3.1.3.16) X-2 (clone EP128) - Arabidopsis thaliana
                   >gi_397590_emb_CAA80312_ (Z22596) protein phosphatase
                   [Arabidopsis thaliana]
                   117985
Seq. No.
Contig ID
                   1117_1.R1010
                   LIB24-067-Q1-E1-B3
5'-most EST
Method
                   BLASTX
                   q1346782
NCBI GI
BLAST score
                   1640
E value
                   0.0e + 00
Match length
                   305
% identity
                   100
NCBI Description
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP-X ISOZYME 1
                   >gi 629549 pir S42558 phosphoprotein phosphatase (EC
                   3.1.3.16) X-1 (clone EP129) - Arabidopsis thaliana
                   >gi_397592_emb_CAA80302_ (Z22587) protein phosphatase
                   [Arabidopsis thaliana] >gi_2623197 (AF030289) protein
                   phosphatase X isoform 1 [Arabidopsis thaliana]
                   >gi_4455195_emb_CAB36518.1_ (AL035440) phosphoprotein
                   phosphatase (PPX-1) [Arabidopsis thaliana]
                   117986
Seq. No.
                   1118 1.R1010
Contig ID
                   jC-atXLIB327417P4b05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1769901
BLAST score
                   2066
                   0.0e + 00
E value
Match length
                   442
% identity
NCBI Description
                   (X95737) proline transporter 1 [Arabidopsis thaliana]
                   >gi 2088642 (AF002109) proline transporter 1 [Arabidopsis
                   thalianal
                   117987
Seq. No.
                   1119 1.R1010
Contig ID
                   jC-atXLIB327409P4b07b1
5'-most EST
```

BLASTX

q1769903

```
BLAST score
                   2080
E value
                   0.0e + 00
Match length
                   439
% identity
                   94
NCBI Description
                   (X95738) proline transporter 2 [Arabidopsis thaliana]
                   117988
Seq. No.
                   1120 1.R1010
Contig ID
5'-most EST
                   g1109741
Method
                   BLASTX
NCBI GI
                   g1172599
BLAST score
                   1120
E value
                   1.0e-123
                   230
Match length
% identity
                   95
NCBI Description
                  PROTEASOME COMPONENT C5 (MULTICATALYTIC ENDOPEPTIDASE
                   COMPLEX SUBUNIT C5) (TAS-F22/FAFP98)
                   >gi 600387 emb CAA47753 (X67338) proteosome subunit
                   [Arabidopsis thaliana]
                   117989
Seq. No.
Contig ID
                   1120_3.R1010
5'-most EST
                   q458761
Method
                  BLASTN
NCBI GI
                  .g577530
BLAST score
                   255
E-value
                   1.0e-141
Match length
                   263
                   100
% identity
NCBI Description A.thaliana mRNA for proteasome subunit
                   117990
Seq. No.
Contig ID
                   1124_1.R1010
5'-most EST
                   PLN_g1402899
Method
                   BLASTX
NCBI GI
                   q1402900
BLAST score
                   1555
E value
                   1.0e-174
Match length
                   305
                   100
% identity
NCBI Description
                   (X98322) peroxidase [Arabidopsis thaliana]
                   >gi 1429219 emb CAA67312 (X98776) peroxidase ATP13a
                   [Arabidopsis thaliana]
                   117991
Seq. No.
                   1126 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327415P2h08b2
Method
                   BLASTX
NCBI GI
                   q1402904
BLAST score
                   1695
                   0.0e + 00
E value
Match length
                   321
% identity
                  (X98313) peroxidase [Arabidopsis thaliana]
NCBI Description
                   117992
Seq. No.
```

1126_2.R1010

```
5'-most EST
                   jC-atXLIB327432P2c08b2
                   BLASTX
Method
NCBI GI
                   g1402904
BLAST score
                   862
E value
                   6.0e-98
Match length
                   228
% identity
                   84
                   (X98313) peroxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   117993
Contig ID
                   1126_3.R1010
5'-most EST
                   jC-atXP112C129O1T7a1
Method
                   BLASTX
                   g1402904
NCBI GI
BLAST score
                   178
                   1.0e-33
E value
Match length
                   110
% identity
                   71
                   (X98313) peroxidase [Arabidopsis thaliana]
NCBI Description
                   117994
Seq. No.
Contig ID
                   1126 4.R1010
5'-most EST
                   LIB3234-033-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q1403136
                   383
BLAST score
E value
                   8.0e-37
Match length
                   95
% identity
                   81
NCBI Description
                  (X98189) peroxidase ATPla [Arabidopsis thaliana]
                   117995
Seq. No.
Contig ID
                   1126_5.R1010
5'-most EST
                   g3450355
Method
                   BLASTX
                   g1402904
NCBI GI
BLAST score
                   231
E value
                   4.0e-43
Match length
                   104
% identity
                   90
NCBI Description
                   (X98313) peroxidase [Arabidopsis thaliana]
                   117996
Seq. No.
Contig ID
                   1126 6.R1010
5'-most EST
                   g2393244
Method
                   BLASTN
NCBI GI
                   g2894557
BLAST score
                   260
E value
                   1.0e-144
Match length
                   390
% identity
                   92
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T805
                   (ESSAII project)
                                        20 €~
Seq. No.
                   117997
                   1126 8.R1010
Contig ID
                   jC-atXLIB327417P4b01b1
5'-most EST
```

```
Method
                   BLASTX
                   q1402904
NCBI GI
                   753
BLAST score
                   5.0e-96
E value
                   192 -
Match length
% identity
                   93
                   (X98313) peroxidase [Arabidopsis thaliana]
NCBI Description
                   117998
Seq. No.
Contig ID
                   1126_9.R1010
5'-most EST
                   jC-atXP78CF4F11T7b1
Method
                   BLASTX.
                   q1402904
NCBI GI
BLAST score
                   1231
                   1.0e-136
E value
                   245
Match length
% identity
                   97
                  (X98313) peroxidase [Arabidopsis thaliana]
NCBI Description
                   117999
Seq. No.
                   1128 1.R1010
Contig ID
5'-most EST
                  LIB2\overline{2}-020-Q1-E1-C12
Method
                  BLASTX
NCBI GI
                   q1402908
                   1750
BLAST score
                   0.0e + 00
E value
                   352
Match length
% identity
NCBI Description
                   (X98315) peroxidase [Arabidopsis thaliana]
                   >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a
                   [Arabidopsis thaliana] >gi_4455802_emb_CAB37193 (AJ133036)
                  peroxidase [Arabidopsis thaliana]
                   118000
Seq. No.
Contig ID
                   1128 2.R1010
5'-most EST
                   jC-atXP44C169L7T7041a1
                   BLASTX
Method
                   q1402908
NCBI GI
BLAST score
                   731
E value
                   2.0e-77
Match length
                   142
% identity
                   (X98315) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a
                   [Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036)
                  peroxidase [Arabidopsis thaliana]
Seq. No.
                   118001
Contig ID
                   1129 1.R1010
                  PLN g1402909
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1402910
BLAST score
                   1602
E value
                   1.0e-179
Match length
                  308
% identity
                  100
NCBI Description (X98316) peroxidase [Arabidopsis thaliana]
```

BLAST score

571

```
thaliana]
                   118002
 Seq. No.
                   1130 1.R1010
 Contig ID
                   jC-atXLIB327427P1b04b1
 5'-most EST
                   BLASTX
 Method
                   g1403138
NCBI GI
                   1621
BLAST score
                   0.0e+00
 E value
                   327
Match length
                   95
 % identity
NCBI Description
                   (X98190) peroxidase ATP2a [Arabidopsis thaliana]
                   >gi_4371288_gb_AAD18146_ (AC006260) putative peroxidase
                   ATP2a [Arabidopsis thaliana]
                   118003
Seq. No.
                   1130 4.R1010
 Contig ID
 5'-most EST
                   jC-atXP102CE2G11T7b1
Method
                   BLASTX
                   g1403138
NCBI GI
BLAST score
                   470
                   6.0e-47
E value
Match length
                   137
% identity
                   75
NCBI Description
                   (X98190) peroxidase ATP2a [Arabidopsis thaliana]
                   >gi 4371288 gb AAD18146 (AC006260) putative peroxidase
                   ATP2a [Arabidopsis thaliana].
                   118004
Seq. No...
                   1130 5.R1010
Contig ID
 5'-most EST
                   q948093
                   BLASTX
Method
                   g1402912
NCBI GI
BLAST score
                   525
                   2.0e-53
E value
Match length
                   120
% identity
                   85
                   (X98317) peroxidase [Arabidopsis thaliana]
NCBI Description
                   118005
Seq. No.
                   1131 1.R1010
Contig ID
5'-most EST
                   LIB3234-060-P1-K1-H7
                   BLASTX
Method
NCBI GI
                   g1402914
BLAST score
                   1826
                   0.0e+00
E value
Match length
                   358
                   100
% identity
NCBI Description
                   (X98318) peroxidase [Arabidopsis thaliana]
                   118006
Seq. No.
                   1132 1.R1010
Contig ID
 5'-most EST
                   jC-atXLIB327408P1c06b1
Method
                   BLASTX
NCBI GI
                   g3021506
```

>gi_1429223_emb_CAA67550_ (X99096) peroxidase [Arabidopsis

```
E value
                   8.0e-59
                   157
Match length
                   71
% identity
                   (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   118007
                   1132 2.R1010
Contig ID
                   jC-atXLIB327409P2g05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1402916
BLAST score
                   1129
                   1.0e-124
E value
                   321
Match length
                   87
% identity
                   (X98319) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >gi 1429217 emb CAA67311 (X98775) peroxidase ATP12a
                   [Arabidopsis thaliana]
                   118008
Seq. No.
                   1133 1.R1010
Contig ID
5'-most EST
                   jC-atX22038Q1E1G12b1
Method
                   BLASTX
                   a1402918
NCBI GI
                   1602
BLAST score
                   1.0e-179
E value
                   336
Match length
% identity
                   (X98320) peroxidase [Arabidopsis thaliana]
NCBI Description
                   >gi 1429215 emb CAA67310 (X98774) peroxidase ATP6a
                   [Arabidopsis thaliana]
Seq. No.
                   118009
                   1134 1.R1010
Contig ID
5'-most EST
                   LIB3177-024-P1-K2-H7
Method
                   BLASTX
NCBI GI
                   q266839
BLAST score
                   1065
E value
                   1.0e-116
Match length
                   212
                   100
% identity
                   PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                   COMPLEX ALPHA SUBUNIT) (TAS-G64) >gi_478764_pir__S29240
                   multicatalytic endopeptidase complex (EC 3.4.99.46) alpha
                   chain - Arabidopsis thaliana >gi_16445_emb_CAA47298
                    (X66825) proteosome alpha subunit [Arabidopsis thaliana]
                   >gi_3421080 (AF043522) 20S proteasome subunit PAD1
[Arabidopsis thaliana] >gi_742351_prf__2009376B
                   proteasome:SUBUNIT=alpha [Arabidopsis thaliana]
                   118010
Seq. No.
Contig ID
                   1135 1.R1010
5'-most EST
                   jC-atXP29C137O18T7067d1
Method
                   BLASTX
                   g2499973
NCBI GI
BLAST score
                   422
                   3.0e-41
E value
```

```
Match length
                  103
                  83
% identity
                  PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T)
NCBI Description
                  >gi 1465366 emb CAA66701 (X98078) photosystem II
                   [Arabidopsis thaliana]
                  118011
Seq. No.
                  1139 1.R1010
Contig ID
                  LIB2\overline{5}-015-Q1-E1-A7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2160174
BLAST score
                  2421
                  0.0e + 00
E value
                  526
Match length
% identity
NCBI Description (AC000132) Identical to A. thaliana PUR2 (gb X74766). ESTs
                  gb_ATTS3927,gb_N96446 come from this gene. [Arabidopsis
                  thaliana]
                  118012
Seq. No.
                  1140 1.R1010
Contig ID
5'-most EST
                  PLN_g398611
Method
                  BLASTX
                  q4512619
NCBI GI
                   345
BLAST score
                  1.0e-149
E value
                  280
Match length
% identity
                   (AC004793) This gene is a member of the formyl transferase
NCBI Description
                   family PF 00551 and may be a pseudogene of gb_X74767
                  phosphoribosylglycinamide formyl transferase (PUR3) from
                  Arabidopsis thaliana since our sequence differs from
                  PUR3... >gi 4753662 emb CAA52779.2 (X74767)
                  phosphoribosylglycinamide formyltransferase [Arabidopsis
                   thaliana]
                   118013
Seq. No.
                   1141 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327438P4h09b2
                   BLASTX
Method
NCBI GI
                   g1363489
BLAST score
                   2675
E value
                   0.0e + 00
Match length
                   509
                   97
% identity
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                   thaliana >gi 984052 emb CAA61592 (X89413) thioglucoside
                   glucohydrolase [Arabidopsis thaliana]
Seq. No.
                   118014
                   1141 2.R1010
Contia ID
                   jC-atXP89C245A3T7012d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2286069
                   757
BLAST score
                   2.0e-80
E value
Match length
                   149
```

```
% identity
                   95
NCBI Description
                  (U72155) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                   118015
                   1141 3.R1010
Contig ID
5'-most EST
                  jC-atXP74C224J15T7042d1
                   BLASTX
Method
                   g1732570
NCBI GI
                   1128
BLAST score
E value
                   1.0e-125
Match length
                   310
% identity
NCBI Description
                  (U72153) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                  118016
                   1141_5.R1010
Contig ID
5'-most EST
                  LIB22-065-Q1-E1-D7
                  BLASTX
Method
                   q2286069
NCBI GI
                   1551
BLAST score
                   1.0e-173
E value
Match length
                   333
% identity
                   93
NCBI Description (U72155) beta-glucosidase [Arabidopsis thaliana]
                   118017
Seq. No.
                   1141 6.R1010
Contig ID
5'-most EST
                  LIB3176-035-P1-K1-D4
                  BLASTX
Method
                   q1363489
NCBI GI
                   835
BLAST score
                   1.0e-89
E value
Match length
                   211
% identity
                   78
NCBI Description
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                   thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                   glucohydrolase [Arabidopsis thaliana]
Seq. No.
                   118018
                  1141 7.R1010
Contig ID
5'-most EST
                   q241\overline{3}104
Method
                  BLASTX
NCBI GI
                  g2286069
BLAST score
                   515
E value
                   3.0e-52
Match length
                  110
                   92
% identity
NCBI Description (U72155) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                   118019
                  1141 8.R1010
Contig ID
5'-most EST
                  q460840
                  BLASTX
Method
NCBI GI
                  g1363489
BLAST score
                  194
E value
                  1.0e-14
Match length
```

```
62
% identity
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                  thaliana >gi 984052 emb CAA61592 (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                   118020
                   1141 9.R1010
Contig ID
                   jC-atXLIB327412P3a08b1
5'-most EST
Method
                   BLASTX
NCBI GI
                  g1732570
BLAST score
                   467
E value
                   1.0e-46
Match length
                   86
                   100
% identity
                  (U72153) beta-glucosidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118021
                   1141 10.R1010
Contig ID
                  jC-atXLIB327409P2h01b1
5'-most EST
                   BLASTX
Method
                   q2286069
NCBI GI
BLAST score
                   487
E value
                   7.0e-49
Match length
                   169
% identity
                   53
                  (U72155) beta-glucosidase [Arabidopsis thaliana]
NCBI Description
                   118022
Seq. No.
                  1141 11.R1010
Contig ID
5'-most EST
                  LIB3176-021-P1-K1-G1
Method
                  BLASTX
                  q1363489
NCBI GI
BLAST score
                   655
                   2.0e-68 ·
E value
Match length
                   160
% identity
                   82
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                   thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
                   118023
Seq. No.
Contig ID
                  1141 12.R1010
                  LIB3177-002-Q1-K1-H5
5'-most EST
Method
                   BLASTX
                   q1076442
NCBI GI
BLAST score
                   163
                   5.0e-11
E value
Match length
                   92
% identity
                   46
NCBI Description
                  beta-glucosidase (EC 3.2.1.21) - rape
                  >gi 757740 emb CAA57913 (X82577) beta-glucosidase
                   [Brassica napus]
                   118024
Seq. No.
Contig ID
                   1141_13.R1010
                  LIB2\overline{2}-068-Q1-E1-C1
5'-most EST
                  BLASTX
Method
```

```
NCBI GI
                  g2286069
BLAST score
                  547
                  3.0e-56
E value
                  104
Match length
                  99
% identity
                  (U72155) beta-glucosidase [Arabidopsis thaliana]
NCBI Description
                  118025
Seq. No.
                  1141 16.R1010
Contig ID
                  LIB3176-117-P2-K1-D7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1732570
                  227
BLAST score
                  9.0e-25
E value
Match length
                  74
                  73
% identity
NCBI Description
                  (U72153) beta-glucosidase [Arabidopsis thaliana]
                  118026
Seq. No.
                  1141 18.R1010
Contig ID
                  LIB3177-005-P1-K2-H4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1732570
BLAST score
                  124
                  1.0e-06
E value
                  97
Match length
                  86
% identity
                  (U72153) beta-glucosidase [Arabidopsis thaliana]
NCBI Description
                  118027
Seq. No.
                  1141 19.R1010
Contig ID
5'-most EST
                  LIB3177-041-P1-K2-H9
Method
                  BLASTX
NCBI GI
                  g1363489
BLAST score
                  712
E value
                  3.0e-89
Match length
                  165
                  98
% identity
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                  thaliana >qi 984052 emb CAA61592 (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
                  118028
Seq. No.
                  1142 1.R1010
Contig ID
                  PLN g443817
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2499945
BLAST score
                   2210
E value
                  0.0e + 00
                   470
Match length
% identity
                   94
                  URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                  PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                  DECARBOXYLASE >gi_1076363_pir__S46440 orotate
                  phosphoribosyltransferase (EC 2.4.2.10) /
                   orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                  Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842)
```

pyrE-F [Arabidopsis thaliana]

```
118029
  Seq. No.
                     1143 1.R1010
  Contig ID
                    LIB3176-044-P1-K1-A10
  5'-most EST
  Method
                     BLASTX
                     q1346929
  NCBI GI
                     1834
  BLAST score
                     0.0e + 00
  E value
  Match length
                     381
  % identity
                     96
                    ASPARTATE CARBAMOYLTRANSFERASE PRECURSOR (ASPARTATE
  NCBI Description
                     TRANSCARBAMYLASE) (ATCASE) >gi_1076293_pir___$46441
                     aspartate carbamoyltransferase (EC 2.1.3.2) - Arabidopsis
                     thaliana >gi_443820_emb_CAA50687_ (X71843) aspartate
                     carbamoyltransferase [Arabidopsis thaliana]
  Seq. No.
                     118030
  Contig ID
                     1144 1.R1010
  5'-most EST
                     jC-atXLIB327431P4a03a1
                     BLASTX
  Method
  NCBI GI
                     q417570
  BLAST score
                     2152
  E value ·
                     0.0e + 00
  Match length
                     434
                     97
  % identity
                    DIHYDROOROTATE DEHYDROGENASE PRECURSOR (DIHYDROOROTATE
  NCBI Description
                    OXIDASE) (DHODEHASE) >gi 478676 pir S23762 dihydroorotate
                    oxidase (EC 1.3.3.1) - Arabidopsis thaliana
                    >gi 16449 emb CAA44695 (X62909) dihydroorotate
                     dehydrogenase [Arabidopsis thaliana]
                     118031
  Seq. No.
  Contig ID
                    1145_1.R1010
  5'-most EST
                    LIB3176-026-P1-K1-G4
  Method
                    BLASTX
  NCBI GI
                     q3915842
  BLAST score
                     1035
  E value
                    1:0e-113
Match length
                     217
                     94
  % identity
                    RAS-RELATED PROTEIN RAB11A >gi 2598229 emb CAA70112
  NCBI Description
                     (Y08904) Rabl1 protein [Arabidopsis thaliana]
  Seq. No.
                     118032
  Contig ID
                     1145_2.R1010
  5'-most EST
                     jC-atXLIB327427P3h05b2
  Method
                     BLASTX
  NCBI GI
                     q3915842
  BLAST score
                     555
  E value
                    1.0e-94
  Match length
                     217
                    83
  % identity
                    RAS-RELATED PROTEIN RAB11A >gi_2598229_emb_CAA70112_
  NCBI Description
                     (Y08904) Rabl1 protein [Arabidopsis thaliana]
```

×.

118033

Seq. No.

1.0

```
Contig ID
                   1145 5.R1010
5'-most EST
                   g936482
Method
                   BLASTX
                   g3024501
NCBI GI
                   483
BLAST score
                   1.0e-48
E value
Match length
                   98
                   96
% identity
                   RAS-RELATED PROTEIN RAB11C >gi 1370146 emb CAA98179
NCBI Description
                   (Z73951) RAB11C [Lotus japonicus]
                   118034
Seq. No.
Contig ID
                   1146 1.R1010
5'-most EST
                   jC-atXLIB327421P4e05b1
Method
                   BLASTX
                   g1370176
NCBI GI
                   962
BLAST score
                   1.0e-104
E value
Match length
                   187
                   100
% identity
                   (Z73937) RAB2A [Lotus japonicus]
NCBI Description
                   118035
Seq. No.
                   1150 1.R1010
Contig ID
5'-most EST
                   g2763338
Method
                   BLASTX
NCBI GI
                   q166834
                   2200
BLAST score
                   0.0e + 00
E value
Match length
                   474
                   97
% identity
                   (M86720) ribulose bisphosphate carboxylase/oxygenase
NCBI Description
                   activase [Arabidopsis thaliana] >gi 2642155 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
                   118036
Seq. No.
Contig ID
                   1150 2.R1010
5'-most EST
                   jC-atXLIB327416Pld12b1
Method
                   BLASTX
NCBI GI
                   g166834
BLAST score
                   428
                   6.0e-42
E value
Match length
                   166
% identity
                   63
NCBI Description
                   (M86720) ribulose bisphosphate carboxylase/oxygenase
                   activase [Arabidopsis thaliana] >gi_2642155 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
                   118037
Seq. No.
Contig ID
                   1152 1.R1010
5'-most EST
                   jC-atXLIB327420Pld10b1
Method
                   BLASTX
NCBI GI
                   g1345595
BLAST score
                   1168
E value
                   1.0e-128
Match length
                   248
% identity
                   94
```

```
NCBI Description
                 14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1)
                  >gi 1084332 pir S53727 14-3-3-like protein (ATF1) -
                  Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like
                  protein 1 [Arabidopsis thaliana] >gi 1549404 (U68545) GF14
                  lambda [Arabidopsis thaliana]
                  118038
Seq. No.
                  1152 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327418P1f05b1
Method
                  BLASTX
NCBI GI
                  g1519251
BLAST score
                  238
E value
                  3.0e-38
Match length
                  174
% identity
                  67
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                  118039
Seq. No.
Contig ID
                  1152_3.R1010
5'-most EST
                  LIB23-056-Q1-E1-A5
                  BLASTX
Method
NCBI GI
                  q1345594
BLAST score
                  1204
                  1.0e-132
E value
Match length
                  248
% identity
                  98
                  14-3-3-LIKE PROTEIN GF14 KAPPA >gi 1022780 (U36447) GF14
NCBI Description
                  Kappa isoform [Arabidopsis thaliana]
                  118040
Seq. No.
Contig ID
                  1152 4.R1010
5'-most EST
                  jC-atXP115C251M22T7031d1
Method
                  BLASTX
NCBI GI
                  q1168201
BLAST score
                  643
E value
                  2.0e-97
Match length
                  204
                  93
% identity
NCBI Description
                  14-3-3-LIKE PROTEIN RCI2 >gi 1076394 pir S47970 RCI1B
                  protein - Arabidopsis thaliana >gi_531379_emb_CAA52238_
                  (X74141) RCI1B [Arabidopsis thaliana]
                  118041
Seq. No.
Contig ID
                  1152 5.R1010
                  jC-aTXLIB327414P4c07a2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1345595
BLAST score
                  530
E value
                  9.0e-54
Match length
                  217
% identity
                  51
NCBI Description 14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1)
                  >gi 1084332 pir S53727 14-3-3-like protein (ATF1) -
                 Arabidopsis thaliana >gi 953221 (U02565) 14-3-3-like
```

lambda [Arabidopsis thaliana]

protein 1 [Arabidopsis thaliana] >gi 1549404 (U68545) GF14

```
118042
Seq. No.
                   1153 1.R1010
Contig ID
                   PLN_g1405836
5'-most EST
                   BLASTX
Method
                   g2129735
NCBI GI
BLAST score
                   3349
                   0.0e+00
E value
Match length
                   661
                   98
% identity
                  serine/threonine-specific kinase (EC 2.7.1.-) precursor -
NCBI Description
                   Arabidopsis thaliana >gi_1405837_emb_CAA62824_ (X91630)
                   receptor-like kinase [Arabidopsis thaliana] >gi 2150023
                   (AF001168) receptor-like kinase LECRK1 [Arabidopsis
                   thaliana]
Seq. No.
                   118043
Contig ID
                   1155 1.R1010
5'-most EST
                  LIB3175-044-P1-K1-G2
                   BLASTX
Method
NCBI GI
                   g3785986
BLAST score
                   2773
                   0.0e+00
E value
Match length
                   587
% identity
                   92
NCBI Description
                  (AC005560) RGA1 protein [Arabidopsis thaliana]
                   118044
Seq. No.
                   1155 2.R1010
Contig ID
5'-most EST
                   jC-atXP125C156J14T7026a1
                   BLASTX
Method
NCBI GI
                   g2339978
BLAST score
                   577
                   2.0e-59
E value
Match length
                   111
% identity
                   98
                  (Y11336) RGA1 protein [Arabidopsis thaliana]
NCBI Description
                  118045
Seq. No.
Contig ID
                   1156 1.R1010
5'-most EST
                   PLN = 2339979
Method
                  BLASTX
                   g2339980
NCBI GI
BLAST score
                   2663
E value
                   0.0e+00
Match length
                   532
                   97
% identity
NCBI Description
                  (Y11337) RGA2 protein [Arabidopsis thaliana]
                  118046
Seq. No.
Contig ID
                  1157 1.R1010
5'-most EST
                  LIB25-113-Q1-E1-A7
                  BLASTX
Method
                   g400976
NCBI GI
BLAST score
                   1008
E value
                  1.0e-110
Match length
                  200
% identity
                  100
```

```
NCBI Description RAS-RELATED PROTEIN RHA1 >gi_478671_pir__S23727 GTP-binding protein RHA1 - Arabidopsis thaliana >gi_16484_emb_CAA41863_
                    (X59152) RHA1 [Arabidopsis thaliana]
                    >gi_397594_emb_CAA80534_ (Z22958) GTP-binding protein
                    [Arabidopsis thaliana]
                    118047
 Seq. No.
                    1157 2.R1010
 Contig ID
 5'-most EST
                    jC-atX35046Q1E1A10b1
Method
                    BLASTX
NCBI GI
                    g2853090
 BLAST score
                    741
E value
                    1.0e-104
Match length
                    200
% identity
                    100
NCBI Description
                    (AL021768) small GTP-binding protein-like [Arabidopsis
                    118048
Seq. No.
                    1158 1.R1010
Contig ID
                    PLN_g840718
 5'-most EST
Method
                    BLASTX
NCBI GI
                    q1710394
 BLAST score
                    1784
                    0.0e + 00
E value
                    340
Match length
                    100
 % identity
NCBI Description
                    RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN
                    (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)
                    >gi 840719 emb CAA54549 (X77336) ribonucleotide reductase
                    R2 [Arabidopsis thaliana]
Seq. No.
                    118049
                    1159 1.R1010
Contig ID
                    LIB3176-006-P1-K1-E10
 5'-most EST
Method
                    BLASTX
NCBI GI
                    q1173309
 BLAST score
                    1225
E value
                    1.0e-135
Match length
                    241
                    100
 % identity
                    MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S10 PRECURSOR
NCBI Description
                    >gi 2119078 pir S66361 ribosomal protein S10 precursor -
                    Arabidopsis thaliana >gi_517331_emb_CAA56711_ (X80694)
                    ribosomal protein S10 [Arabidopsis thaliana]
                    118050
Seq. No.
 Contig ID
                    1161 1.R1010
 5'-most EST
                    jC-atX25113Q1E1H06b1
Method
                    BLASTX
NCBI GI
                    q2149021
BLAST score
                    2609
E value
                    0.0e + 00
Match length
                    522
 % identity
                    98
NCBI Description
                    (U72290) ADPG pyrophosphorylase large subunit [Arabidopsis
                    thaliana]
```

```
118051
Seq. No.
                  1163 1.R1010
Contig ID
5'-most EST
                  PLN g312718
                  BLASTX
Method
NCBI GI
                  g1707931
BLAST score
                  968
                  1.0e-105
E value
Match length
                  182
                  100
% identity
                  GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 3
NCBI Description
                   (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)
                   (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE)
                  >gi_312719 emb CAA51776 (X73364) glucose-1-phosphate
                  adenylyltransferase [Arabidopsis thaliana]
                  118052
Seq. No.
                  1164 1.R1010
Contig ID
                  jC-atXLIB327424P4d03b1
5'-most EST
                  BLASTX
Method
                  g3015514
NCBI GI
BLAST score
                  2500
E value
                  0.0e + 00
Match length
                  520
                  94
% identity
NCBI Description
                  (U72351) ADPG pyrophosphorylase small subunit [Arabidopsis
                  thaliana]
                  118053
Seq. No.
                  1165 1.R1010
Contig ID
                  PLN g456508
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1170714
BLAST score
                  1507
                  0.0e + 00
E value
                  409
Match length
% identity
                  98
NCBI Description
                  SHAGGY RELATED PROTEIN KINASE ASK-GAMMA
                  >gi_541850_pir__S41597 protein kinase ASK-gamma (EC
                  2.7.1.-) - Arabidopsis thaliana >gi_456509_emb_CAA53180_
                   (X75431) ASK-gamma (Arabidopsis shaggy-related kinase)
                   [Arabidopsis thaliana] >gi 2059329 emb CAA73247 (Y12710)
                  shaggy-like kinase gamma [Arabidopsis thaliana]
Seq. No.
                  118054
                  1165_2.R1010
Contig ID
5'-most EST
                  LIB23-061-Q1-E1-G6
Method
                  BLASTX
NCBI GI
                  g1170711
BLAST score
                  2162
E value
                  0.0e + 00
Match length
                  405
                  100
% identity
                  SHAGGY RELATED PROTEIN KINASE ASK-ALPHA
NCBI Description
                  >gi_541901 pir_S41596 protein kinase ASK-alpha (EC
                  2.7.1.-) - Arabidopsis thaliana >gi 460832 emb CAA53181_
```

(X75432) shaggy related kinase [Arabidopsis thaliana]

```
protein kinase [Arabidopsis thaliana]
                  118055
Seq. No.
                   1165 3.R1010
Contig ID
5'-most EST
                  9471\overline{4}024
Method
                   BLASTX
                   g2598601
NCBI GI
                   1121
BLAST score
                   1.0e-150
E value
                   364
Match length
                   71
% identity
NCBI Description
                   (AJ002314) shaggy-like kinase 111 [Nicotiana tabacum]
                   118056
Seq. No.
                   1165 4.R1010
Contig ID
5'-most EST
                  ARABL1-025-Q1-B1-G12
                  BLASTX
Method
                   g1170714
NCBI GI
BLAST score
                   545
                   9.0e-56
E value
                   99
Match length
                   100
% identity
NCBI Description
                  SHAGGY RELATED PROTEIN KINASE ASK-GAMMA
                   >gi_541850_pir__S41597 protein kinase ASK-gamma (EC
                   2.7.1.-) - Arabidopsis thaliana >gi_456509_emb_CAA53180_
                   (X75431) ASK-gamma (Arabidopsis shaggy-related kinase)
                   [Arabidopsis thaliana] >gi_2059329 emb_CAA73247 (Y12710)
                   shaggy-like kinase gamma [Arabidopsis thaliana]
                   118057
Seq. No.
                   1165 5.R1010
Contig ID
                   jC-atXP65C207O19T7068d1
5'-most EST
Method
                   BLASTX
                   g1170714
NCBI GI
BLAST score
                   1191
E value
                   1.0e-136
Match length
                   267
% identity
                  89
NCBI Description
                  SHAGGY RELATED PROTEIN KINASE ASK-GAMMA
                   >gi 541850 pir S41597 protein kinase ASK-gamma (EC
                   2.7.1.-) - Arabidopsis thaliana >gi 456509 emb CAA53180
                   (X75431) ASK-gamma (Arabidopsis shaggy-related kinase)
                   [Arabidopsis thaliana] >gi_2059329_emb_CAA73247_ (Y12710)
                   shaggy-like kinase gamma [Arabidopsis thaliana]
                  118058
Seq. No.
                  1165 6.R1010
Contig ID
                   jC-a\overline{t}XLIB327420P1e08b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2351066
BLAST score
                   260
E value
                  1.0e-144
Match length
                   436
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOP9, complete sequence [Arabidopsis thaliana]
```

>gi 1769889 emb CAA48538 (X68525) serine /threonine

```
Seq. No.
                  118059
                  1165 7.R1010
Contig ID
                  jC-aTXLIB327428P4e06b2
5'-most EST
                  BLASTX
                  g1170714
NCBI GI
                  342
BLAST score
                   5.0e-32
E value
Match length
                  70
                  97
% identity
NCBI Description
                  SHAGGY RELATED PROTEIN KINASE ASK-GAMMA
                  >gi_541850_pir__S41597 protein kinase ASK-gamma (EC
                  2.7.1.-) - Arabidopsis thaliana >gi_456509_emb_CAA53180_
                   (X75431) ASK-gamma (Arabidopsis shaggy-related kinase)
                   [Arabidopsis thaliana] >gi_2059329_emb_CAA73247_ (Y12710)
                  shaggy-like kinase gamma [Arabidopsis thaliana]
                  118060
Seq. No.
                  1167_1.R1010
Contig ID
                  jC-aTXLIB327435P2d12a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1890352
BLAST score
                  890
E value
                  7.0e-96
Match length
                  171
% identity
NCBI Description
                  (X91398) transcription factor L2 [Arabidopsis thaliana]
                  118061
Seq. No.
                  1167 2.R1010
Contig ID
5'-most EST
                  g2413981
Method
                  BLASTX
NCBI GI
                  q2088643
BLAST score
                  255
E value
                  9.0e-22
Match length
                  92
% identity
NCBI Description
                   (AF002109) transcription factor SF3 isolog [Arabidopsis
                  thaliana]
Seq. No.
                  118062
                  1167 3.R1010
Contig ID
5'-most EST
                  ARABLI-15-Q1-B1-H9
Method
                  BLASTX
NCBI GI
                  g1890352
BLAST score
                   372
E value
                  2.0e-35
Match length
                  83
                  49
% identity
                  (X91398) transcription factor L2 [Arabidopsis thaliana]
NCBI Description
                  118063
Seq. No.
Contig ID
                  1168 1.R1010
5'-most EST
                  jC-atXLIB327409P2g06b1
Method
                  BLASTX
NCBI GI
                  g480725
```

```
E value
                     0.0e + 00
Match length
                     584
                     99
% identity
                     beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis
NCBI Description
                     thaliana >gi_402740_emb_CAA52619_ (X74514)
                     beta-fructofuranosidase [Arabidopsis thaliana]
                     >gi_757536_emb_CAA52620_ (X74515) beta-fructofuranosidase
                     [Arabidopsis thaliana]
Seq. No.
                     118064
                     1171 1.R1010
Contig ID
                     LIB22-031-Q1-E1-G8
5'-most EST
Method
                     BLASTX
NCBI GI
                     q1345644
BLAST score
                     2030
E value
                     0.0e + 00
Match length
                     513
                     100
% identity
                     CYTOCHROME P450 86A1 (CYPLXXXVI) >gi_940446 emb CAA62082
NCBI Description
                     (X90458) cytochrome p450 [Arabidopsis thaliana]
Seq. No.
                     118065
Contig ID
                     1173 1.R1010
5'-most EST
                     PLN_g1495270
                     BLASTX
Method
NCBI GI
                     q3913437
BLAST score
                     264
E value
                     6.0e-22
Match length
                     1039
% identity
                     PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                     \label{eq:helicase} \begin{array}{lll} \texttt{HELICASE} > & \texttt{gi\_1402875\_emb\_CAA66825\_} & \texttt{(X98130)} & \texttt{RNA helicase} \\ \texttt{[Arabidopsis thaliana]} > & \texttt{gi\_1495271\_emb\_CAA66613\_} & \texttt{(X97970)} \end{array}
                     RNA helicase [Arabidopsis thaliana]
Seq. No.
                     118066
Contig ID
                     1174 1.R1010
5'-most EST
                     jC-atXLIB327411P2d12b1
Method
                     BLASTX
NCBI GI
                     q2129634
BLAST score
                     1220
E value
                     1.0e-135
Match length
                     272
% identity
                     92
                     lectin-like protein - Arabidopsis thaliana
NCBI Description
                     >gi_995619_emb_CAA62665_ (X91259) lectin like protein
                    [Arabidopsis thaliana]
Seq. No.
                     118067
                     1174 2.R1010
Contig ID
5'-most EST
                     q906802
Method
                     BLASTN
NCBI GI
                     g995618
BLAST score
                     164
E value
                     6.0e-87
Match length
                     288
% identity
                     90
```

Method

BLASTX

```
NCBI Description A.thaliana mRNA for lectin-like protein
Seq. No.
                  118068
                  1174 3.R1010
Contig ID
5'-most EST
                  ARABL1-039-Q1-E1-D3
Method
                  BLASTN
NCBI GI
                  q995618
BLAST score
                  57
E value
                  4.0e-23
Match length
                  114
% identity
                  93
                  A.thaliana mRNA for lectin-like protein
NCBI Description
                  118069
Seq. No.
                  1175 1.R1010
Contig ID
5'-most EST
                  PLN g1149570
Method
                  BLASTX
NCBI GI
                  g2129754
BLAST score
                  2238
E value
                  0.0e + 00
Match length
                  471
% identity
                  93
NCBI Description
                  translation elongation factor Tu precursor - Arabidopsis
                  thaliana >gi_1149571_emb_CAA61511_ (X89227) mitochondrial
                  elongation factor Tu [Arabidopsis thaliana]
Seq. No.
                  118070
                  1175 2.R1010
Contig ID
5'-most EST
                  LIB3176-005-P1-K1-D5
                  BLASTX
Method
NCBI GI
                  g3924612
BLAST score
                  429
E value
                  3.0e-42
Match length
                  97
% identity
                  87
NCBI Description
                  (AF069442) mitochondrial elongation factor Tu [Arabidopsis
                  thaliana] >gi 4263511 gb AAD15337 (AC004044) mitochondrial
                  elongation factor Tu [Arabidopsis thaliana]
                  118071
Seq. No.
                  1176 1.R1010
Contig ID
5'-most EST
                  jC-atXP89C242K20T7089d1
Method
                  BLASTX
NCBI GI
                  g1709498
BLAST score
                  1288
E value
                  1.0e-142
Match length
                  244
% identity
NCBI Description
                  OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                  >qi 1362001 pir S57524 osmotin precursor - Arabidopsis
                  thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                   [Arabidopsis thaliana]
                  118072
Seq. No.
                  1178 1.R1010
Contig ID
                  PLN g16487
5'-most EST
```

NCBI GI

```
NCBI GI
                    q585914
BLAST score
                    6063
                    0.0e+00
E value
                    1188
Match length
% identity
                    98
                    DNA-DIRECTED RNA POLYMERASE II 135 KD POLYPEPTIDE (RNA
NCBI Description
                    POLYMERASE II SUBUNIT 2) >gi_421848_pir__S30228
                    DNA-directed RNA polymerase (EC 2.7.7.6) II second largest
                    chain - Arabidopsis thaliana >gi_16488_emb_CAA79527
                    (Z19120) RNA polymerase II second largest subunit
                    [Arabidopsis thaliana]
                    118073
Seq. No.
                    1184 1.R1010
Contig ID
                    LIB25-060-Q1-E1-B10
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3661603
BLAST score
                    4205
                    0.0e + 00
E value
Match length
                    814
                    99
% identity
NCBI Description
                    (AF092841) ribonucleoside-diphosphate reductase large
                    subunit [Arabidopsis thaliana]
                    118074
Seq. No.
                    1184 2.R1010
Contig ID
                    jC-atXLIB327411P3h02b1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3661603
BLAST score
                    201
E value
                    9.0e-69
Match length
                    167
% identity
                    86
NCBI Description
                    (AF092841) ribonucleoside-diphosphate reductase large
                    subunit [Arabidopsis thaliana]
Seq. No.
                    118075
                    11:87 1.R1010
Contig ID
                    \mathtt{LIB2}\overline{5} \mathtt{-025}\mathtt{-Q1}\mathtt{-E1}\mathtt{-F12}
5'-most EST
Method
                    BLASTX
NCBI GI
                    g133028
BLAST score
                    806
E value
                    4.0e-86
Match length
                    177
                    93
% identity
                    50S RIBOSOMAL PROTEIN L9, CHLOROPLAST PRECURSOR (CL9)
NCBI Description
                    >gi_71257_pir__R5MUL9 ribosomal protein L9 precursor,
                    chloroplast - Arabidopsis thaliana >gi_16499_emb_CAA77480_(Z11129) plastid ribosomal protein CL9 [Arabidopsis
                    thaliana] >gi 16501 emb CAA77594_ (Z11509) Chloroplast
                    ribosomal protein CL9 [Arabidopsis thaliana]
                    118076
Seq. No.
Contig ID
                    1189 1.R1010
                    PLN_g572522
5'-most EST
                    BLASTX
Method
```

g1076398

```
BLAST score
                   704
                   4.0e-74
E value
Match length
                   150
% identity
                   87
NCBI Description
                   ribosomal protein L2 - Arabidopsis thaliana
                   >gi_572523_emb_CAA57902_ (X82556) ribosomal protein L2
                   [Arabidopsis thaliana]
Seq. No.
                   118077
                   1190 1.R1010
Contig ID
5'-most EST
                   LIB25-030-Q1-E1-E9
Method
                   BLASTX
NCBI GI
                   q1710424
BLAST score
                   876
E value
                   2.0e-94
Match length
                   204
% identity
                   87
NCBI Description
                   50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21)
                   >gi 2129718 pir S71282 ribosomal protein L21 - Arabidopsis
                   tha\overline{1}iana \overline{9} 11\overline{49}573 emb CAA89887 (Z49787) chloroplast
                   ribosomal large subunit protein L21 [Arabidopsis thaliana]
Seq. No.
                   118078
                   1193 1.R1010
Contig ID
5'-most EST
                   PLN g3559763
                   BLASTX
Method
NCBI GI
                   q2801433
BLAST score
                   1108
E value
                   1.0e-121
Match length
                   221
                   92
% identity
                   (AF017991) salt stress inducible small GTP binding protein
NCBI Description
                   Ran1 homolog [Arabidopsis thaliana] >gi 3559764 (U75601)
                   unknown [Arabidopsis thaliana]
Seq. No.
                   118079
                   1194 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327410P4b12b1
Method
                   BLASTX
                   q2058282
NCBI GI
BLAST score
                   668
E value
                   9.0e-70
Match length
                   153
% identity
NCBI Description
                   (X97377) atranbpla [Arabidopsis thaliana]
                   118080
Seq. No.
                   1194_2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327428P1q04b2
Method
                   BLASTX
NCBI GI
                   q2058284
BLAST score
                   839
E value
                   7.0e-90
Match length
                   217
% identity
                   79
```

NCBI Description (X97378) atranbp1b [Arabidopsis thaliana]

```
Seq. No.
                   118081
                   1194 10.R1010
Contig ID.
                   jC-alXLIB327435P3a05b1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2058281
BLAST score
                   397
                   0.0e + 00
E value
                   504
Match length
                   97
% identity
NCBI Description
                  A.thaliana mRNA for AtRanBPla protein
Seq. No.
                   118082
                   1196 1.R1010
Contig ID
5'-most EST
                   PLN_g1707365
                  BLASTX
Method
                   q4033467
NCBI GI
BLAST score
                   1190
E value
                   1.0e-131
Match length
                   251
% identity
                   91
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP31
NCBI Description
                  >gi_1707366_emb_CAA67798_ (X99435) splicing factor
                   [Arabidopsis thaliana]
                   118083
Seq. No.
Contig ID
                  1196_2.R1010
                  LIB24-122-Q1-E1-F11
5'-most EST
Method
                  BLASTX
                   q4033467
NCBI GI
BLAST score
                   189
                   3.0e-14
E value
Match length
                   36
% identity
                   100
NCBI Description
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP31
                  >gi_1707366_emb_CAA67798_ (X99435) splicing factor
                   [Arabidopsis thaliana]
                  118084
Seq. No.
Contig ID
                  1197_1.R1010
                  PLN_g2582640
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4033468
BLAST score
                   1267
E value
                   1.0e-140
Match length
                   350
                  73
% identity
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP40
NCBI Description
                  >gi_2582641_emb_CAA67800_ (X99437) splicing factor
                   [Arabidopsis thaliana] >gi_2980800_emb_CAA18176_ (AL022197)
                  splicing factor At-SRp40 [Arabidopsis thaliana]
                  118085
Seq. No.
                  1197 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327402Pla03b1
Method
                  BLASTX
NCBI GI
                  q4033469
```

```
E value
                  1.0e-134
Match length
                  341
                  73
% identity
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP41
NCBI Description
                  >gi 1707370 emb CAA67799 (X99436) splicing factor
                  [Arabidopsis thaliana]
Seq. No.
                  118086
                  1197_3.R1010
Contig ID
5'-most EST
                  LIB23-035-Q1-E112-E2
Method
                  BLASTX
NCBI GI
                  q4033469
                  199
BLAST score
                  2.0e-15
E value
                  40
Match length
                  93
% identity
NCBI Description
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP41
                  >gi 1707370 emb CAA67799 (X99436) splicing factor
                  [Arabidopsis thaliana]
                  118087
Seq. No.
Contig ID
                  1197 4.R1010
5'-most EST
                  LIB24-096-Q1-E1-E10
Method
                  BLASTX
NCBI GI
                  a4033468
                  194
BLAST score
                  7.0e-15
E value
Match length
                  36
                  100
% identity
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP40
NCBI Description
                  >gi 2582641 emb CAA67800 (X99437) splicing factor
                  [Arabidopsis thaliana] >gi_2980800_emb_CAA18176_ (AL022197)
                  splicing factor At-SRp40 [Arabidopsis thaliana]
                  118088
Seq. No.
Contig ID
                  1197 5.R1010
                  jC-atXLIB327409P2b03b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  a4033469
                  703
BLAST score
                  6.0e-74
E value
Match length
                  248
% identity
                  52
NCBI Description
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP41
                  >gi_1707370_emb_CAA67799_ (X99436) splicing factor
                  [Arabidopsis thaliana]
                  118089
Seq. No.
                  1199_1.R1010
Contig ID
5'-most EST
                  g315663
Method
                  BLASTX
                  q3435096
NCBI GI
                  497
BLAST score
                  7.0e-50
E value
Match length
                  129
                  75
% identity
                  (AF033587) SRZ21 [Arabidopsis thaliana]
NCBI Description
```

```
118090
Seq. No.
                   1200 1.R1010
Contig ID
                   jC-atXLIB327423P3g11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                  g3281869
BLAST score
                   509
E value
                   3.0e-51
Match length
                   200
% identity
                   55
NCBI Description
                   (AL031004) RSZp22 splicing factor [Arabidopsis thaliana]
                   >gi_3435094_gb_AAD12769.1_ (AF033586) 9G8-like SR protein
                   [Arabidopsis thaliana]
                   118091
Seq. No.
Contig ID
                   1200 2.R1010.
5'-most EST
                   jC-atXP114C231O16T7s1
                   BLASTN
Method
NCBI GI
                   q2582644
BLAST score
                   352
                   0.0e + 00
E value
Match length
                   375
% identity
                   99
NCBI Description Arabidopsis thaliana mRNA for RSZp22 splicing factor
                   118092
Seq. No.
                   1201 1.R1010
Contig ID
5'-most EST
                  LIB35-015-Q1-E1-H12
                  BLASTX
Method
NCBI GI
                   q1565227
BLAST score
                   1001
E value
                  1.0e-109
Match length
                   227
% identity
                   83
NCBI Description
                   (X95573) salt-tolerance zinc finger protein [Arabidopsis
                   thaliana]
                   118093
Seq. No.
Contig ID
                   1202 1.R1010
5'-most EST
                   jC-atXLIB327417P2g12b1
Method
                   BLASTX
NCBI GI
                   q4056504
BLAST score
                   689
E value
                   4.0e-83
Match length
                   178
% identity
                   (AC005896) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   118094
Contig ID
                   1203 1.R1010
5'-most EST
                   PLN g1418336
Method
                  BLASTX
NCBI GI
                  g1418325
BLAST score
                   549
E value
                   3.0e-82
Match length
                   160
```

```
% identity
                   (X98674) zinc finger protein [Arabidopsis thaliana]
NCBI Description
                   >gi 1418337 emb CAA67231 (X98673) zinc finger protein
                   [Arabidopsis thaliana]
                   118095
Seq. No.
                   1204 1.R1010
Contig ID
                   jC-aTXP118C144L6T7022d2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1418327
BLAST score
                   1296
                   1.0e-143
E value
                   284
Match length
% identity
                   89
                   (X98675) zinc finger protein [Arabidopsis thaliana]
NCBI Description
                   >gi 1418339 emb CAA67236 (X98678) zinc finger protein
                   [Arabidopsis thaliana]
                   118096
Seq. No.
                   1208 1.R1010
Contig ID
                   jC-atXP87CG10G5T7b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2244750
BLAST score
                   2471
                   0.0e + 00
E value
                   485
Match length
                   97
% identity
NCBI Description
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                   >qi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
                   118097
Seq. No.
Contig ID
                   1208 2.R1010
                   jC-atXP96C248G6T7b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2244750
BLAST score
                   842
E value
                   2.0e-90
Match length
                   161
                   99
% identity
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
NCBI Description
                   >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
                   118098
Seq. No.
                   1208 3.R1010
Contig ID
                   jC-aTXP92C246M24T7010d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2244750
BLAST score
                   63
                   1.0e-26
E value
Match length
                   67
                   90
% identity
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
NCBI Description
                   >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
```

[Arabidopsis thaliana]

```
Seq. No.
                   118099
                   1208 4.R1010
Contig ID
                   jC-atXLIB327416P3d12b1
5'-most EST
                   BLASTX .
Method
                   q2244750
NCBI GI
BLAST score
                   429
                   5.0e-42
E value
                   81
Match length
% identity
                   100
NCBI Description
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                   >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
                   118100
Seq. No.
Contig ID
                   1208_6.R1010
                   q435\overline{1}76
5'-most EST
Method
                   BLASTX
                   g2244750
NCBI GI
                   169
BLAST score
                   1.0e-11
E value
Match length
                   36
                   86
% identity
NCBI Description
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                   >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
                   118101
Seq. No.
Contig ID
                   1208 7.R1010
5'-most EST
                   jC-atXP95CH2A1T7071b1
Method
                   BLASTN
                   g984910
NCBI GI
BLAST score
                   41
                   1.0e-13
E value
Match length
                   53
                   48
% identity
                   Plasmid pBSL168 cloning vector, complete sequence
NCBI Description
                   118102
Seq. No.
Contig ID
                   1208 10.R1010
5'-most EST
                   jC-atXP95CH2A1T7071d1
Method
                   BLASTX
NCBI GI
                   g3242075
BLAST score
                   342
E value
                   8.0e-32
Match length
                   177
                   95
% identity
                   (Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis
NCBI Description
                   thaliana]
                   118103
Seq. No.
Contig ID
                   1208_11.R1010
5'-most EST
                   g2748444
Method
                   BLASTX
                  _..g2244750
NCBI GI
BLAST score
                   1333
E value
                   1.0e-147
Match length
                   445
```

```
67
% identity
NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
               >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
                   118104
Seq. No.
                   1208 12.R1010
Contig ID
5'-most EST
                   jC-atXP44C170K7T7030a1
Method
                   BLASTX
                   q1710840
NCBI GI
                   753
BLAST score
                   5.0e-80
E value
                   147
Match length
                   94
% identity
                   ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) (CYTOKININ BINDING PROTEIN CBP57) >gi_441217_dbj_BAA03709_ (D16138) S-adenosyl-L-homocystein
                   hydrolase [Nicotiana sylvestris] >gi_1857024_dbj_BAA08142
                   (D45204) S-adenosyl-L-homocysteine hydrolase [Nicotiana
                   tabacum] >gi 2588781 dbj BAA23164 (D49804)
                   S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum]
                   118105
Seq. No.
                   1208 13.R1010
Contig ID
5'-most EST
                   g2748561
Method
                   BLASTN
                   g2244747
NCBI GI
BLAST score
                   257
E value
                   1.0e-142
                   398
Match length
% identity
                   94
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   118106
                   1210 1.R1010
Contig ID
                   g2762232
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2129733
BLAST score
                   1973
E value
                   0.0e + 00
Match length
                   391
% identity
                   97
                   serine O-acetyltransferase (EC 2.3.1.30) SAT1 precursor -
NCBI Description
                   Arabidopsis thaliana >gi 1184048 (U22964) serine
                   acetyltransferase [Arabidopsis thaliana]
                   118107
Seq. No.
                   1211 1.R1010
Contig ID
                   PLN \overline{g}3660466
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3660467
BLAST score
                   1719
                   0.0e+00
E value
Match length
                   347
                   97
% identity
                  (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis
NCBI Description
```

thaliana] Seq. No. 118108 1212 1.R1010 Contig ID 5'-most EST jC-atXLIB327422P1a06b1 Method BLASTX NCBI GI g3660469 BLAST score 2104 E value 0.0e+00Match length 421 % identity 100 NCBI Description (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] >gi_4512693_gb_AAD21746.1 (AC006569) succinyl-CoA ligase beta subunit [Arabidopsis thaliana] 118109 Seq. No. 1212 2.R1010 Contig ID 5'-most EST q906907 Method BLASTX NCBI GI q3660469 BLAST score 875 E value 3.0e-94 304 Match length % identity 61 NCBI Description (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] >gi 4512693 gb AAD21746.1 (AC006569) succinyl-CoA ligase beta subunit [Arabidopsis thaliana] Seq. No. 118110 Contig ID 1213 1.R1010 jC-aIX24006Q1E1D11b1 5'-most EST Method BLASTX NCBI GI q1711572 BLAST score 1674 E value 0.0e + 00Match length 345 94 % identity SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR NCBI Description (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) >gi_1076415_pir__S30579 succinate--CoA ligase (GDP-forming) (EC 6.2.1.4) alpha chain - Arabidopsis thaliana (fragment) >gi_16510_emb_CAA48891_ (X69138) succinate--CoA ligase (GDP-forming) [Arabidopsis thaliana] Seq. No. 118111 Contig ID 1214 1.R1010 5'-most EST LIB23-017-Q1-E1-E10 -Method BLASTX

5'-most EST LIB23-017
Method BLASTX

NCBI GI g3660471

BLAST score 3074

E value 0.0e+00

Match length 634

% identity 92

NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha

subunit [Arabidopsis thaliana]

Seq. No. 118112

NCBI GI

q322596

```
1214 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327415P1d06b1
Method
                  BLASTX
NCBI GI
                  g3660471
BLAST score
                  1004
E value
                  1.0e-109
Match length
                  191
                  99
% identity
NCBI Description
                  (AJ001809) succinate dehydrogenase flavoprotein alpha
                  subunit [Arabidopsis thaliana]
Seq. No.
                  118113
Contig ID
                  1215 1.R1010
5'-most EST
                  LIB3176-034-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2244970
BLAST score
                  3271
E value
                  0.0e + 00
Match length
                  647
% identity
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 2326365 emb CAA74765 (Y14423) putative cell wall
                  protein [Arabidopsis thaliana]
Seq. No.
                  118114
                  1217 1.R1010
Contig ID
                  jC-atXLIB327431P1b09a1
5'-most EST
Method
                  BLASTX
                  q1944518
NCBI GI
BLAST score
                  2482
                  0.0e + 00
E value
                  472
Match length
% identity
                  100
NCBI Description
                  (Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana]
                  >gi_3047105 (AF058919) protein kinase [Arabidopsis
                  thaliana]
                  118115
Seq. No.
Contig ID
                  1219 1.R1010
5'-most EST
                  LIB23-067-Q1-E1-C8
                  BLASTX
Method
NCBI GI
                  q1076416
BLAST score
                  3172
E value
                  0.0e + 00
Match length
                  642
% identity
                  sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor -
NCBI Description
                  Arabidopsis thaliana >gi_2129745_pir__S71437 sulfite
                  reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis
                  thaliana >gi_804953_emb_CAA89154_ (Z49217) sulfite
                  reductase [Arabidopsis thaliana]
                  118116
Seq. No.
                  1221_1.R1010
Contig ID
5'-most EST
                  PLN_g1742968
Method
                  BLASTX
```

```
BLAST score
                   2608
E value
                   0.0e+00
Match length
                   512
                   97
% identity
                  serine/threonine protein kinase (EC 2.7.-.-) AK21 -
NCBI Description
                  Arabidopsis thaliana >gi_166600 (M93023) SNF1-related
                  protein kinase [Arabidopsis thaliana]
                  >gi 1742969 emb CAA64384 (X94757) ser/thr protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   118117
                   1223 1.R1010
Contig ID
                   jC-atXP34C153A24T7a1
5'-most EST
                  BLASTX
Method
NCBI GI
                   q2501448
BLAST score
                   469
E value
                   1.0e-46
Match length
                   90
                   100
% identity
                  UBIQUITIN-LIKE PROTEIN SMT3 >gi_1707372_emb_CAA67923
NCBI Description
                   (X99609) ubiquitin-like protein [Arabidopsis thaliana]
Seq. No.
                   118118
                   1223 2.R1010
Contig ID
                  LIB22-018-Q1-E1-F11
5'-most EST
                   BLASTX
Method
NCBI GI
                  a2501448
BLAST score
                   475
E value
                   1.0e-47
Match length
                   99
                   95
% identity
                  UBIQUITIN-LIKE PROTEIN SMT3 >gi_1707372_emb_CAA67923
NCBI Description
                   (X99609) ubiquitin-like protein [Arabidopsis thaliana]
Seq. No.
                   118119
Contig ID
                  1224 1.R1010
                  jC-atXLIB327404P2d05b1
5'-most EST
                   BLASTX
Method
NCBI GI
                  q2462081
BLAST score
                   500
E value
                   3.0e-50
Match length
                   123
                   80
% identity
NCBI Description
                   (Y09427) squamosa-promoter binding protein like 3
                   [Arabidopsis thaliana]
                   118120
Seq. No.
Contig ID
                   1225 1.R1010
                   jC-atXLIB327405P2c02b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1765899
BLAST score
                   3258
E value
                   0.0e + 00
Match length
                   607
% identity
NCBI Description
                   (Y07917) Spot 3 protein [Arabidopsis thaliana] >gi 1839244
```

(U86700) EGF receptor like protein [Arabidopsis thaliana]

```
Seq. No.
                   118121
 Contig ID
                   1227_1.R1010
                   PLN g479046
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   q629561
                   1755
 BLAST score
 E value
                   0.0e + 00
Match length
                   358
                   96
 % identity
                   SRG1 protein - Arabidopsis thaliana
 NCBI Description
                   >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis
                   thaliana
                   118122
 Seq. No.
                   1229 2.R1010
 Contig ID
                   jC-atXLIB327426P3g05a1
 5'-most EST
 Method
                   BLASTN
 NCBI GI
                   g1405439
 BLAST score
                   450
                   0.0e + 00
 E value
                   450
Match length
                   100
 % identity
NCBI Description A.thaliana mRNA for SRG3 protein, 5'
Seq. No.
                   118123
                   1230_1.R1010
Contig ID
                   LIB23-061-Q1-E1-B5
 5'-most EST
                   BLASTX
Method
                   g2208946
NCBI GI
BLAST score
                   520
                   2.0e-52
E value
Match length
                   116
                   91
 % identity
NCBI Description
                   (Y10116) signal recognition particle subunit 14
                   [Arabidopsis thaliana]
Seq. No.
                   118124
                   1231_1.R1010
· Contig ID
 5'-most EST
                   jC-alXLIB327436P2e04b1
Method
                   BLASTX
 NCBI GI
                   g2129532
 BLAST score
                   1975
                   0.0e + 00
 E value
Match length
                   407
                   93
 % identity
                   acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -
 NCBI Description
                   Arabidopsis thaliana >gi_1107507_emb_CAA63746_ (X93461)
                   acyl-[acyl-carrier protein] desaturase [Arabidopsis
                   thaliana]
 Seq. No.
                   118125
                   1231_2.R1010
 Contig ID
 5'-most EST
                   g2749180
                   BLASTN
Method
 NCBI GI
                   g2281081
```

Method

BLASTX

```
0.0e+00
E value
Match length
                  420
% identity
                  96
                  Arabidopsis thaliana chromosome II BAC F18019 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  118126
Seq. No.
                  1232 1.R1010
Contig ID
5'-most EST
                  PLN g1419387
Method
                  BLASTX
NCBI GI
                  q1419388
BLAST score
                  1437
E value
                  1.0e-160
Match length
                  295
                  92
% identity
                  (X98925) stromal ascorbate peroxidase [Arabidopsis
NCBI Description
                  thaliana]
                  118127
Seq. No.
                  1232 2.R1010
Contig ID
                  jC-atXP92C249A12T7067d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4263818
BLAST score
                  651
                  6.0e-68
E value
                  187
Match length
% identity
                  65
NCBI Description
                  (AC006067) unknown protein [Arabidopsis thaliana]
Seq. No.
                  118128
                  1232 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327427P2e01b1
Method
                  BLASTN
NCBI GI
                  q4263813
BLAST score
                  275
                  1.0e-153
E value
Match length
                  513
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T13P21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  118129
Seq. No.
                  1232 4.R1010
Contig ID
                  jC-atXLIB327427P4f05b2
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4263813
                  271
BLAST score
E value
                  1.0e-150
Match length
                  387
% identity
                  95
                  Arabidopsis thaliana chromosome II BAC T13P21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  118130
Seq. No.
Contig ID
                  1233 1.R1010
5'-most EST
                  LIB3168-015-P1-K1-D5
```

```
NCBI GI
                  q1061040
                  1879
BLAST score
                  0.0e + 00
E value
                  353
Match length
% identity
                  100
NCBI Description
                  (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]
                  >gi 1587694_prf 2207220A sterol C-methyltransferase
                  [Arabidopsis thaliana]
                  118131
Seq. No.
Contig ID
                  1233_3.R1010
5'-most EST
                  g2763202
Method
                  BLASTX
                  q1061040
NCBI GI
BLAST score
                  508
E value
                  2.0e-51
Match length
                  104
% identity
                  93
NCBI Description
                  (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]
                  >gi_1587694_prf__2207220A sterol C-methyltransferase
                  [Arabidopsis thaliana]
                  118132
Seq. No.
Contig ID
                  1234 1.R1010
5'-most EST
                  LIB25-061-Q1-E1-F9
                  BLASTX
Method
NCBI GI
                  g1565225
BLAST score
                  1208
E value
                  1.0e-133
Match length
                  248
                  92
% identity
NCBI Description
                  (X95572) salt-tolerance protein [Arabidopsis thaliana]
Seq. No.
                  118133
                  1235 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327409P2h11b1
Method
                  BLASTX
NCBI GI
                  q134976
BLAST score
                  2581
E value
                  0.0e + 00
Match length
                  522
% identity
                  95
                  GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi 81619 pir S12042
NCBI Description
                  glucose transport protein STP1 - Arabidopsis thaliana
                  >gi_16520_emb_CAA39037_ (X55350) glucose transporter
                  [Arabidopsis thaliana]
                  118134
Seq. No.
Contig ID
                  1235_3.R1010
5'-most EST
                  g906549
Method
                  BLASTX
NCBI GI
                  g134976
BLAST score
                  212
E value
                  8.0e-20
Match length
                  65
% identity
                  86
NCBI Description
                  GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi_81619_pir__S12042
```

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```
[Arabidopsis thaliana]
                   118135
Seq. No.
Contig ID
                   1236 1.R1010
                   jC-atXLIB327415P2a01b2
5'-most EST'
                   BLASTX
Method
NCBI GI
                   g99758
BLAST score
                   2523
                   0.0e + 00
E value
Match length
                   514
% identity
                   95
                  monosaccharid transport protein STP4 - Arabidopsis thaliana
NCBI Description
                   >gi_16524_emb_CAA47325_ (X66857) sugar transport protein
                   [Arabidopsis thaliana]
                   118136
Seq. No.
                   1237 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327412P3c06b1
Method
                   BLASTX
                   g2501056
NCBI GI
BLAST score
                   2345
E value
                   0.0e + 00
Match length
                   451
% identity
                   100
                  SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
NCBI Description
                  >gi 2129737 pir S71293 seryl-tRNA synthetase - Arabidopsis
                  thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA
                   Synthetase [Arabidopsis thaliana]
                   118137
Seq. No.
                   1239 1.R1010
Contig ID
5'-most EST
                   jC-atX24048Q1E2C11b1
Method
                  BLASTX
                   g3287687
NCBI GI
BLAST score
                   2578
                   0.0e + 00
E value
Match length
                   512
                   98
% identity
                   (AC003979) Match to sucrose-proton symporter (SUC2) gene
NCBI Description
                  gb X75382 from A. thaliana. [Arabidopsis thaliana]
                  118138
Seq. No.
Contig ID
                  1240 1.R1010
5'-most EST
                   jC-atXLIB327432P4g09b1
Method
                  BLASTX
NCBI GI
                  g481132
BLAST score
                   2453
E value
                  0.0e + 00
Match length
                  513
                  93
% identity
                  sucrose transport protein SUC1 - Arabidopsis thaliana
NCBI Description
                  >gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter
                   [Arabidopsis thaliana]
```

glucose transport protein STP1 - Arabidopsis thaliana >gi_16520_emb_CAA39037_ (X55350) glucose transporter

118139

Seq. No.

```
1240 3.R1010
Contig ID
                   jC-a\overline{1}X25084Q1E1C08b1
5'-most EST
Method
                   BLASTX
                   q481132
NCBI GI
                   490
BLAST score
E value
                   1.0e-49
Match length
                   114
                   82
% identity
                   sucrose transport protein SUC1 - Arabidopsis thaliana
NCBI Description
                   >gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter
                   [Arabidopsis thaliana]
Seq. No.
                   118140
                   1241 1.R1010
Contig ID
                   LIB2\overline{2}-019-Q1-E1-C2
5'-most EST
                   BLASTX
Method
                   g1495273
NCBI GI
BLAST score
                   3181
                   0.0e+00
E value
                   734
Match length
                   86
% identity
NCBI Description (Z50752) sugar transporter [Arabidopsis thaliana]
                   118141
Seq. No.
                   1242 1.R1010
Contig ID
                   jC-atXLIB327408P2h10b1
5'-most EST
Method
                   BLASTX
                   g2072626
NCBI GI
BLAST score
                   283
                   4.0e-60
E value
                   134
Match length
                   92
% identity
                   (Y12904) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3281856_emb_CAA19751_ (AL031004) Transcription factor
                   II homolog [Arabidopsis thaliana]
                   118142
Seq. No.
                   1242 5.R1010
Contig ID
5'-most EST
                   g958<u>1</u>58
Method
                   BLASTN
                   g2072625
NCBI GI
BLAST score
                   169
                   4.0e-90
E value
                   313
Match length
                   98
% identity
                   A.thaliana mRNA for homologue of human TAFII30 and yeast
NCBI Description
                   TAFII25/23
                   118143
Seq. No.
                   1243_1.R1010
Contig ID
                   LIB3177-062-P1-K1-C9
5'-most EST
                   BLASTX
Method
                   g1419390
NCBI GI
                   1906
BLAST score
                   0.0e + 00
E value
Match length
                   380
                   96
% identity
```

```
NCBI Description (X98926) thylakoid-bound ascorbate peroxidase [Arabidopsis
                  thaliana]
                  118144
Seq. No.
                  1243 3.R1010
Contig ID
                  g204<del>7</del>578
5'-most EST
Method
                  BLASTN
                  g1419389
NCBI GI
BLAST score
                  377
                  0.0e + 00
E value
                  431
Match length
                  98
% identity
NCBI Description A.thaliana mRNA for thylakoid-bound ascorbate peroxidase
Seq. No.
                  118145
                  1244 1.R1010
Contig ID
                  LIB3175-019-P1-K1-F5
5'-most EST
                  BLASTX
Method
                  g2196466
NCBI GI
BLAST score
                  2542
                  0.0e + 00
E value
Match length
                  527
                  95
% identity
                  (Y13673) TATA binding protein-associated factor
NCBI Description
                  [Arabidopsis thaliana]
                  118146
Seq. No.
                  1249 1.R1010
Contig ID
                  PLN_{g}^{-1}6545
5'-most EST
                  BLASTX
Method
                  g135627
NCBI GI
                  998
BLAST score
E value
                  1.0e-108
Match length
                  197
                  100
% identity
                  TRANSCRIPTION INITIATION FACTOR TFIID-2 (TATA-BOX FACTOR 2)
NCBI Description
                  (TATA SEQUENCE-BINDING PROTEIN 2) (TBP-2)
                  >gi_99764_pir__S10945 transcription initiation factor IID
                  (clone At-1) - Arabidopsis thaliana >gi_16546_emb_CAA38742_
                  (X54995) transcription initiation factor II [Arabidopsis
                  thaliana] >gi_4204264 (AC005223) 43453 [Arabidopsis
                  thaliana] >gi 227073 prf 1613452A transcription initiation
                  factor TFIID-1 [Arabidopsis thaliana]
                  118147
Seq. No.
                  1249 2.R1010
Contig ID
5'-most EST
                  g935930
Method
                  BLASTX
                  g135626
NCBI GI
BLAST score
                  1014
                  1.0e-110
E value
Match length
                  200
% identity
                  100
NCBI Description
                  TRANSCRIPTION INITIATION FACTOR TFIID-1 (TATA-BOX FACTOR 1)
                  (TATA SEQUENCE-BINDING PROTEIN 1) (TBP-1)
                  >gi 99763 pir S10946 transcription initiation factor IID
                  (clone At-2) - Arabidopsis thaliana >gi_1943466_pdb_1VOK_A
```

```
Chain A, Arabidopsis Thaliana Tbp (Dimer)
>gi 1943467_pdb_1VOK_B Chain B, Arabidopsis Thaliana Tbp
(Dimer) >gi_1943469 pdb 1VOL B Chain B, Tfiib (Human Core
Domain) TBP (A. THALIANA) TATA ELEMENT Ternary Complex
>gi_16548_emb_CAA38743_ (X54996) transcription initiation
factor II [Arabidopsis thaliana] >gi 227074 prf 1613452B
transcription initiation factor TFIID-2 [Arabidopsis
thaliana]
```

```
118148
Seq. No.
                   1251 1.R1010
Contig ID
                   PLN g16549
5'-most EST
                   BLASTX
Method
                   g320563
NCBI GI
BLAST score
                   1889
                   0.0e + 00
E value
                   368
Match length
% identity
NCBI Description
```

118149

transcription factor tgal - Arabidopsis thaliana >gi_16550_emb_CAA48189_ (X68053) transcription factor [Arabidopsis thaliana]

Seq. No. 1251 3.R1010 Contig ID 5'-most EST g2758892 Method BLASTX g320563 NCBI GI BLAST score 490 E value 2.0e-49 Match length 150 % identity 68

transcription factor tgal - Arabidopsis thaliana NCBI Description >gi_16550_emb_CAA48189_ (X68053) transcription factor [Arabidopsis thaliana]

118150 Seq. No. 1252 2.R1010 Contig ID 5'-most EST jC-atXLIB327410P2c05a1 Method BLASTN

NCBI GI g2924729 BLAST score 426 0.0e + 00E value Match length 438 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MNA5, complete sequence [Arabidopsis thaliana]

Seq. No. 118151 1254 1.R1010 Contig ID 5'-most EST PLN g516864 BLASTX Method NCBI GI g1168251 BLAST score 1675 E value 0.0e+00 Match length 313 100 % identity

PROBABLE CYSTEINE PROTEINASE A494 PRECURSOR NCBI Description

Seq. No.

Contig ID 5'-most EST

118156

q2748230

1259_3.R1010

```
>gi_1076384_pir__S46535 probable cysteine proteinase (EC
3.4.22.-) (clone A1494) - Arabidopsis thaliana (fragment)
>gi_516865_emb_CAA52403_ (X74359) putative thiol protease
                     [Arabidopsis thaliana]
                    118152
Seq. No.
                    1255 1.R1010
Contig ID
                    PLN g_{992959}
5'-most EST
Method
                    BLASTX
                    q2117426
NCBI GI
BLAST score
                    609
                    3.0e-63
E value
Match length
                    118
% identity
                    100
                    thioredoxin - Arabidopsis thaliana >gi 992960 emb CAA84610
NCBI Description
                     (Z35473) thioredoxin [Arabidopsis thaliana]
Seq. No.
                    118153
                    1258 1.R1010
Contig ID
5'-most EST
                    jC-atXLIB327427P4c01b2
Method
                    BLASTX
NCBI GI
                    q2117425
BLAST score
                    610
E value
                    3.0e-63
Match length
                    118
                    100
% identity
NCBI Description
                    thioredoxin - Arabidopsis thaliana >gi 992966 emb CAA84613
                     (Z35476) thioredoxin [Arabidopsis thaliana]
                    118154
Seq. No.
                    1259 1.R1010
Contig ID
5'-most EST
                    LIB3177-050-P1-K2-B7
Method
                    BLASTX
NCBI GI
                    q2262173
BLAST score
                    1808
E value
                    0.0e + 00
Match length
                    379
% identity
                    94
NCBI Description
                    (AC002329) NADPH thioredoxin reductase [Arabidopsis
                    thalianal
                    118155
Seq. No.
Contig ID
                    1259 2.R1010
5'-most EST
                    PLN_g468525
Method
                    BLASTX
NCBI GI
                    g2500129
BLAST score
                    1654
E value
                    0.0e + 00
Match length
                    332
% identity
                    96
                    THIOREDOXIN REDUCTASE 1 (NADPH-DEPENDENT THIOREDOXIN
NCBI Description
                    REDUCTASE 1) (NTR 1) >gi 468526 emb_CAA80656_ (Z23109)
                    Thioredoxin reductase [Arabidopsis thaliana]
```

```
BLASTX
Method
NCBI GI
                   g2262173
BLAST score
                   304
E value
                   2.0e-27
                   109
Match length
                   62
% identity
                   (AC002329) NADPH thioredoxin reductase [Arabidopsis
NCBI Description
                   thaliana]
                   118157
Seq. No.
                   1265 1.R1010
Contig ID
                   LIB3175-026-P1-K1-F10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q267146
BLAST score
                   4178
                   0.0e + 00
E value
                   913
Match length
                   89
% identity
                   DNA TOPOISOMERASE I >gi_99762_pir__S22864 DNA topoisomerase
NCBI Description
                   (EC 5.99.1.2) I - Arabidopsis thaliana
                   >gi_16558_emb_CAA40763_ (X57544) topoisomerase I
[Arabidopsis thaliana] >gi_445137_prf__1908437A
                   topoisomerase I [Arabidopsis thaliana]
                   118158
Seq. No.
                   1265 2.R1010
Contig ID
5'-most EST
                   jC-alXLIB327436P2d02b1
Method
                   BLASTX
NCBI GI
                   g267146
BLAST score
                   137
                   2.0e-63
E value
Match length
                   139
% identity
                   93
NCBI Description
                   DNA TOPOISOMERASE I >gi 99762 pir S22864 DNA topoisomerase
                   (EC 5.99.1.2) I - Arabidopsis thaliana
                   >gi_16558_emb_CAA40763_ (X57544) topoisomerase I
                   [Arabidopsis thaliana] >qi 445137 prf 1908437A
                   topoisomerase I [Arabidopsis thaliana]
Seq. No.
                   118159
                   1266 1.R1010
Contig ID
5'-most EST
                   PLN g1865676
Method
                   BLASTX
NCBI GI
                   g1865677
BLAST score
                   4535
                   0.0e+00
E value
Match length
                   942
                   93
% identity
NCBI Description
                   (Y08568) trehalose-6-phosphate synthase [Arabidopsis
                   thalianal
                   118160
Seq. No.
                   1268 2.R1010
Contig ID
                   LIB3177-033-P1-K2-H11
5'-most EST
                   BLASTN
Method
                   q3702315
NCBI GI
```

E value

```
E value
                  1.0e-134
                   473
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T3F17 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                   118161
Seq. No.
                   1268_3.R1010
Contig ID
                   jC-atXP95CH2A12T7080d1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q2894445
BLAST score
                   3584
                   0.0e + 00
E value
Match length
                   739
% identity
                  (Y14333) transketolase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118162
                  1268 4.R1010
Contig ID
5'-most EST
                   jC-aTXP73CF2G3T7d2
Method
                  BLASTX
NCBI GI
                  q2244912
BLAST score
                 583
E value
                  7.0e-60
Match length
                  129
% identity
                  91
NCBI Description
                  (Z97339) similar to transketolase [Arabidopsis thaliana]
Seq. No.
                  118163
                  1268_5.R1010
Contig ID
                  LIB25-030-Q1-E1-C12
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2894445
BLAST score
                   430
E value
                  2.0e-42
Match length
                  101
% identity .
                  81
                  (Y14333) transketolase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118164
                  1268 8.R1010
Contig ID
5'-most EST
                   jC-atxP95CH2A12T7080b1
Method
                  BLASTX
NCBI GI
                  g2244912
BLAST score
                  142
E value
                  1.0e-08
Match length
                  29
% identity
                  100
                  (Z97339) similar to transketolase [Arabidopsis thaliana]
NCBI Description
                  118165
Seq. No.
                  1269_1.R1010
Contig ID
5'-most EST
                  PLN_g3617769
                  BLASTX
Method
NCBI GI
                  q3617770
BLAST score
                  3453
                  0.0e + 00
```

```
·Match length
                    682
 % identity
                    96
 NCBI Description
                    (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
                    118166
 Seq. No.
                    1271 1.R1010
 Contig ID
                    PLN g_{1841398}
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g1841399
 BLAST score
                    1461
 E value
                    1.0e-163
 Match length
                    297
 % identity
                    96
 NCBI Description
                   (Z34661) AtTFIIB2 [Arabidopsis thaliana]
                    118167
 Seq. No.
 Contig ID
                    1272 1.R1010
 5'-most EST
                    jC-atXLIB327405P3f11b1
 Method
                    BLASTX
 NCBI GI
                    q3929364
 BLAST score
                    1093
 E value
                    1.0e-119
 Match length
                    222
% identity
                    95
                    NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR
 NCBI Description
                    (COMPLEX I-23KD) (CI-23KD) >gi_1076356_pir__S52380 NADH
                    dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana
                    >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase
                    [Arabidopsis thaliana] >gi 3152573 (AC002986) Match to
                    NADH: ubiquinone oxidoreductase gb X84318 from A.thaliana.
                    ESTs gb_Z27005, gb_T04711, gb_T45\overline{0}78 and gb_Z28689 come
                    from this gene. [Arabidopsis thaliana]
 Seq. No.
                    118168
 Contig ID
                    1272_3.R1010
 5'-most EST
                    jC-atXP112C129H11T7a1
 Method
                    BLASTX
 NCBI GI
                    q3929364
 BLAST score
                    615
 E value
                    7.0e-64
 Match length
                    139
 % identity
                    83
                    NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR
 NCBI Description
                    (COMPLEX I-23KD) (CI-23KD) >gi 1076356 pir S52380 NADH
                    dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana
                    >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase
                    [Arabidopsis thaliana] >gi_3152573 (AC002986) Match to
                    NADH: ubiquinone oxidoreductase gb_X84318 from A.thaliana.
                    ESTs gb_Z27005, gb_T04711, gb_T\overline{45078} and gb_Z28689 come
                    from this gene. [Arabidopsis thaliana]
 Seq. No.
                    118169
                    1272 4.R1010
 Contig ID
 5'-most EST
                    jC-atXP31C144L7T7d2
 Method
                    BLASTX
```

NCBI GI g3929364 BLAST score 546

```
6.0e-58
E value
Match length
                   127
% identity
                   91
                  NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-23KD) (CI-23KD) >gi_1076356_pir__ S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana
                   >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase
                   [Arabidopsis thaliana] >gi_3152573 (AC002986) Match to
                   NADH: ubiquinone oxidoreductase gb X84318 from A.thaliana.
                   ESTs gb_Z27005, gb_T04711, gb_T45078 and gb_Z28689 come
                   from this gene. [Arabidopsis thaliana]
                   118170
Seq. No.
                   1274 1.R1010
Contiq .ID
                   LIB3175-039-P1-K1-E8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g462273
BLAST score
                   1115
E value
                   1.0e-122
Match length
                   270
                   83
% identity
NCBI Description
                   IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (IGPD) >gi 437213
                   (U02689) imidazoleglycerolphosphate dehydratase
                   [Arabidopsis thaliana]
                   118171
Seq. No.
Contia ID
                   1275 1.R1010
5'-most EST
                   PLN g541564
Method
                  BLASTX
NCBI GI
                   g115766
BLAST score
                   96
E value
                   6.0e-66
Match length
                   224
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR
                   (CAB) >gi_82243_pir__S00442 chlorophyll a/b-binding protein
                   precursor - garden petunia >gi_169214 (M21317) chlorophyll
                   binding protein precursor [Petunia hybrida]
                   >gi 226259 prf 1503272A chlorophyll binding protein
                   [Petunia sp.]
                   118172
Seq. No.
Contig ID
                   1277 1.R1010
                  LIB22-008-Q1-E1-B5
5'.-most EST
Method
                  BLASTX
NCBI GI
                   q729882
BLAST score
                   1413
E value
                   1.0e-157
Match length
                   282
% identity
                   93
NCBI Description
                  CASEIN KINASE II BETA' CHAIN (CK II)
                  >gi 1076300 pir S47968 casein kinase II (EC 2.7.1.-) beta
                  chain CKB2 - Arabidopsis thaliana >gi 467975 (U03984)
                  casein kinase II beta subunit CKB2 [Arabidopsis thaliana]
                  >gi 2245122 emb CAB10544 (Z97343) unnamed protein product
```

[Arabidopsis thaliana]

```
118173
Seq. No.
                  1278 1.R1010
Contig ID
                  LIB22-008-Q1-E1-H5
5'-most EST
                  BLASTX
Method
                  g3080449
NCBI GI
                  2555
BLAST score
                  0.0e+00
E value
                  511
Match length
% identity
                  97
                   (AL022605) myo-inositol-1-phosphate synthase [Arabidopsis
NCBI Description
                  thaliana]
                  118174
Seq. No.
                  1278 2.R1010 .
Contig ID
                  LIB3177-094-P1-K1-B12
5'-most EST
Method
                  BLASTX
                  g973313
NCBI GI
BLAST score
                  2634
                  0.0e + 00
E value
                  509
Match length
% identity
                  100
NCBI Description
                  (U30250) myo-inositol 1-phosphate synthase isozyme-2
                   [Arabidopsis thaliana]
                  118175
Seq. No.
                  1278 3.R1010
Contig ID
5'-most EST
                  jC-atXP67C215B1T7012a1
Method
                  BLASTX
                  g1352463
NCBI GI
BLAST score
                  269
                  2.0e-23
E value
Match length
                  57
% identity
                  89
NCBI Description
                  MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi 1161312
                  (U04876) myo-inositol-1-phosphate synthase [Arabidopsis
                  thaliana]
Seq. No.
                  118176
                  1278 6.R1010
Contig ID
5'-most EST
                  jC-atX24025Q1E1F10b1
Method
                  BLASTX
                  g973313
NCBI GI
BLAST score
                  156
E value
                  5.0e-20
                  52
Match length
% identity
                  100
NCBI Description
                  (U30250) myo-inositol 1-phosphate synthase isozyme-2
                  [Arabidopsis thaliana]
                  118177
Seq. No.
                  1279 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327428P4d12b2
Method
                  BLASTX
NCBI GI
                  g452470
BLAST score
                  2363
                  0.0e+00
E value
```

463

Match length

```
% identity
                  (U05218) ATP sulfurylase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118178
                  1279 2.R1010
Contig ID
                  g496480
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3421109
BLAST score
                  1047
E value
                  1.0e-114
Match length
                  204
% identity
                  100
                  (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  118179
                  1279 3.R1010
Contig ID
5'-most EST
                  LIB3168-043-P1-K1-E1
                  BLASTX
Method
                  g2129744
NCBI GI
                  2432
BLAST score
E value
                  0.0e + 00
Match length
                  465
                  100
% identity
                  sulfate adenylyltransferase (EC 2.7.7.4) precursor (clone
NCBI Description
                  APS3) - Arabidopsis thaliana >gi 459144 (U06275) ATP
                  sulfurylase [Arabidopsis thaliana]
                  118180
Seq. No.
                  1279 4.R1010
Contig ID
                  jC-atXmonuni25Aa06b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3421109
                  465
BLAST score
E value
                  1.0e-46
Match length
                  98
                   96
% identity
                   (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
NCBI Description
                  thaliana]
                   118181
Seq. No.
                  1279 10.R1010
Contig ID
5'-most EST
                  ARABL1-045-Q1-E1-C1
Method
                  BLASTX
                  g452470
NCBI GI
BLAST score
                   251
                   1.0e-21
E value
Match length
                   45
                  100
% identity
NCBI Description (U05218) ATP sulfurylase [Arabidopsis thaliana]
                   118182
Seq. No.
                   1281 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327422P4h08a1
Method
                   BLASTX
                   g1076366
NCBI GI
```

Contig ID

```
E value
                  4.0e-84
Match length
                  148
                  100
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis
NCBI Description
                  thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans
                  isomerase [Arabidopsis thaliana] >gi 992643 (U32186)
                  cyclophilin [Arabidopsis thaliana]
                  >gi 1091580 prf 2021266A peptidyl-Pro cis-trans isomerase
                  [Arabidopsis thaliana]
Seq. No.
                  118183
Contig ID
                  1281_2.R1010
                  jC-atXP89C245E7T7056d1
5'-most EST
Method
                  BLASTX
                  q1076366
NCBI GI
BLAST score
                  911
E value
                  2.0e-98
Match length
                  172
                  100
% identity
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis
                  thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans
                  isomerase [Arabidopsis thaliana] >gi 992643 (U32186)
                  cyclophilin [Arabidopsis thaliana]
                  >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase
                  [Arabidopsis thaliana]
                  118184
Seq. No.
Contig ID
                  1281 4.R1010
5'-most EST
                  q935818
Method
                  BLASTX
                  g1076366
NCBI GI
BLAST score
                  621
E value
                  1.0e-64
Match length
                  155
% identity
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis
                  thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans
                  isomerase [Arabidopsis thaliana] >gi 992643 (U32186)
                  cyclophilin [Arabidopsis thaliana]
                  >gi 1091580 prf 2021266A peptidyl-Pro cis-trans isomerase
                  [Arabidopsis thaliana]
Seq. No.
                  118185
Contig ID
                  1283_1.R1010
                  jC-aTXLIB327416P4c10b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g520478
BLAST score
                  1762
                  0.0e + 00
E value
Match length
                  363
% identity
                  (U09137) pyruvate dehydrogenase El beta subunit
NCBI Description
                  [Arabidopsis thaliana] >gi_1090498_prf__2019230A pyruvate
                  dehydrogenase [Arabidopsis thaliana]
                  118186
Seq. No.
```

1283 2.R1010

```
g3449704
5'-most EST
                  BLASTX
Method
                  g520478
NCBI GI
                   192
BLAST score
                   2.0e-14
E value
                 40
Match length
                  95
% identity
                   (U09137) pyruvate dehydrogenase E1 beta subunit
NCBI Description
                   [Arabidopsis thaliana] >gi_1090498_prf__2019230A pyruvate
                  dehydrogenase [Arabidopsis thaliana]
                  118187
Seq. No.
Contig ID
                  1283 4.R1010
5'-most EST
                  g2763095
                  BLASTX
Method
                  g520478
NCBI GI
BLAST score
                   258
                   6.0e-27
E value
                  92
Match length
                  79
% identity
                   (U09137) pyruvate dehydrogenase El beta subunit
NCBI Description
                   [Arabidopsis thaliana] >gi_1090498_prf__2019230A pyruvate
                  dehydrogenase [Arabidopsis thaliana]
                  118188
Seq. No.
Contig ID
                  1289 1.R1010
                  LIB24-071-Q1-E1-F8
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2980771
                   2281
BLAST score
                  0.0e+00
E value
Match length
                   448
                  94
% identity
                   (AL022198) chloroplast omega-6 fatty acid desaturase (fad6)
NCBI Description
                   [Arabidopsis thaliana]
                  118189
Seq. No.
                  1290 1.R1010
Contig ID
5'-most EST
                  PLN g1709235
Method
                  BLASTX
                  g2507222
NCBI GI
BLAST score
                  2824
                  0.0e+00
E value
                  581
Match length
                  95
% identity
                  KINASE ASSOCIATED PROTEIN PHOSPHATASE >gi_1709236 (U09505)
NCBI Description
                  kinase associated protein phosphatase [Arabidopsis
                  thaliana]
                  118190
Seq. No.
Contig ID
                  1292_1.R1010
5'-most EST
                  LIB23-067-Q1-E1-E12
Method
                  BLASTX
NCBI GI
                  g1171771
BLAST score
                  1847
E value
                  0.0e + 00
Match length
                  355
```

```
% identity
                   NITRILASE 4 >qi 508737 (U09961) nitrilase [Arabidopsis
NCBI Description
                    thaliana]
                    118191
Seq. No.
                    1293 1.R1010
Contig ID
                   LIB22-029-Q1-E1-F8
5'-most EST
                   BLASTX
Method
NCBI GI
                    g2494174
BLAST score
                    2607
E value
                    0.0e + 00
Match length
                    502
% identity
                    100
                   GLUTAMATE DECARBOXYLASE 1 (GAD 1) >qi 497979 (U10034)
NCBI Description
                   glutamate decarboxylase [Arabidopsis thaliana]
Seq. No.
                    118192
                    1294 1.R1010
Contig ID
                    PLN g1353238
5'-most EST
                   BLASTX
Method
NCBI GI
                    q1353239
BLAST score
                    5972
E value
                    0.0e + 00
                    1291
Match length
                    90
% identity
                   (U10245) putative RNA helicase A [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    118193
                    1295 1.R1010
Contig ID
5'-most EST
                   LIB22-033-Q1-E2-H2
                   BLASTX
Method
NCBI GI
                    q571330
BLAST score
                    4155
E value
                    0.0e + 00
Match length
                    802
% identity
                   (U11034) ent-kaurene synthetase A [Arabidopsis thaliana]
NCBI Description
                   >gi_4263508_gb_AAD15334_ (AC004044) ent-kaurene synthetase
                   A [Arabidopsis thaliana]
                    118194
Seq. No.
                    1296 1.R1010
Contig ID
5'-most EST
                   PLN_{g}511795
Method
                   BLASTX
NCBI GI
                    g2129611
BLAST score
                    936
E value
                    1.0e-101
Match length
                    195
                    95
% identity
NCBI Description
                   heat shock protein HSP22.0 - Arabidopsis thaliana
                   >gi_511796 (U11501) AtHSP22.0 [Arabidopsis thaliana]
>gi_3695402 (AF096373) contains similarity to heat shock
                   hsp20 proteins (Pfam: PF00011, E=1.2e-46 [Arabidopsis
                   thaliana] >gi_4538954_emb_CAB39778.1_ (AL049488) heat shock protein 22.0 [Arabidopsis thaliana]
                   >gi 1094856 prf 2106413A small heat shock protein
                    [Arabidopsis thaliana]
```

```
118195
Seq. No.
                   1297 1.R1010
Contig ID
                   g936<del>2</del>63
5'-most EST
Method
                   BLASTX
                   q1169837
NCBI GI
BLAST score
                   339
                   1.0e-31
E value
Match length
                   99 -
                   75
% identity
NCBI Description
                   GIBBERELLIN-REGULATED PROTEIN 3 PRECURSOR
                   >qi 2129590 pir S60231 GAST1 protein homolog (clone GASA3)
                   - Arabidopsis thaliana >qi 887935 (U11764) GAST1 protein
                   homolog [Arabidopsis thaliana]
                   118196
Seq. No.
                   1298 1.R1010
Contig ID
5'-most EST ·
                   g2763430
Method
                   BLASTX
NCBI GI
                   g1169838
BLAST score
                   330
E value
                   1.0e-30
Match length
                   93
% identity
                   70
                  GIBBERELLIN-REGULATED PROTEIN 2 PRECURSOR
NCBI Description
                   >gi 2129589_pir__S60230 GAST1 protein homolog (clone GASA2)
                   - Arabidopsis thaliana >qi 887937 (U11765) GAST1 protein
                  homolog [Arabidopsis thaliana]
                   118197
Seq. No.
                   1299 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327431P1e05a1
Method
                   BLASTX
NCBI GI
                   q2146733
BLAST score
                   458
E value
                   2.0e-45
Match length
                   98
% identity
                   83
                  GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana
NCBI Description
                   118198
Seq. No.
                   1299 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327426P2d02b1
Method
                   BLASTX
                   q2739383
NCBI GI
BLAST score
                   554
E value
                   1.0e-56
                   122
Match length
                   91
% identity
                  (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                   118199
Seq. No.
                   1299 4.R1010
Contig ID
                  LIB35-019-Q1-E1-B9
5'-most EST
                  BLASTX
Method
                  g2146733
NCBI GI
```

```
7.0e-40
 E value
                    75
 Match length
 % identity
                   . 93
 NCBI Description GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana
                    118200
 Seq. No.
                   1300 1.R1010
 Contig ID
                   LIB2\overline{5}-029-Q1-E1-G11
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g1346106
 BLAST score
                    1935
 E value
                    0.0e + 00
 Match length
                    377
 % identity
                    96
                   GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >qi 557694
 NCBI Description
                    (U12232) GTP binding protein beta subunit [Arabidopsis
                    thaliana] >gi_3096915_emb_CAA18825.1 (AL023094) GTP
                   binding protein beta subunit [Arabidopsis thaliana]
                    118201
 Seq. No.
 Contig ID
                    1302_1.R1010
 5'-most EST
                    PLN_g533706
 Method
                   BLASTX
 NCBI GI
                    q533707
 BLAST score
                    3709
· E value
                    0.0e + 00
 Match length
                    715
 % identity
                    100
 NCBI Description
                    (U12536) 3-methylcrotonyl-CoA carboxylase precursor
                    [Arabidopsis thaliana]
                    118202
 Seq. No.
                    1302 3.R1010
 Contig ID
 5'-most EST
                   q2749538
 Method
                    BLASTN
 NCBI GI
                    q4580745
 BLAST score
                    342
 E value
                    0.0e + 00
 Match length
                    443
                    98
 % identity
 NCBI Description
                   Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
                   complete sequence
 Seq. No.
                    118203
                    1304 1.R1010
 Contig ID
 5'-most EST
                    LIB146-013-Q1-E1-C9
 Method
                   BLASTX
 NCBI GI
                    q625973
 BLAST score
                    4476
 E value
                    0.0e + 00
 Match length
                    909
 % identity
                    95
 NCBI Description
                   disease resistance protein RPS2 - Arabidopsis thaliana
                   >gi 548086 (U14158) RPS2 [Arabidopsis thaliana] >gi 549979
                    (U12860) RPS2 [Arabidopsis thaliana]
                   >gi 4538938 emb CAB39674.1 (AL049483) disease resistance
                    protein RPS2 [Arabidopsis thaliana]
```

Contig ID

```
118204
Seq. No.
                   1306 1.R1010
Contig ID
                   PLN g537445
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1170149
BLAST score
                   4191
E value
                   0.0e + 00
Match length
                   896
% identity
NCBI Description
                   HEAT SHOCK PROTEIN 101 >gi 537446 (U13949) AtHSP101
                   [Arabidopsis thaliana]
                   118205
Seq. No.
Contig ID
                   1307 1.R1010
5'-most EST
                   PLN \overline{g}602421
Method
                   BLASTX
NCBI GI
                   q1168493
BLAST score
                   1669
                   0.0e + 00
E value
                   337
Match length
% identity
                   97
                   {\tt ARGINASE} > \!\! gi\_602422 \text{ (U15019) arginase [Arabidopsis}
NCBI Description
                   thaliana] >gi_4325373_gb_AAD17369_ (AF128396) Arabidopsis
                   thaliana arginase (SW:P46637) (Pfam: PF00491, Score=419.6,
                   E=3.7e-142 N=1) [Arabidopsis thaliana]
                   118206
Seq. No.
                   1308 1.R1010
Contig ID
5'-most EST
                   LIB24-092-Q1-E1-B11
Method
                   BLASTX
NCBI GI
                   q1168256
BLAST score
                   2269
                   0.0e + 00
E value
Match length
                   430
% identity
                   100
                   ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi_693688 (U15026) aspartate
NCBI Description
                   aminotransferase [Arabidopsis thaliana] >gi 3201622
                    (AC004669) aspartate aminotransferase [Arabidopsis
                   thaliana]
                   118207
Seq. No.
Contig ID
                   1309 1.R1010
5'-most EST
                   LIB3176-015-P1-K1-E4
                   BLASTX
Method
NCBI GI
                   q1168257
BLAST score
                   2084
                   0.0e + 00
E value
Match length
                   405
                   100
% identity
                   ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC ISOZYME 1
NCBI Description
                    (TRANSAMINASE A) >gi 693690 (U15033) aspartate
                   aminotransferase [Arabidopsis thaliana]
                   118208
Seq. No.
```

1310_1.R1010

Match length

```
jC-atXLIB327439P1a06b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1168258
BLAST score
                  2214
E value
                  0.0e+00
Match length
                  449
% identity
                  96
                  ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (TRANSAMINASE A) >gi 693692 (U15034) aspartate
                  aminotransferase [Arabidopsis thaliana]
Seq. No.
                  118209
                  1310 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327438P3a06b1
Method
                  BLASTX
NCBI GI
                  g1168258
BLAST score
                  800
E value
                  2.0e-85
Match length
                  206
                  77
% identity
NCBI Description
                  ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR
                  (TRANSAMINASE A) >gi_693692 (U15034) aspartate
                  aminotransferase [Arabidopsis thaliana]
Seq. No.
                  118210
                  1311 1.R1010
Contia ID
5'-most EST
                  PLN g693693
Method
                  BLASTX
NCBI GI
                  g1168259
BLAST score
                  2077
E value
                  0.0e + 00
Match length
                  403
% identity
                  100
                  ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC ISOZYME 2
NCBI Description
                  (TRANSAMINASE A) >gi 693694 (U15035) aspartate
                  aminotransferase [Arabidopsis thaliana]
Seq. No.
                  118211
                  1315 1.R1010
Contig ID
5'-most EST
                  jC-atXP89C245F9T7096d1
Method
                  BLASTX
NCBI GI
                  g1172977
BLAST score
                  918
E value
                   3.0e-99
Match length
                  187
                  97
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
                  ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                  118212
                  1315 2.R1010
Contig ID
                  LIB22-064-Q1-E1-F6
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1172977
BLAST score
                  532
                  3.0e-54
E value
```

```
97
% identity
                  60S RIBOSOMAL PROTEIN L18 >qi 606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                  118213
                  1315 4.R1010
Contig ID
5'-most EST .
                  jC-atXLIB327426P3f08b1
Method
                  BLASTX
NCBI GI
                  g1172977 -
BLAST score
                   613
E value
                  1.0e-63
Match length
                  145
                  87
% identity
                  60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                  118214
                  1315 7.R1010
Contig ID
5'-most EST
                  LIB25-080-Q1-E1-G6
                  BLASTX
Method
NCBI GI
                  q1172977
BLAST score
                  89
E value
                  1.0e-30
Match length
                  82
                  90
% identity
                  60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                  118215
                  1318 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327438P4c12a2
Method
                  BLASTX
NCBI GI
                  g600855
BLAST score
                  1703
E value
                  0.0e + 00
Match length
                  369
% identity
                   90
NCBI Description (U17887) bZIP protein [Arabidopsis thaliana]
Seq. No.
                  118216
                  1318 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327406P2f12b1
Method
                  BLASTX
                  g600855
NCBI GI
                  276
BLAST score
                  3.0e-24
E value
Match length
                  53
                  98
% identity
NCBI Description
                  (U17887) bZIP protein [Arabidopsis thaliana]
                  118217
Seq. No.
                  1321 1.R1010
Contig ID
                  jC-atXP19C113B23T7080a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3005688
BLAST score
                  277
                  1.0e-154
E value
```

Contig ID

```
Match length
                   557
% identity
                   100
                  Arabidopsis thaliana AT4 mRNA sequence
NCBI Description
Seq. No.
                   118218
                   1321 2.R1010
Contig ID
                   PLN g603055
5'-most EST
                   BLASTN
Method
NCBI GI
                   q603055
BLAST score
                   869
E value
                   0.0e + 00
                   977
Match length
% identity
                   100
                  Arabidopsis thaliana inner mitochondrial membrane protein
NCBI Description
                   mRNA, complete cds
                   118219
Seq. No.
                   1322 1.R1010
Contig ID
5'-most EST
                   ARABL1-029-Q1-B1-H7
Method
                   BLASTX
NCBI GI
                   g1362003
BLAST score
                   2680
E value
                   0.0e + 00
Match length
                   513
                                                                                 . .ā... .
% identity
                   100
                   protein phosphatase 2A B regulatory chain 55K - Arabidopsis
NCBI Description
                   thaliana >gi_710330 (U18129) 55 kDa B regulatory subunit of
                   phosphatase ZA [Arabidopsis thaliana]
Seq. No.
                   118220
                   1323 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327415P3c04b1
Method
                   BLASTX
NCBI GI
                   g1361982
BLAST score
                   2715
                   0.0e + 00
E value
Match length
                   561
% identity
                   96
                   4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis
NCBI Description
                   thaliana >gi 609340 (U18675) 4-coumarate--coenzyme A ligase
                   [Arabidopsis thaliana]
Seq. No.
                   118221
                   1323 3.R1010
Contig ID
                   g272\overline{2}499
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1361982
BLAST score
                   288
E value
                   6.0e-26
Match length
                   63
                   89
% identity
                   4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis
NCBI Description
                   thaliana >gi_609340 (U18675) 4-coumarate--coenzyme A ligase
                   [Arabidopsis thaliana]
                   118222
Seq. No.
```

1324 1.R1010

% identity

```
5'-most EST
                   LIB3175-025-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g2146739
BLAST score
                   2320
E value
                   0.0e + 00
                   496
Match length
                   93
% identity
                   hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >qi 881521
NCBI Description
                   (U28214) hexokinase 1 [Arabidopsis thaliana]
Seq. No.
                   118223
                   1324 2.R1010
Contig ID
                   g2393573
5'-most EST
Method
                   BLASTN
                   q881520
NCBI GI
BLAST score
                   354
                   0.0e + 00
E value
Match length
                   420
% identity
                   97
NCBI Description
                   Arabidopsis thaliana hexokinase 1 (AtHXK1) mRNA, complete
                   118224
Seq. No.
                   1325 1.R1010
Contig ID
                   iC-atxLIB327438P1d11a1
5'-most EST
Method
                   BLASTX
                   g4587610
NCBI GI
BLAST score
                   1946
                   0.0e + 00
E value
                   404
Match length
% identity
                   96
NCBI Description
                   (AC006951) putative indole-3-glycerol phosphate synthase
                   precursor [Arabidopsis thaliana]
Seq. No.
                   118225
                   1328 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327415P4f10b1
Method
                   BLASTX
                   g2119046
NCBI GI
BLAST score
                   1116
                   1.0e-122
E value
Match length
                   250
% identity
                   88
                   small nuclear ribonucleoprotein U1A - Arabidopsis thaliana
NCBI Description
                   >gi_1050430_emb_CAA90283_ (Z49991) UlsnRNP-specific protein
[Arabidopsis thaliana] >gi_2529669 (AC002535)
                   UlsnRNP-specific protein, UlA [Arabidopsis thaliana]
Seq. No.
                   118226
                   1329 1.R1010
Contig ID
                   LIB3176-042-P1-K1-A2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g790582
BLAST score
                   468
E value
                   0.0e+00
Match length
                   500
```

```
NCBI Description Arabidopsis thaliana putative pathogenesis-related protein
                  (ATOZI1) mRNA, complete cds
                  118227
Seq. No.
                  1330 1.R1010
Contig ID
5'-most EST
                  g2048061
Method
                  BLASTX
                  q4263525
NCBI GI
                  971
BLAST score
                  1.0e-105
E value
Match length
                  208
% identity
                  90
                  (AC004044) putative photosystem I reaction center subunit
NCBI Description
                  II precursor [Arabidopsis thaliana]
                  118228
Seq. No.
                  1330 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327414P1f08a1
Method
                  BLASTX
                  g4587564
NCBI GI
BLAST score
                  941
                  1.0e-102
E value
Match length
                  182
% identity
                  100
NCBI Description
                  (ACOO6550) Strong similarity to gb_X14017 photosystem I
                  reaction centre subunit II precursor (psaD) from Spinacia
                  oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133,
                  gb N65521, gb T42498, gb T41918, gb N38024
                  118229
Seq. No.
                  1330 4.R1010
Contig ID
                  jC-atXP19C111J15T7050a1
5'-most EST
Seq. No.
                  118230
Contig ID
                  1330_6.R1010
5'-most EST
                  g406837
Method
                  BLASTX
                  q2129549
NCBI GI
BLAST score
                  2758
                  0.0e + 00
E value
Match length
                  533
% identity
                  100
                  calcium-dependent protein kinase (EC 2.7.1.-) CDPK19 -
NCBI Description
                  Arabidopsis thaliana >gi_2129551_pir__S71778
                  calcium-dependent protein kinase 19 - Arabidopsis thaliana
                  >gi 836942 (U20624) calcium-dependent protein kinase
                  [Arabidopsis thaliana] >gi_836948 (U20627)
                  calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.
                  118231
                  1330 7.R1010
Contig ID
5'-most EST
                  jC-atXLIB327426P1d06b1
                  BLASTN
Method
NCBI GI
                  q2582640
BLAST score
                  35
                  6.0e-10
E value
Match length
                  47
```

```
% identity
NCBI Description
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                   factor, RSp40
Seq. No.
                   118232
                   1330 8.R1010
Contig ID
5'-most EST
                   LIB3175-042-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q4587564
BLAST score
                   506
E value
                   3.0e-51
Match length
                   96
                   100
% identity
NCBI Description
                   (AC006550) Strong similarity to gb X14017 photosystem I
                   reaction centre subunit II precursor (psaD) from Spinacia
                   oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133,
                   gb N65521, gb T424\overline{9}8, gb T419\overline{1}8, gb N380\overline{2}4
                   118233
Seq. No.
                   1330 9.R1010
Contig ID
                   jC-a\(\bar{1}\)XLIB327434P4f05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1399277
BLAST score
                   2767
                   0.0e + 00
E value
Match length
                   535
% identity
                   100
NCBI Description
                   (U31836) calmodulin-domain protein kinase CDPK isoform 7
                   [Arabidopsis thaliana]
                   118234
Seq. No.
                   1330 13.R1010
Contig ID
                   LIB2\overline{2}-059-Q1-E1-D5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2129549
BLAST score
                   473
                   2.0e-47
E value
Match length
                   88
% identity
                   calcium-dependent protein kinase (EC 2.7.1.-) CDPK19 -
NCBI Description
                   Arabidopsis thaliana >gi_2129551_pir__S71778
                   calcium-dependent protein kinase 19 - Arabidopsis thaliana
                   >gi 836942 (U20624) calcium-dependent protein kinase
                   [Arabidopsis thaliana] >gi_836948 (U20627)
                   calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.
                   118235
Contig ID
                   1331 1.R1010
5'-most EST
                   PLN_g710399
Method
                   BLASTX
                   g1709446
NCBI GI
BLAST score
                   1959
E value
                   0.0e+00
Match length
                   389
% identity
                   96
                  PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT
NCBI Description
                   PRECURSOR (PDHE1-A) >gi_2117533_pir__JC4358 pyruvate
```

```
dehydrogenase (lipoamide) (EC 1.2.4.1) complex E1 alpha
chain - Arabidopsis thaliana mitochondrion >gi_710400
(U21214) pyruvate dehydrogenase E1 alpha subunīt
[Arabidopsis thaliana]
```

```
Seq. No.
                  118236
                  1331_3.R1010
Contig ID
5'-most EST
                  LIB3176-119-P2-K1-F8
                  BLASTX
Method
NCBI GI
                  q2829869
BLAST score
                  465
E value
                  2.0e-46
                  108
Match length
% identity
                  89
                  (AC002396) pyruvate dehydrogenase E1 alpha subunit
NCBI Description
                  [Arabidopsis thaliana]
                  118237
Seq. No.
                  1331 4.R1010
Contig ID
```

 $jC-a\overline{1}X24090Q1E1H04b1$ 5'-most EST Method BLASTX NCBI GI g2829869 BLAST score 612 E value 1.0e-63 Match length 135 % identity 91

(AC002396) pyruvate dehydrogenase E1 alpha subunit NCBI Description

[Arabidopsis thaliana]

118238 Seq. No. 1333 1.R1010 Contig ID PLN g1020154 5'-most EST Method BLASTX q1020155 NCBI GI BLAST score 1273 1.0e-141 E value

236 Match length % identity 100

NCBI Description (U26936) DNA-binding protein [Arabidopsis thaliana]

118239 Seq. No. 1335 1.R1010 Contig ID

jC-atXP73C224A3T7b15'-most EST

Method BLASTX NCBI GI g2146773 BLAST score 664 4.0e-97 E value Match length 182 % identity

NCBI Description senescence-associated protein sen1 - Arabidopsis thaliana

>gi 1046268 (U26944) senescence-associated protein

[Arabidopsis thaliana]

118240 Seq. No. Contig ID 1335_4.R1010 g634811 5'-most EST Method BLASTX

```
NCBI GI
                   g2146773
BLAST score
                   492
E value
                   1.0e-51
Match length
                   129
% identity
                   87
NCBI Description
                   senescence-associated protein sen1 - Arabidopsis thaliana
                   >gi 1046268 (U26944) senescence-associated protein
                   [Arabidopsis thaliana]
Seq. No.
                   118241
Contig ID
                   1335 5.R1010
                   jC-atXP104CE10C5T7b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2129730
BLAST score
                   296
E value
                   2.0e-58
Match length
                   120
% identity
NCBI Description
                   senescence-associated protein sen1 - Arabidopsis thaliana
                   (fragment)
Seq. No.
                   118242
Contig ID
                   1335 6.R1010
5'-most EST
                   q937943
                   BLASTX
Method
                   a2146773
NCBI GI
BLAST score
                   475
E value
                   1.0e-47
Match length
                   112
                   87
% identity
                   senescence-associated protein sen1 - Arabidopsis thaliana
NCBI Description
                   >gi 1046268 (U26944) senescence-associated protein
                   [Arabidopsis thaliana]
Seq. No.
                   118243
                   1335_7.R1010
Contig ID
5'-most EST
                   q1158999
Method
                   BLASTX
NCBI GI
                   q2129729
BLAST score
                   423
E value
                   2.0e-41
Match length
                   158
% identity
                   49
NCBI Description
                   senescence-associated protein sen1 - Arabidopsis thaliana
                   >gi 1046270 (U26945) senescence-associated protein
                   [Arabidopsis thaliana] >gi_3367595_emb_CAA20047_ (AL031135) senescence-associated protein sen1 [Arabidopsis thaliana]
                   >gi_3805843_emb_CAA21463_ (AL031986) senescence-associated
                   protein sen1 [Arabidopsis thaliana]
                   118244
Seq. No.
                   1336 1.R1010
Contig ID
5'-most EST
                   PLN g1353265
Method
                   BLASTX
NCBI GI
                   g1353266
BLAST score
                   1664
```

0.0e + 00

E value

E value

```
Match length
                  339
% identity
                  98
                   (U27590) Fe(II) transport protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3250678 emb CAA19686.1 (AL024486) Fe(II) transport
                  protein [Arabidopsis thaliana] >gi 1589711 prf 2211425A Zn
                transporter [Saccharomyces cerevisiae]
                  118245
Seq. No.
                  1337 1.R1010
Contig ID
                  jC-a\(\bar{1}\)XLIB327435P4f03b1
5'-most EST
Method
                  BLASTX
                  q3219858
NCBI GI
BLAST score
                  601
                  3.0e-62
E value
Match length
                  116
% identity
                  100
                  DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE
NCBI Description
                  >gi 2129724_pir__S71204 RNA polymerase II 13.6 kDa chain -
                  Arabidopsis thaliana >gi 881501 (U28048) RNA polymerase II
                  13.6 kDa subunit [Arabidopsis thaliana]
                  >gi 4678938 emb CAB41329.1 (AL049711) DNA-directed RNA
                  polymerase II 13.6K chain [Arabidopsis thaliana]
                  118246
Seq. No.
                  1338 1.R1010
Contig ID
5'-most EST
                  PLN g1777442
Method
                  BLASTX
NCBI GI
                  g1777443
BLAST score
                  2488
E value
                  0.0e + 00
Match length
                  608
% identity
NCBI Description
                  (U28422) CCA1 [Arabidopsis thaliana] >gi_3510263 (AC005310)
                  DNA-binding protein CCAl [Arabidopsis thaliana] >gi 4090569
                   (U79156) CCA1 [Arabidopsis thaliana]
Seq. No.
                  118247
Contig ID
                  1339 1.R1010
5'-most EST
                  LIB3177-096-P1-K1-D10-
Method
                  BLASTX
NCBI GI
                  g1173327
BLAST score
                  899
E value
                  6.0e-97
Match length
                  249
% identity
                  75
NCBI Description
                  U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A')
                  >gi_322619_pir__S30580 U2 snRNP protein A' - Arabidopsis
                  thaliana >gi_17669_emb_CAA48890_ (X69137) U2 small nuclear
                  ribonucleoprotein A' [Arabidopsis thaliana]
                  118248
Seq. No.
                  1340 1.R1010
Contig ID
5'-most EST
                  PLN g1041703
Method
                  BLASTX
NCBI GI
                  g1041704
BLAST score
                  1050
```

1.0e-114

```
Match length
                  241
% identity
NCBI Description
                  (U30478) expansin At-EXP5 [Arabidopsis thaliana]
                  118249
Seq. No.
Contig ID
                  1341 1.R1010
5'-most EST
                  jC-atXP46C173O7T7078d1
                  BLASTX
Method
NCBI GI
                  q3461837
BLAST score
                  1330
E value
                  1.0e-147
Match length
                  257
                  95
% identity
                  (AC005315) putative expansin [Arabidopsis thaliana]
NCBI Description
                  >gi 3927842 (AC005727) expansin AtEx6 [Arabidopsis
                 · thaliana]
                  118250
Seq. No.
                  1342 1.R1010
Contig ID
                  PLN_g1041707
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1041708
BLAST score
                 1350
E value
                  1.0e-150
Match length
                  244
% identity
                  100
NCBI Description (U30481) expansin At-EXP2 [Arabidopsis thaliana]
                  118251
Seq. No.
                  1343 1.R1010
Contig ID
                  LIB25-056-Q1-E1-B4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1351221
BLAST score
                  1539
E value
                  1.0e-172
Match length
                  312
% identity
                  96
                  TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi_945085
NCBI Description
                  (U31096) transcription factor TFIIB [Arabidopsis thaliana]
                  >gi_2618697 (AC002510) transcription factor TFIIB
                  [Arabidopsis thaliana]
                  118252
Seq. No.
Contig ID
                  1343_2.R1010
5'-most EST
                  LIB25-027-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  q1351221
BLAST score
                  432
                  1.0e-42
E value
Match length
                  130
% identity
                  71
                  TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi 945085
NCBI Description
                  (U31096) transcription factor TFIIB [Arabidopsis thaliana]
                  >gi 2618697 (AC002510) transcription factor TFIIB
                  [Arabidopsis thaliana]
```

118253

Seq. No.

```
1344 1.R1010
Contig ID
                  LIB23-029-Q1-E1-E5
5'-most EST
                  BLASTX
Method
                  g1399265
NCBI GI
BLAST score
                  2654
                   0.0e + 00
E value
                   541
Match length
% identity
                   96
NCBI Description
                   (U31751) calmodulin-domain protein kinase CDPK isoform 9
                   [Arabidopsis thaliana]
Seq. No.
                  118254
                  1344 4.R1010
Contig ID
                  g2048480
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1399264
BLAST score
                  375
E value
                , 0.0e+00
Match length
                  486
                  96
% identity
NCBI Description
                  Arabidopsis thaliana calmodulin-domain protein kinase CDPK
                  isoform 9 (CPK9) mRNA, complete cds
                  118255
Seq. No.
                  1345 1.ŔÎ010
Contig ID
                                                   S. 2 L.
5'-most EST
                  PLN g1399270
Method
                  BLASTX
NCBI GI
                  q1399271
BLAST score
                   3130
E value
                  0.0e + 00
Match length
                   646
% identity
                   95
NCBI Description
                   (U31833) calmodulin-domain protein kinase CDPK isoform 2
                   [Arabidopsis thaliana]
Seq. No.
                  118256
                  1349 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327420P4b09b1
Method
                  BLASTX
NCBI GI
                  q1709825
BLAST score
                  874
E value
                  3.0e-94
Match length
                  171
% identity
                  100
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                   (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                  118257
                  1349 2.R1010
Contig ID
                  LIB23-054-Q1-E1-E7
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2618601
BLAST score
                  485
E value
                  0.0e + 00
Match length
                  627
% identity
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

Contig ID

5'-most EST

```
MHJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   118258
                   1349 4.R1010
Contig ID
5'-most EST
                   g935793
Method
                   BLASTX
                   g1709825
NCBI GI
BLAST score
                   323
E value
                   2.0e-54
Match length
                   168
% identity
                   73
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
                   118259
Seq. No.
Contig ID
                   1350 1.R1010
5'-most EST
                   jC-atXLIB327403P1g07b1
                   BLASTX
Method
NCBI GI
                   g1709794
BLAST score
                   1427
                   1.0e-158
E value
Match length
                   366
% identity
                   80
                   26S PROTEASOME REGULATORY SUBUNIT SSA (MULTIUBIQUITIN CHAIN
NCBI Description
                   BINDING PROTEIN) >gi_1165206 (U33269) MBP1 [Arabidopsis thaliana] >gi_4467150_emb_CAB37519_ (AL035540)
                   multiubiquitin chain binding protein (MBP1) [Arabidopsis
                   thaliana]
                   118260
Seq. No.
                   1351 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327430P1e04b1
Method
                   BLASTX
NCBI GI
                   q3912998
BLAST score
                   1192
E value
                   1.0e-131
Match length
                   237
                   100
% identity
                   FLORAL HOMEOTIC PROTEIN AGL8 >qi 2129536 pir S71208 AGL8
NCBI Description
                   protein - Arabidopsis thaliana >gi 10043\overline{6}5 (\overline{U3}3473) AGL8
                   [Arabidopsis thaliana]
Seq. No.
                   118261
Contig ID
                   1353 1.R1010
5'-most EST
                   jC-alXLIB327435P3c07b1
Method
                   BLASTX
NCBI GI
                   g1345592
BLAST score
                   1206
E value
                   1.0e-133
Match length
                   248
                   96
% identity
NCBI Description 14-3-3-LIKE PROTEIN GF14 EPSILON >gi 1022778 (U36446) GF14
                   epsilon isoform [Arabidopsis thaliana]
                   118262
Seq. No.
                   1356 1.R1010
```

jC-atXLIB327427P3h10b2

NCBI Description

```
Method
                  BLASTX
                  g2129597
NCBI GI
                   2150
BLAST score
                  0.0e+00
E value
Match length
                   411
                   100
% identity
                  glutamate dehydrogenase 1 - Arabidopsis thaliana
NCBI Description
                  >gi 1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis
                   thaliana] >gi 1293095 (U53527) glutamate dehydrogenase 1
                   [Arabidopsis thaliana]
                  118263
Seq. No.
                  1357 1.R1010
Contig ID
                  LIB23-014-Q1-E1-A6
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2129538
BLAST score
                   1842
                  0.0e+00
E value
Match length
                   350
                  100
% identity
NCBI Description
                  AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232)
                  AT103 [Arabidopsis thaliana]
                   118264
Seq. No.
                  1358 1.R1010
Contig ID
5'-most EST
                  LIB3168-044-P1-K1-A9
Method
                  BLASTX
NCBI GI
                   g1053093
BLAST score
                   2817
                   0.0e + 00
E value
Match length
                   558
% identity
                   97
                   (U38550) zeta-carotene desaturase precursor [Arabidopsis
NCBI Description
                  thaliana]
                   118265
Seq. No.
                  1359 1.R1010
Contig ID
                  PLN \overline{g}1145626
5'-most EST
                  BLASTX
Method
                  g2129636
NCBI GI
BLAST score
                   1973
                  0.0e+00
E value
Match length
                   368
                  100
% identity
NCBI Description
                  lipase - Arabidopsis thaliana >gi 1145627 (U38916) lipase
                   [Arabidopsis thaliana]
                  118266
Seq. No.
                  1359 2.R1010
Contig ID
                   jC-atXLIB327406P3h07b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1350680
BLAST score
                  948
                  1.0e-103
E value
Match length
                  188
                  99
% identity
                  60S RIBOSOMAL PROTEIN L1
```

```
Seq. No.
                  118267
                  1359_3.R1010
Contig ID
                  jC-aTXLIB327409P4g07b1
5'-most EST
                  BLASTX
Method
                  g1350680
NCBI GI
BLAST score
                   729
                  2.0e-77
E value
                  145
Match length
% identity
                   96
NCBI Description
                  60S RIBOSOMAL PROTEIN L1
                  118268
Seq. No.
                  1360 1.R1010
Contig ID
                  LIB3177-055-P1-K1-H8
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1063684
BLAST score
                   556
                  7.0e-57
E value
Match length
                  201
                   58
% identity
NCBI Description
                  (U39072) AtGRP2b [Arabidopsis thaliana]
Seq. No.
                  118269
Contig ID
                  1361_1.R1010
5'-most EST
                   jC-atXLIB327427P1f12b1
                  BLASTX
Method
NCBI GI
                  g2494610
BLAST score
                   1546
E value
                  1.0e-172
Match length
                   413
                  79
% identity
NCBI Description
                  CELL DIVISION PROTEIN FTSZ CHLOROPLAST HOMOLOG PRECURSOR
                  >gi_1079732 (U39877) cpFtsZ [Arabidopsis thaliana]
                  118270
Seq. No.
Contig ID
                  1362_1.R1010
5'-most EST
                  PLN_g1122532
Method
                  BLASTX
NCBI GI
                  g2129613
                   2371
BLAST score
                  0.0e+00
E value
Match length
                   610
% identity
                  77
                  homeotic protein BEL1 - Arabidopsis thaliana >gi_1122533
NCBI Description
                   (U39944) BELL1 [Arabidopsis thaliana]
                  118271
Seq. No.
                  1363_1.R1010
Contig ID
5'-most EST
                  PLN_g1100897
Method
                  BLASTX
NCBI GI
                  g1100898
                  3886
BLAST score
                  0.0e + 00
E value
Match length
                  802
% identity
                  (U40154) potassium channel [Arabidopsis thaliana]
NCBI Description
```

. . . .

```
118272
Seq. No.
Contig ID
                   1364 1.R1010
5'-most EST
                   PLN g1209098
                   BLASTX
Method
NCBI GI
                   g2129537
BLAST score
                   2619
                   0.0e + 00
E value
                   553
Match length
% identity
                   90
NCBI Description
                   AP2 domain-containing protein - Arabidopsis thaliana
                   >gi_1209099 (U40256) AINTEGUMENTA [Arabidopsis thaliana]
                   >gi_1244708 (U41339) ANT [Arabidopsis thaliana]
                   >gi_4490720_emb_CAB38923.1_ (AL035709) ovule development
protein aintegumenta (ANT) [Arabidopsis thaliana]
Seq. No.
                   118273
                   1368 1.R1010
Contig ID
                   jC-a\overline{1}XLIB327436P3d11b1
5'-most EST
                   BLASTX
Method
                   q2493541
NCBI GI
BLAST score
                   2667
E value
                   0.0e + 00
Match length
                   492
                   99
% identity
                   CATALASE 1 >qi 1518450 (U43340) catalase 1 [Arabidopsis
NCBI Description
                   thalianal
                   118274
Seq. No.
                   1368 2.R1010
Contig ID
                   jC-atXLIB327408P1h10b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1345684
BLAST score
                   589
E value
                   1.0e-138
Match length
                   317
                   74
% identity
                   CATALASE ISOZYME 3 >gi 536787 emb_CAA85426_ (Z36977)
NCBI Description
                   catalase [Nicotiana plumbaginifolia]
                   118275
Seq. No.
                   1369 1.R1010
Contig ID
                   LIB23-063-Q1-E1-F10
5'-most EST
Method
                   BLASTX
                   q2129770
NCBI GI
BLAST score
                   1690
E value
                   0.0e + 00
Match length
                   332
% identity
                   96
                   xyloglucan endotransglycosylase-related protein XTR-2 -
NCBI Description
                   Arabidopsis thaliana >qi 1244756 (U43487) xyloglucan
                   endotransqlycosylase-related protein [Arabidopsis thaliana]
                   >gi 2154611 dbj BAA20290 (D63510) endoxyloglucan
                   transferase related protein [Arabidopsis thaliana]
```

118276

1369 3.R1010

Seq. No.

Contig ID

BLAST score

```
5'-most EST
                   q402941
Method
                   BLASTN
                   q2351065
NCBI GI
BLAST score
                   251
E value
                   1.0e-139
Match length
                   304
                   95
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MHF15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   118277
                   1370 1.R1010
Contig ID
5'-most EST
                   LIB23-030-Q1-E1-D11
Method
                   BLASTX
NCBI GI
                   q2129771
BLAST score
                   1535
E value
                   1.0e-171
Match length
                   286
                   100
% identity
                   xyloglucan endotransglycosylase-related protein XTR-6 -
NCBI Description
                   Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan
                   endotransglycosylase-related protein [Arabidopsis thaliana]
                   >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1,
4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]
                   118278
Seq. No.
Contig ID
                   1371_1.R1010
5'-most EST
                   a936363
                   BLASTX
Method
NCBI GI
                   q2129772
BLAST score
                   1481
E value
                   1.0e-165
Match length
                   289
% identity
NCBI Description
                   xyloglucan endotransglycosylase-related protein XTR-7 -
                   Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan
                   endotransglycosylase-related protein [Arabidopsis thaliana]
Seq. No.
                   118279
                   1371 2.R1010
Contia ID
                   g1565876
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2129772
BLAST score
                   383
E value
                   9.0e-37
Match length
                   152
                   57
% identity
                   xyloglucan endotransglycosylase-related protein XTR-7 -
NCBI Description
                   Arabidopsis thaliana >gi 1244760 (U43489) xyloglucan
                   endotransglycosylase-related protein [Arabidopsis thaliana]
                   118280
Seq. No.
Contig ID
                   1373 1.R1010
5'-most EST
                   PLN g1754986
Method
                   BLASTX
NCBI GI
                   q3024665
```

```
0.0e + 00
E value
Match length
                     318
                     100
% identity
                    STRICTOSIDINE SYNTHASE 3 PRECURSOR >gi 1754987 (U43946)
NCBI Description
                     strictosidine synthase [Arabidopsis thaliana]
Seq. No.
                     118281
                     1375_1.R1010
Contig ID
                     PLN_g1174152
5'-most EST
                     BLASTX
Method
                     g4115925
NCBI GI
BLAST score
                     1603
E value
                     1.0e-179
Match length
                     336
                     93
% identity
                     (AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
NCBI Description
                     >gi 4539439 emb CAB40027.1 (AL049523) RNA-binding protein
                     [Arabidopsis thaliana]
                     118282
Seq. No.
                     1375 2.R1010
Contig ID
                     jC-atXP74C225C19T7085d1
5'-most EST
Method
                     BLASTX
                     g4115925
NCBI GI
BLAST score
                     637
E value
                     4.0e-66
                     328
Match length
                     46
% identity
                     (AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
NCBI Description
                     >gi 4539439 emb CAB40027.1 (AL049523) RNA-binding protein
                     [Arabidopsis thaliana]
                     118283
Seq. No.
                     1375_3.R1010
Contig ID
5'-most EST
                    LIB23-013-Q1-E1-D7
Method
                     BLASTX
                     g2129727
NCBI GI
BLAST score
                     191
                     3.0e-14
E value
Match length
                     74
                     59
% identity
                    RNA-binding protein 37 - Arabidopsis thaliana >gi_1174153
NCBI Description
                     (U44134) RNA-binding protein [Arabidopsis thaliana]
                     118284
Seq. No.
                     1378_1.R1010
Contig ID
5'-most EST
                     PLN g1184980
Method
                     BLASTX
NCBI GI
                     g2129604
                     1052
BLAST score
E value
                     1.0e-115
                     205
Match length
% identity
                    GTP-binding protein 1 - Arabidopsis thaliana
NCBI Description
                     >gi_2129607_pir__S71584 GTP-binding protein ATBG1 -
```

```
[Arabidopsis thaliana]
                   118285
 Seq. No.
                   1378 2.R1010
 Contig, ID
                   LIB35-007-Q1-E1-C5
 5'-most EST
 Method
                   BLASTX
                   g2129604
 NCBI GI
 BLAST score
                   511
                   5.0e-52
 E value
                   98
 Match length
                   100
 % identity
                   GTP-binding protein 1 - Arabidopsis thaliana
 NCBI Description
                   >gi 2129607 pir S71584 GTP-binding protein ATBG1 -
                   Arabidopsis thaliana >gi 1184981 (U46924) ATGB1
                   [Arabidopsis thaliana]
                   118286
 Seq. No.
 Contig ID
                   1379 1.R1010
 5'-most EST
                   jC-atXLIB327414P2a08b1
 Method
                   BLASTX
                   g2129605
 NCBI GI
 BLAST score
                   1097
                   1.0e-120
 E value
                   211
 Match length
                   100
 % identity
                   GTP-binding protein 2 - Arabidopsis thaliana
 NCBI Description
                   >gi_2129702_pir__S71585 Rab2 homolog GTP-binding protein
                   ATGB2 - Arabidopsis thaliana >gi 1184983 (U46925) ATGB2
                   [Arabidopsis thaliana] >gi_3805852 emb_CAA21472 (AL031986)
                   GTP-binding protein GB2 [Arabidopsis thaliana]
 Seq. No.
                   118287
                   1380 1.R1010
 Contig ID
                   q2757583
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   q4490750
BLAST score
                   1018
                   1.0e-111
 E value
 Match length
                   202
                   100
 % identity
 NCBI Description
                   (AL035708) GTP-binding protein GB3 [Arabidopsis thaliana]
                   118288
 Seq. No.
                   1382 1.R1010
 Contig ID
 5'-most EST
                   jC-atXLIB327426P2e07b1
 Method
                   BLASTX
 NCBI GI
                   g1408473
 BLAST score
                   715
                   2.0e-75
 E value
 Match length
                   137
                   100
 % identity
 NCBI Description
                   (U48939) actin depolymerizing factor 2 [Arabidopsis
                   thaliana]
```

Arabidopsis thaliana >gi 1184981 (U46924) ATGB1

118289

1382 3.R1010

Seq. No.

Contig ID

```
5'-most EST
                  LIB3175-004-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g1408473
BLAST score
                  337
                  2.0e-31
E value
Match length
                  79
% identity
                  84
                  (U48939) actin depolymerizing factor 2 [Arabidopsis
NCBI Description
                  thaliana]
                  118290
Seq. No.
                  1383 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327428P1f10b2
                  BLASTX
Method
                  g2500026
NCBI GI
                  2250
BLAST score
                  0.0e+00
E value
                  480
Match length
                  91
% identity
                  ADENYLOSUCCINATE SYNTHETASE PRECURSOR (IMP--ASPARTATE
NCBI Description
                  LIGASE) >gi 1616657 (U49389) adenylosuccinate synthetase
                   [Arabidopsis thaliana] >gi 4678286 emb CAB41194.1
                   (AL049660) adenylosuccinate synthetase [Arabidopsis
                  thaliana]
                  118291
Seq. No.
                  1383 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327428P1f10a2
Method
                  BLASTX
                  g2500026
NCBI GI
BLAST score
                  231
                  2.0e-22
E value
Match length
                  78
                  76
% identity
                  ADENYLOSUCCINATE SYNTHETASE PRECURSOR (IMP--ASPARTATE
NCBI Description
                  LIGASE) >gi 1616657 (U49389) adenylosuccinate synthetase
                   [Arabidopsis thaliana] >gi 4678286 emb CAB41194.1
                   (AL049660) adenylosuccinate synthetase [Arabidopsis
                  thaliana]
                  118292
Seq. No.
                  1386 1.R1010
Contig ID
5'-most EST
                  LIB22-021-Q1-E1-E4
                  BLASTX
Method
                  q1590814
NCBI GI
BLAST score
                  3479
                  0.0e + 00
E value
                  702
Match ·length
                  95
% identity
                  (U52851) arginine decarboxylase [Arabidopsis thaliana]
NCBI Description
                  118293
Seq. No.
                  1386 2.R1010
Contig ID
5'-most EST
                  jC-a TXLIB327435P2d06a1
                  BLASTX
Method
                  g2271485
NCBI GI
                  3478
BLAST score
```

Contig ID

```
0.0e + 00
E value
Match length
                   711
                   96
% identity
                   (AF009647) arginine decarboxylase [Arabidopsis thaliana]
NCBI Description
                  >gi 3096940 emb_CAA18850.1_ (AL023094) arginine
                   decarboxylase SPE2 [Arabidopsis thaliana]
                   118294
Seq. No.
                   1386 3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327409P1g06b1
Method
                   BLASTX
                  g2271485
NCBI GI
BLAST score
                   1025
                   1.0e-112
E value
                   236
Match length
% identity
                   86
                   (AF009647) arginine decarboxylase [Arabidopsis thaliana]
NCBI Description
                   >gi 3096940 emb CAA18850.1 (AL023094) arginine
                   decarboxylase SPE2 [Arabidopsis thaliana]
Seq. No.
                   118295
Contig ID
                  1386 4.R1010
                  LIB3234-016-P1-K1-G7 :
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4589969
BLAST score
                   394
E value
                   0.0e + 00
Match length
                   478
% identity
                   95
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F1P15 genomic
                   sequence, complete sequence
Seq. No.
                   118296
Contig ID
                   1390 1.R1010
5'-most EST
                   jC-atXLIB327419P2c02b2
Method
                   BLASTX
NCBI GI
                  q1336084
BLAST score
                  2159
E value
                   0.0e + 00
Match length
                   411
% identity
                   100
                   (U56635) Arabidopsis thaliana glutamate dehydrogenase 2
NCBI Description
                   (GDH2) mRNA, complete cds. [Arabidopsis thaliana]
                   118297
Seq. No.
                   1390 3.R1010
Contig ID
5'-most EST
                   g1520887
Method
                  BLASTN
NCBI GI
                  g304040
BLAST score
                   346
E value
                  0.0e + 00
Match length
                   446
% identity
                  95
NCBI Description Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene
Seq. No.
                  118298
```

1390 4.R1010

```
5'-most EST
                  jC-atXP82CG2B12T7d3
                  BLASTX
Method
NCBI GI
                  g1335862
BLAST score
                  1859
                  0.0e+00
E value
Match length
                  418
                  87
% identity
                  (U42608) clathrin heavy chain [Glycine max]
NCBI Description
                  118299
Seq. No.
                  1390 8.R1010
Contig ID
                  LIB25-049-Q1-E1-A4
5'-most EST
                  BLASTX
Method
                  q1336084
NCBI GI
BLAST score
                  200
E value
                  8.0e-48
                  102
Match length
                  98
% identity
                   (U56635) Arabidopsis thaliana glutamate dehydrogenase 2
NCBI Description
                   (GDH2) mRNA, complete cds. [Arabidopsis thaliana]
Seq. No.
                  118300
                  1390 9.R1010
Contig ID
                  LIB3177-019-P1-K2-A11
5'-most EST
                  BLASTX
Method
                  q1335862
NCBI GI
BLAST score
                  324
                  4.0e-30
E value
Match length
                  86
% identity
                  69
                  (U42608) clathrin heavy chain [Glycine max]
NCBI Description
                  118301
Seq. No.
                  1390 10.R1010
Contig ID
5'-most EST
                  g2758561
Method
                  BLASTX
                  q1335862
NCBI GI
BLAST score
                  935
                  1.0e-101
E value
                  202
Match length
% identity
                  91
                  (U42608) clathrin heavy chain [Glycine max]
NCBI Description
                  118302
Seq. No.
                  1391 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P3b12b1
Method
                  BLASTX
NCBI GI
                  g3334323
                  825
BLAST score
                  2.0e-88
E value
                  193
Match length
                  83
% identity
                  GTP-BINDING PROTEIN SAR1A >gi 131,4860 (U56929) Sar1 homolog
NCBI Description
                   [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1
                   (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis
                  thaliana] >gi 2104550 (AF001535) AGAA.4 [Arabidopsis
```

thaliana]

Match length

```
Seq. No.
                   118303
                   1392 1.R1010
Contig ID
                   jC-atXLIB327408P1f12b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1488265
BLAST score
                   1894
                   0.0e+00
E value
Match length
                   446
% identity
                   85
NCBI Description
                   (U57411) high affinity calcium antiporter CAX1 [Arabidopsis
                  thaliana]
Seq. No.
                   118304
                   1392 3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327408P1f12a1
Method
                  BLASTX
NCBI GI
                  q1488265
BLAST score
                   411
E value
                   4.0e-40
Match length
                  76
% identity
                   99
NCBI Description
                  (U57411) high affinity calcium antiporter CAX1 [Arabidopsis
                  thaliana]
                  118305
Seq. No.
Contig ID
                  1393 1.R1010
5'-most EST
                  PLN_g1488266
                  BLASTX
Method
NCBI GI
                  q1488267
BLAST score
                   1966
E value
                  0.0e + 00
Match length
                   399
                   98
% identity
                  (U57412) low affinity calcium antiporter CAX2 [Arabidopsis
NCBI Description
                  thaliana]
                  118306
Seq. No.
Contig ID
                  1393 2.R1010
5'-most EST
                  jC-atXLIB327429P1f06b1
Method
                  BLASTX
NCBI GI
                  q1488267
BLAST score
                   60
E value
                  3.0e-14
Match length
                  173
% identity
                  (U57412) low affinity calcium antiporter CAX2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  118307
Contig ID
                  1393 3.R1010
                  jC-atXLIB327429P1f08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1488267 ·
BLAST score
                  420
E value
                  5.0e-41
```

```
% identity
                  41
                  (U57412) low affinity calcium antiporter CAX2 [Arabidopsis
NCBI Description
                  thaliana]
                  118308
Seq. No.
Contig ID
                  1394 1.R1010
                  LIB25-081-Q1-E1-G10
5'-most EST
                  BLASTX
Method
                  q1762428
NCBI GI
                  3315
BLAST score
                  0.0e + 00
E value
                  622
Match length
                  100
% identity
                  (U59467) aromatic rich glycoprotein JP630 [Arabidopsis
NCBI Description
                  thaliana]
                  118309
Seq. No.
                  1396 1.R1010
Contig ID
                  jC-atXLIB327431P4d02a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1432083
BLAST score
                  691
                  1.0e-72
E value
Match length
                  160
% identity
                  86
                  (U60981) homolog to Skplp, an evolutionarily conserved
NCBI Description
                  kinetochore protein in budding yeast [Arabidopsis thaliana]
                  >gi 3068807 (AF059294) Skpl homolog [Arabidopsis thaliana]
                  >gi 3719209 (U97020) UIP1 [Arabidopsis thaliana]
Seq. No.
                  118310
                  1396 2.R1010
Contig ID
5'-most EST
                  q241\overline{4}083
Method
                  BLASTX
                  g1432083
NCBI GI
                  164
BLAST score
E value
                  5.0e-11
                  82
Match length
                  52
% identity
                  (U60981) homolog to Skplp, an evolutionarily conserved
NCBI Description
                  kinetochore protein in budding yeast [Arabidopsis thaliana]
                  >gi 3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana]
                  >gi 3719209 (U97020) UIP1 [Arabidopsis thaliana]
                  118311
Seq. No.
                  1396 3.R1010
Contig ID
5'-most EST
                  q937736
                  BLASTX
Method
NCBI GI
                  g1432083
BLAST score
                  184
                  5.0e-48
E value
Match length
                  131
% identity
                  80
                  (U60981) homolog to Skplp, an evolutionarily conserved
NCBI Description
                  kinetochore protein in budding yeast [Arabidopsis thaliana]
                  >gi 3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana]
```

12825

>gi 3719209 (U97020) UIP1 [Arabidopsis thaliana]

NCBI GI

```
118312
Seq. No.
                   1398 1.R1010
Contig ID
                   PLN g1502429
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1502430
BLAST score
                   2411
                   0.0e + 00
E value
Match length
                   534
% identity
NCBI Description
                   (U62331) phosphate transporter [Arabidopsis thaliana]
                   >gi_2564661 (AF022872) phosphate transporter [Arabidopsis
                   thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)
                   phosphate transporter, AtPT2 [Arabidopsis thaliana]
Seq. No.
                   118313
Contig ID
                   1401 1.R1010
                   jC-aTXLIB327422P2f08b2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1732509
BLAST score
                   800
E value
                   4.0e-85
                   183
Match length
% identity
                   85
                   (U62741) putative cytoskeletal protein [Arabidopsis
NCBI Description
                   thalianal
                   118314
Seq. No.
                   1401 2.R1010
Contig ID
                   LIB3176-033-P1-K1-E11
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4376087
BLAST score
                   266
E value
                   1.0e-148
Match length
                   433
                   99
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
                   118315
Seq. No.
                   1402 1.R1010
Contig ID
5'-most EST
                   LIB3176-097-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   q1732511
BLAST score
                   830
                   6.0e-89
E value
Match length
                   162
% identity
                   100
NCBI Description
                   (U62742) Ran binding protein 1 homolog [Arabidopsis
                   thalianal
                   118316
Seq. No.
                   1404 1.R1010
Contig ID
                   jC-atXLIB327405P3b04b1
5'-most EST
Method
                   BLASTN
```

q1732514

Contig ID

```
BLAST score
                   1307
E value
                   0.0e+00
Match length
                   1307
                   100
% identity
NCBI Description
                  Arabidopsis thaliana myosin heavy chain-like protein mRNA,
                   complete cds
                   118317
Seq. No.
                   1405 1.R1010
Contig ID
                  LIB22-032-Q1-E1-E7
5'-most EST
Method
                  BLASTX
NCBI GI
                   g1732517
BLAST score
                   3685
                   0.0e + 00
E value
                   754
Match length
% identity
                   94
                   (U62745) putative cytoskeletal protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   118318
Contig ID
                   1407 1.R1010
5'-most EST
                   LIB3177-092-P1-K1-B12
Method
                  BLASTX
NCBI GI
                   q1762584
BLAST score
                   3076
E value
                   0.0e + 00
Match length
                   610
% identity
                   (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   118319
                   1407_3.R1010
Contig ID
5'-most EST
                   jC-atX24076Q1E1G04a1
Method
                   BLASTX
                   q3176680
NCBI GI
                   180
BLAST score
E value
                   4.0e-13
Match length
                   79
                   97
% identity
                   (AC003671) Identical to polygalacuronase isoenzyme 1 beta
NCBI Description
                   subunit homolog mRNA gb U63373. EST gb AA404878 comes from
                   this gene. [Arabidopsis thaliana]
                   118320
Seq. No.
                  1409 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327420P1f03b1
Method
                  BLASTX
NCBI GI
                  q1498064
BLAST score
                   135
                   2.0e-51
E value
Match length
                  106
                  93
% identity
NCBI Description
                  (U64825) AtEl [Arabidopsis thaliana]
                  118321
Seq. No.
```

1410 1.R1010

% identity

```
5'-most EST
                   PLN g1518058
Method
                   BLASTX
                   g1518059
NCBI GI
BLAST score
                   618
                   4.0e-64
E value
                   222
Match length
                   59
% identity
                   (U65650) blue-copper binging protein III [Arabidopsis
NCBI Description
                   thaliana] >gi_3395770 (AF039404) uclacyanin 3 [Arabidopsis
                   thaliana]
                   118322
Seq. No.
Contig ID
                   1411 1.R1010
5'-most EST
                   LIB3234-089-P1-K1-A12
                   BLASTX
Method
NCBI GI
                   g1778141
BLAST score
                   1810
                   0.0e + 00
E value
                   408
Match length
                   90
% identity
                   (U66321) phosphate/phosphoenolpyruvate translocator
NCBI Description
                   precursor; PPT [Arabidopsis thaliana]
                   118323
Seq. No.
                   1414_1.R1010
Contig ID
                   LIB3177-088-P1-K1-D7
5'-most EST
                   BLASTX
Method
                   g1575699
NCBI GI
BLAST score
                   1780
                   0.0e + 00
E value
                   356
Match length
                   96
% identity
                   (U70478) putative leucoanthocyanidin dioxygenase
NCBI Description
                   [Arabidopsis thaliana] >gi_3292813_emb_CAA19803_ (AL031018)
                   putative leucoanthocyanidin dioxygenase (LDOX) [Arabidopsis
                   thaliana]
Seq. No.
                   118324
Contig ID
                   1416 1.R1010
5'-most EST
                   PLN g1575751
Method
                   BLASTX
                   g1575752
NCBI GI
BLAST score
                   604
                   1.0e-102
E value
Match length
                   212
% identity
                   93
                   (U70672) glutathione S-transferase [Arabidopsis thaliana]
NCBI Description
                   118325
Seq. No.
                   1420 1.R1010
Contig ID
5'-most EST
                   jC-a\overline{1}XLIB327436P3b07b1
Method
                   BLASTX
NCBI GI
                   g1657617
BLAST score
                   1742
                   0.0e + 00
E value
Match length
                   392
```

5'-most EST

```
NCBI Description (U72503) G2p [Arabidopsis thaliana] >qi 3068707 (AF049236)
                  putative nuclear DNA-binding protein G2p [Arabidopsis
                  thaliana]
Seq. No.
                  118326
                  1421 1.R1010
Contig ID
                  PLN g1657618
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1657619
BLAST score
                  3073
E value
                  0.0e + 00
Match length
                  588
% identity
                  100
                  (U72504) G5p [Arabidopsis thaliana] >qi 3068710 (AF049236)
NCBI Description
                  putative transmembrane protein G5p [Arabidopsis thaliana]
Seq. No.
                  118327
                  1422 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327416P4d03b1
Method
                  BLASTX
NCBI GI
                  q1657621
BLAST score
                  2207
E value
                  0.0e + 00
Match length
                  436
% identity
                  97
                  (U72505) G6p [Arabidopsis thaliana] >qi 3068711 (AF049236)
NCBI Description
                  putative acyl-coA dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  118328
                  1422 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327423P4g02b1
Method
                  BLASTN
NCBI GI
                  g3068702
BLAST score
                  416
E value
                  0.0e + 00
Match length
                  443
% identity
                  99
NCBI Description
                  Arabidopsis thaliana putative transmembrane protein Glp
                  (AtG1), putative nuclear DNA-binding protein G2p (AtG2),
                  Eml protein (ATEM1), putative chlorophyll synthetase
                  (AtG4), putative transmembrane protein G5p (AtG5), put
Seq. No.
                  118329
                  1422 4.R1010
Contig ID
                  g2047751
5'-most EST
Method
                  BLASTN
NCBI GI
                  q1657620
BLAST score
                  333
E value
                  0.0e + 00
Match length ·
                  455
% identity
                  95
                  Arabidopsis thaliana putative acyl-coA dehydrogenase G6p
NCBI Description
                  (AtG6) mRNA, complete cds
Seq. No.
                  118330
                  1424 1.R1010
Contig ID
```

jC-atXLIB327424P1d09b2

5'-most EST

```
BLASTX
Method
                   g1644427
NCBI GI
                   1274
BLAST score
                   1.0e-141
E value
Match length
                   256
                   96
% identity
NCBI Description
                   (U74610) glyoxalase II [Arabidopsis thaliana]
Seq. No.
                   118331
                   1424 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327424P1e10b2
Method
                   BLASTX
                   g1644427
NCBI GI
BLAST score
                   688
                   4.0e-72
E value
Match length
                   281
                   79
% identity
                   (U74610) glyoxalase II [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118332
                   1424_3.R1010
LIB25-051-Q1-E1-H4
Contig ID
5'-most EST
Method
                   BLASTN
                   g1644426
NCBI GI .
BLAST score
                   96
                   2.0e-46
E value
Match length
                   252
% identity
                   99
                   Arabidopsis thaliana putative glyoxalase II mRNA, complete
NCBI Description
                   cds
Seq. No.
                   118333
                   1424 4.R1010
Contig ID
5'-most EST
                   jC-atXLIB327424P1e09a1
Method
                   BLASTX
NCBI GI
                   g1644427
BLAST score
                   453
E value
                   4.0e-45
Match length
                   93
% identity
                   95
                   (U74610) glyoxalase II [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118334
                   1429 1.R1010
Contig ID
                   PLN g1769567
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2443751
BLAST score
                   2503
E value
                   0.0e + 00
Match length
                   492
% identity
                   100
                   (AF020303) fumarase [Arabidopsis thaliana] >qi 2529676
NCBI Description
                   (AC002535) putative fumarase [Arabidopsis thaliana]
                   118335
Seq. No.
                   1431 1.R1010
Contig ID
```

jC-atXLIB327409P2h04b1

```
Method
                  BLASTX
                  g1800147
NCBI GI
BLAST score
                  1235
                  1.0e-136
E value
Match length
                  265
                  89
% identity
                  (U83655) membrane associated protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118336
                  1431 4.R1010
Contig ID
                  q2749640
5'-most EST
Method
                  BLASTX
                  q1800147
NCBI GI
BLAST score
                  344
                  3.0e-32
E value
Match length
                  95
                  75
% identity
                  (U83655) membrane associated protein [Arabidopsis thaliana]
NCBI Description
                  118337
Seq. No.
Contig ID
                  1433 1.R1010
                  PLN g1814423
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1814424
BLAST score
                  3469
E value
                  0.0e + 00
Match length
                  737
% identity
                  92
                  (U85254) homeodomain protein AHDP [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118338
Contig ID
                  1436 1.R1010
5'-most EST
                  PLN g22657
Method
                  BLASTX
                  q1174853
NCBI GI
BLAST score
                  397
E value
                  3.0e-38
Match length
                  154
% identity
                  52
                  UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)
                  >gi 481811 pir S39483 ubiquitin-conjugating enzyme UBC2-1
                  - Arabidopsis thaliana >gi 22658 emb CAA48378 (X68306)
                  ubiquitin-conjugating enzyme [Arabidopsis thaliana]
                  118339
Seq. No.
Contig ID
                  1439 1.R1010
5'-most EST
                  jC-atX25094Q1E1H06b1
Method
                  BLASTX
NCBI GI
                  q2129759
BLAST score
                  1817
                  0.0e + 00
E value
Match length
                  351
% identity
                  99
                  UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana
NCBI Description
                  >gi 1143392 emb CAA90941 (Z54214) uridine diphosphate
```

glucose epimerase [Arabidopsis thaliana]

5'-most EST

```
118340
Seq. No.
                  1440 1.R1010
Contig ID
                  LIB23-020-Q1-E1-H4
5.'-most EST
                  BLASTX
Method
                  g1155261
NCBI GI
BLAST score
                  2233
                  0.0e+00 ··
E value
Match length
                  436
                  100
% identity
NCBI Description
                  (U40217) eukaryotic release factor 1 homolog [Arabidopsis
                  thalianal
Seq. No.
                  118341
                  1442 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327424P1c01b2
Method
                  BLASTX
NCBI GI
                  g3600058
BLAST score
                  1152
E value
                  1.0e-126
Match length
                  230
% identity
                  100
NCBI Description
                  (AF080120) similar to vacuolar ATPases [Arabidopsis
                  thaliana]
                  118342
Seq. No.
Contia ID
                  1442 7.R1010
5'-most EST
                  jC-atXLIB327425P1h03b1
Method
                  BLASTX
NCBI GI
                  g3334409
BLAST score
                  143
E value
                  7.0e-45
Match length
                  101
% identity
                  96
NCBI Description
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
                  >gi 2129765 pir S71261 V-type proton-ATPase - Arabidopsis
                  thaliana >gi_11.43394_emb_CAA63086_ (X92117) V-type
                  proton-ATPase [Arabidopsis thaliana]
                  118343
Seq. No.
                  1444 1.R1010
Contig ID
5'-most EST
                  g1216724
Method
                  BLASTX
NCBI GI
                  g1172806
BLAST score
                  1172
E value
                  1.0e-129
Match length
                  220
% identity
                  100
NCBI Description
                  60S RIBOSOMAL PROTEIN L10 (WILM'S TUMOR SUPPRESSOR PROTEIN
                  HOMOLOG) >gi_478401_pir__JQ2244 ribosomal protein L10.e,
                  cytosolic - Arabidopsis thaliana >gi_17682_emb_CAA78856_
                  (Z15157) Wilm's tumor suppressor homologue [Arabidopsis
                  thaliana]
Seq. No.
                  118344
                  1444_3.R1010
Contig ID
```

LIB35-042-Q1-E1-C12

```
BLASTX
Method
NCBI GI
                   g4262180
BLAST score
                   673
                   1.0e-70
E value
Match length
                   180
% identity
                   68
                   (AC005508) 29621 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118345
                   1444 4.R1010
Contig ID
5'-most EST
                   jC-atXLIB327408P1b10b1
Method
                   BLASTX
NCBI GI
                   q4262180
BLAST score
                   900
E value
                   3.0e-97
Match length
                   181
% identity
                   94
NCBI Description
                   (AC005508) 29621 [Arabidopsis thaliana]
Seq. No.
                   118346
Contig ID
                   1444 6.R1010
5'-most EST
                   jC-atXLIB327418P4c06b1
Method
                   BLASTX
                   q1172806
NCBI GI
BLAST score
                   89
                   3.0e-02
E value
Match length
                   140
% identity
                   79
                   60S RIBOSOMAL PROTEIN L10 (WILM'S TUMOR SUPPRESSOR PROTEIN
NCBI Description
                   HOMOLOG) >gi_478401_pir__JQ2244 ribosomal protein L10.e,
                   cytosolic - Arabidopsis thaliana >gi_17682_emb_CAA78856_
                   (Z15157) Wilm's tumor suppressor homologue [Arabidopsis
                   thaliana]
Seq. No.
                   118347
Contig ID
                   1444 8.R1010
                   LIB24-056-Q1-E2-E1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1172813
BLAST score
                   207
E value
                   2.0e-31
Match length
                   72
                   92
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPRESSOR SG12)
                   >gi_1076752_pir__S49596 ribosomal protein L10.e, cytosolic - rice >gi_575357_emb_CAA57340_ (X81692) putative tumor
                   supressor [Oryza sativa]
                   118348
Seq. No.
                   1444 9.R1010
Contig ID
5'-most EST
                   jC-atXP102CE2G6T7081d1
Method
                   BLASTX
NCBI GI
                   g1172813
BLAST score
                   328
E value
                   1.0e-39
Match length
                   114
% identity
                   76
```

```
NCBI Description
                    60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPRESSOR SG12)
                     >gi_1076752_pir__S49596 ribosomal protein L10.e, cytosolic
                     - rice >gi_575357_emb_CAA57340_ (X81692) putative tumor
                     supressor [Oryza sativa]
                     118349
...Seq. No.
                     1445_1.R1010
  Contig ID
                     jC-atXP95CG12E3T7067b1
  5'-most EST
  Method
                     BLASTX
  NCBI GI
                    g2440035
  BLAST score
                     2502
  E value
                     0.0e + 00
                     492
  Match length
                     96
  % identity
                     (X98544) endo-1,4-beta-glucanase [Arabidopsis thaliana]
  NCBI Description
                     118350
  Seq. No.
  Contig ID
                     1446 1.R1010
  5'-most EST
                     PLN g1769906
  Method
                     BLASTX
  NCBI GI
                     g1769907
  BLAST score
                     1441
  E value
                    1.0e-160
  Match length
                     293
  % identity
                     91
  NCBI Description
                    (X92975) xyloglucan endo-transglycosylase [Arabidopsis
                    thaliana]
  Seq. No.
                     118351
                     1447 1.R1010
  Contig ID
  5'-most EST
                    PLN g_{2330567}
  Method
                    BLASTX
  NCBI GI
                    g2330568
  BLAST score
                    5026
  E value
                     0.0e + 00
  Match length
                     976
  % identity
                     99
                    (Y08137) mitochondrial single-subunit DNA-dependent RNA
  NCBI Description
                    polymerase [Arabidopsis thaliana]
                    118352
  Seq. No.
                    1449 1.R1010
  Contig ID
  5'-most EST
                    PLN g2065014
  Method
                    BLASTX
  NCBI GI
                     g3914521
  BLAST score
                    1072
  E value
                    1.0e-117
  Match length
                    203
  % identity
                    100
                    RAS-RELATED PROTEIN RAB7 >gi_2065015_emb_CAA70951_ (Y09821)
  NCBI Description
                    GTP-binding protein Rab7 [Arabidopsis thaliana]
                    >gi_2505866_emb_CAA72904_ (Y12227) GTP-binding protein Rab7
                     [Arabidopsis thaliana] >gi_3287684 (AC003979) Strong
                    similaity to gb_Y09821 GTP-binding protein Rab7 from A.
                    thaliana. EST gb_T76449 comes from this gene. [Arabidopsis
                    thaliana]
```

```
Seq. No.
                   118353
                   1452 1.R1010
Contig ID
                   PLN g2065020
5'-most EST
Method
                   BLASTX
NCBI GI
                   g421855
BLAST score
                   1028
                                    453
E value
                  1.0e-112
Match length
                   251
% identity
                   86
NCBI Description
                  alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana
Seq. No.
                   118354
Contig ID
                   1453 1.R1010
5'-most EST
                   PLN g2072627
Method
                  BLASTX
NCBI GI
                  g2072628 -
BLAST score
                   657
E value
                   4.0e-70
Match length
                   151
                   91
% identity
NCBI Description
                  (Y12641) superoxide dismutase [Arabidopsis thaliana]
Seq. No.
                  118355
Contig ID
                  1454 1.R1010
5'-most EST
                  LIB146-010-Q1-E1-F7
                  BLASTX
Method
NCBI GI
                  q2959730
BLAST score
                   998
E value
                   1.0e-108
Match length
                  263
                  74
% identity
NCBI Description
                   (Y13648) homologous to GATA-binding transcription factors
                   [Arabidopsis thaliana]
Seq. No.
                  118356
Contig ID
                   1454 2.R1010
5'-most EST
                   jC-atXLIB327410P3c07b1
Method
                  BLASTN
NCBI GI
                  a2959729
BLAST score
                   347
E value
                  0.0e + 00
Match length
                  371
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for GATA transcription factor
                  118357
Seq. No.
Contig ID
                  1455 1.R1010
5'-most EST
                  jC-atXLIB327411P2h02b1
Method
                  BLASTX
NCBI GI
                  q2959732
BLAST score
                  1047
E value
                  1.0e-114
Match length
                  264
% identity
                  77
NCBI Description
                  (Y13649) homologous to GATA-binding transcription factors
```

[Arabidopsis thaliana]

```
118358
 Seq. No.
                    1456 1.R1010
 Contig ID
 5'-most EST
                    jC-aTXLIB327408P3b01b1
 Method
                    BLASTX
 NCBI GI
                    g2959734 . .
 BLAST score
                   1316
 E value
                    1.0e-146
 Match length
                    269
 % identity
                    93
 NCBI Description
                    (Y13650) homologous to GATA-binding transcription factors
                    [Arabidopsis thaliana]
 Seq. No.
                    118359
                    1456 3.R1010
 Contig ID
                    LIB3<u>1</u>76-008-P1-K2-F5
 5'-most EST
 Method
                    BLASTX
                    g2959734
 NCBI GI
                    289
 BLAST score
                    7.0e-26
 E value
 Match length
                    61
 % identity
                    93
 NCBI Description
                    (Y13650) homologous to GATA-binding transcription factors
                    [Arabidopsis thaliana]
 Seq. No.
                    118360
                    1457 1.R1010
 Contig ID
 5'-most EST
                    g315832
 Method
                    BLASTX
 NCBI GI
                    g2959736
 BLAST score
                    1005
 E value
                    1.0e-109
 Match length
                    240
 % identity
                    79
 NCBI Description
                    (Y13651) homologous to GATA-binding transcription factors
                    [Arabidopsis thaliana]
 Seq. No.
                    118361
                    1458 1.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327439P1b07b2
 Method
                    BLASTX
                    g3281858
 NCBI GI
 BLAST score
                    956
                    1.0e-103
 E value
 Match length
                    250
% identity
                    77
 NCBI Description
                    (AL031004) ribosomal protein S6 - like [Arabidopsis
                    thaliana]
 Seq. No.
                    118362
                    1458 2.R1010
 Contig ID
 5'-most EST
                    q1053498
 Method
                    BLASTX
 NCBI GI
                    g3123271
 BLAST score
                    1078
 E value
                    1.0e-118
 Match length
                    249
```

BLAST score

```
87
% identity
                  40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052)
NCBI Description
                  ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                  118363
                  1458 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327426P2e08b1
                  BLASTX
Method
NCBI GI
                  q3123271
BLAST score
                  344
E value
                  1.0e-74
Match length
                  181
                  79
% identity
                  40S RIBOSOMAL PROTEIN S6 >qi 2224751 emb CAA74381 (Y14052)
NCBI Description
                  ribosomal protein S6 [Arabidopsis thaliana]
                  118364
Seq. No.
                  1458 4.R1010
Contig ID
                  g2762252
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3123271
BLAST score
                  418
E value
                  7.0e-41
Match length
                  109
% identity
                  80
NCBI Description
                  40S RIBOSOMAL PROTEIN S6 >gi 2224751 emb CAA74381 (Y14052)
                  ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                  118365
                  1458_7.R1010
Contig ID
5'-most EST
                  g398616
Method
                  BLASTN
NCBI GI
                  q3281847
BLAST score
                  268
E value
                  1.0e-149
Match length
                  292
% identity
                  98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20
                  (ESSAII project)
Seq. No.
                  118366
Contig ID
                  1462 1.R1010
5'-most EST
                  g933364
Method
                  BLASTX
NCBI GI
                  q2315153
BLAST score
                  1909
E value
                  0.0e + 00
Match length
                  372
% identity
                  98
NCBI Description
                 (Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
                  118367
Seq. No.
                  1463 1.R1010
Contig ID
5'-most EST
                  LIB3175-068-P1-K1-C6
Method
                  BLASTX
                  g2288887
NCBI GI
```

```
0.0e + 00
E value
Match length
                   463
                   97
% identity
                   (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
NCBI Description
                   thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate
                  diphosphate decarboxylase [Arabidopsis thaliana]
                  >gi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                   [Arabidopsis thaliana]
                  118368
Seq. No.
                   1463 2.R1010
Contig ID
5'-most EST
                   jC-atXP123C118M9T7015a1
Method
                  BLASTX
                  g2288887
NCBI GI
BLAST score
                   595
E value
                  2.0e-61
Match length
                  136
% identity
                  85
                   (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
NCBI Description
                   thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate
                  diphosphate decarboxylase [Arabidopsis thaliana]
                  >gi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                   [Arabidopsis thaliana]
Seq. No.
                  118369
                  1463 3.R1010
Contig ID
5'-most EST
                  iC-atXLIB327422P2g07b2
Method
                  BLASTX
NCBI GI
                  g2288887
BLAST score
                   631
E value
                  7.0e-66
Match length
                  129
% identity
                   92
NCBI Description
                   (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
                  thaliana] > gi_3250736\_emb\_CAA76803\_ (Y17593) mevalonate
                  diphosphate decarboxylase [Arabidopsis thaliana]
                  >gi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                   [Arabidopsis thaliana]
Seq. No.
                  118370
                  1464 1.R1010
Contig ID
5'-most EST
                  LIB2\overline{3}-013-Q1-E1-F1
Method
                  BLASTN
NCBI GI
                  g2765441
BLAST score
                  722
E value
                  0.0e + 00
Match length
                  1572
% identity
                  98
NCBI Description
                  Arabidopsis thaliana mRNA for ethylene-regulated transcript
Seq. No.
                  118371
                  1467 1.R1010
Contig ID
                  LIB24-077-Q1-E1-D4
5'-most EST
Method
                  BLASTX
                  q2760086
NCBI GI
BLAST score
                  2717
```

0.0e + 00

E value

BLAST score

```
583
Match length
                   94
% identity
                   (Y16046) leucine-rich repeat protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118372
                  1468 1.R1010*
Contig ID
                  PLN g3096946
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3096947
BLAST score
                   3589
E value
                  0.0e + 00
                  716
Match length
                   97
% identity
                   (Y16327) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
                  118373
Seq. No.
                  1469 1.R1010
Contig ID
                  PLN g3096948
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3096949
BLAST score
                   3524
                  0.0e + 00
E value
                  726
Match length
                   92
% identity
                   (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana] >gi 3894399 (AF067798) cyclic
                  nucleotide-gated cation channel [Arabidopsis thaliana]
                  118374
Seq. No.
                  1470 1.R1010
Contig ID ·
5'-most EST
                  LIB3175-033-P1-K1-A6
                  BLASTX
Method
NCBI GI
                  g3043415
BLAST score
                   3121
                  0.0e + 00
E value
Match length
                  649
% identity
                  95
                  (Y17053) At-hsc70-3 [Arabidopsis thaliana]
NCBI Description
                  118375
Seq. No.
                  1470 2.R1010
Contig ID
5'-most EST
                  g2580683
                  BLASTX
Method
NCBI GI
                  g1621205
BLAST score
                   289
E value
                  1.0e-25
Match length
                  68
% identity
                  82
                  (Y08903) HSC70-G7 protein [Arabidopsis thaliana]
NCBI Description
                  118376
Seq. No.
                  1470 3.R1010
Contig ID
                  g2413543
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3043414
```

Method

```
E value
                   1.0e-97
Match length
                   373
                   92
% identity
NCBI Description Arabidopsis thaliana mRNA for At-hsc70-3 protein
Seq. No.
                   118377
                   1471 1.R1010
Contig ID
                   jC-a\overline{t}XLIB327437P3c12a1
5'-most EST
                   BLASTX
Method
                   g3766248
NCBI GI
BLAST score
                   561
E value
                   3.0e-57
Match length
                   124
                   85
% identity
                   (Y18227) blue copper binding-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   118378
Seq. No.
                   1476 1.R1010
Contig ID
5'-most EST
                  PLN_g2246375
                  BLASTX
Method
                   g2246376
NCBI GI
BLAST score
                   1504
E value ...
                   1.0e-168
Match length
                   339
% identity
                   88
                  (Z86093) b-Zip DNA binding protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118379
                   1478 1.R1010
Contig ID
5'-most EST
                  PLN g2246379
Method
                  BLASTX
NCBI GI
                   g2246380
BLAST score
                   1073
                   1.0e-117
E value
Match length
                   221
% identity
                   94
                   (Z86095) peptidyl-prolyl cis-trans isomerase [Arabidopsis
NCBI Description
                   thaliana]
                   118380
Seq. No.
                   1479 1.R1010
Contig ID
5'-most EST
                   q438331
Method
                   BLASTX
                   g1174870
NCBI GI
BLAST score .
                   290
E value
                   6.0e-26
Match length
                  72
% identity
                  76
NCBI Description
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN
                  >gi_633685_emb_CAA55861_ (X79274) ubiquinol--cytochrome c
                   reductase [Solanum tuberosum]
                  118381
Seq. No.
Contig ID
                  1479_2.R1010
5'-most EST
                  LIB24-112-Q1-E1-C7
```

BLASTX

5'-most EST

```
NCBI GI
                   q1064883
BLAST score
                   2326
E value
                   0.0e+00
Match length
                   463
% identity
                   97
NCBI Description
                  (X92976) ZAP1 [Arabidopsis thaliana]
                   118382
Seq. No.
Contig ID
                   1483 1.R1010
5'-most EST
                   jC-atXLIB327424P4d07b1
Method
                  BLASTX
NCBI GI
                   q2266985
BLAST score
                   3005
E value
                  0.0e + 00
Match length
                   616
                   94
% identity
NCBI Description (Y13943) METRS [Arabidopsis thaliana]
                  118383
Seq. No.
                  1484_1.R1010
Contig ID
5'-most EST
                  PLN_g1777311
Method
                  BLASTX
NCBI GI
                  q1777312
BLAST score
                  2016
                  0.0e + 00
E value
Match length
                   421
                   93
% identity
NCBI Description
                  (D30622) novel serine/threonine protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  118384
                  1484 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P4h02b1
                  BLASTN
Method
NCBI GI
                  q1777311
BLAST score
                  246
                  1.0e-136
E value
Match length
                   434
% identity
                  98
                  Arabidopsis thaliana mRNA for novel serine/threonine
NCBI Description
                  protein kinase, complete cds
Seq. No.
                  118385
Contig ID
                  1486 1.R1010
5'-most EST
                  jC-atXLIB327405P3a07b1
Method
                  BLASTX
NCBI GI
                  q1747310
BLAST score
                  3951
E value
                  0.0e + 00
Match length
                  844
                  92
% identity
NCBI Description
                  (D58424) Myb-like DNA binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  118386
Contig ID
                  1487_1.R1010
```

 $PLN_{g}^{2154608}$

```
Method
                  BLASTX
NCBI GI
                   g2154609
BLAST score
                   1785
                  0.0e+00
E value
Match length
                   333
                   100
% identity
                   (D63509) endoxyloglucan transferase related protein
NCBI Description
                   [Arabidopsis thaliana] >gi 4522010 gb AAD21783.1
                   (AC007069) endoxyloglucan transferase [Arabidopsis
                   thaliana]
                   118387
Seq. No.
                   1487 2.R1010
Contig ID
                   jC-atXLIB327427P1d12a2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2154609
BLAST score
                   289
E value
                   8.0e-26
Match length
                   71
% identity
                   80
NCBI Description
                   (D63509) endoxyloglucan transferase related protein
                   [Arabidopsis thaliana] >qi 4522010 qb AAD21783.1
                   (AC007069) endoxyloglucan transferase [Arabidopsis
                   thaliana]
....
                   118388
Seq. No.
Contig ID
                   1489 1.R1010
                   PLN g992920
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1526422
BLAST score
                  1188
E value
                   1.0e-131
Match length
                   256
% identity
                   93
NCBI Description
                  (D64139) LEA protein in group 5 [Arabidopsis thaliana]
Seq. No.
                   118389
Contig ID
                   1490 1.R1010
                  LIB3234-060-P1-K1-D11
5'-most EST
Method
                  BLASTX
NCBI GI
                   g1526424
BLAST score
                   1780
E value
                   0.0e + 00
Match length
                   448
% identity
                   81
NCBI Description
                  (D64140) LEA protein in group 3 [Arabidopsis thaliana]
Seq. No.
                   118390
                   1492 1.R1010
Contig ID
                  LIB22-076-Q1-E1-H1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3164126
BLAST score
                   2392
E value
                   0.0e + 00
Match length
                   459
% identity
                   100
                  (D78598) cytochrome P450 monooxygenase [Arabidopsis
NCBI Description
```

NCBI GI

E value

BLAST score

q3164138

0.0e + 00

2316

thaliana] 118391 Seq. No. 1492 4.R1010 Contig ID g1217085 5'-most EST Method BLASTX g3164126 NCBI GI BLAST score 56 E value 1.0e-37 Match length 154 % identity 69 (D78598) cytochrome P450 monooxygenase [Arabidopsis NCBI Description thaliana] Seq. No. 118392 Contig ID 1494 1.R1010 5'-most EST PLN_g3164129 Method BLASTX NCBI GI q3164130 BLAST score 2240 E value 0.0e + 00Match length 495 % identity 91 (D78600) cytochrome P450 monooxygenase [Arabidopsis NCBI Description thaliana] 118393. Seq. No. Contig ID 1496_1.R1010 5'-most EST PLN_g3164133 Method BLASTX NCBI GI q3164134 BLAST score 2513 E value 0.0e + 00Match length 501 % identity 97 NCBI Description (D78602) cytochrome P450 monooxygenase [Arabidopsis thaliana] Seq. No. 118394 1497 1.R1010 Contig ID 5'-most EST jC-atXLIB327440P1h03a1 Method BLASTX NCBI GI q3164136 BLAST score 2440 E value 0.0e + 00Match length 483 97 % identity NCBI Description (D78603) cytochrome P450 monooxygenase [Arabidopsis thaliana] 118395 Seq. No. Contig ID 1498 1.R1010 5'-most EST jC-atXP76C226P8T7d1 Method BLASTX

```
Match length
                  503
% identity
                  90
NCBI Description
                  (D78604) cytochrome p450 monooxygenase [Arabidopsis
                  thaliana] >gi_4115378 (AC005967) cytochrome p450
                  monooxygenase [Arabidopsis thaliana]
Seq. No.
                  118396
                  1499 1.R1010
Contig ID
                  PLN g3164139
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3164140
BLAST score
                  2541
E value
                  0.0e + 00
Match length
                  502
                  98
% identity
                  (D78605) cytochrome P450 monooxygenase [Arabidopsis
NCBI Description
                  thaliana]
                  118397
Seq. No.
                  1500_1.R1010
Contig ID
                  PLN_g3164141
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3164142
                  2470
BLAST score
E value
                  0.0e + 00
Match length
                  500
% identity
                  96
                  (D78606) cytochrome P450 monooxygenase [Arabidopsis
NCBI Description
                  thaliana]
                  118398
Seq. No.
                  1501 1.R1010
Contig ID
5'-most EST
                  PLN_g3164143
Method
                  BLASTX
NCBI GI
                  q3164144
BLAST score
                  2541
                  0.0e + 00
E value
Match length
                  484
% identity
                  100
                  (D78607) cytochrome P450 monooxygenase [Arabidopsis
NCBI Description
                  thalianal
                  118399
Seq. No.
Contig ID
                  1501 2.R1010
                  g2047582
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3164144
BLAST score
                  418
E value
                  2.0e-41
Match length
                  137
% identity
                  74
                  (D78607) cytochrome P450 monooxygenase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  118400
                  1501_3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327404P2c02b1
```

```
Method
                   BLASTX
NCBI GI
                   q3164144
BLAST score
                   138
E value
                   4.0e-08
Match length
                   144
% identity
                   (D78607) cytochrome P450 monooxygenase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   118401
Contig ID
                   1502_1.R1010
5'-most EST
                   g1327679
                   BLASTN
Method
                   g4006885
NCBI GI
BLAST score
                   748
                   0.0e + 00
E value
Match length
                   1378
% identity
                   99
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
                   118402
Seq. No.
Contig ID
                   1505 1.R1010
                   LIB3176-073-P1-K1-D8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1483150
                   2330
BLAST score
E value
                   .0.0e+00
Match length
                   534
% identity
                   92
                   (D84417) monodehydroascorbate reductase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   118403
Contig ID
                   1505_2.R1010
5'-most EST
                   g2393393
Method
                   BLASTX
                   q1483150
NCBI GI
BLAST score
                   243
                   3.0e-50
E value
                   127
Match length
% identity
                   (D84417) monodehydroascorbate reductase [Arabidopsis
NCBI Description
                   thaliana]
                   118404
Seq. No.
                   1509 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327405P1f02b1
Method
                   BLASTX
NCBI GI
                   q2055273
                   1909
BLAST score
                   0.0e + 00
E value
                   386
Match length
% identity
                   95
NCBI Description (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]
```

118405

Seq. No.

```
Contig ID
                  1509 2.R1010
5'-most EST
                  -jC-atXP75C225M7T7d1
Method
                 - BLASTX -
                  g2055273
NCBI GI
BLAST score
                   253
                   2.0e-21
E value
                   83
Match length
                   65
% identity
                   (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]
NCBI Description
                   118406
Seq. No.
                   1509 3.R1010
Contig ID
                   jC-atXLIB327423P3h02b1
5'-most EST
                  BLASTX
Method
                   g2129511
NCBI GI
BLAST score
                   462
                   2.0e-55
E value
                   166
Match length
                   68
% identity
                   glycerate dehydrogenase (EC 1.1.1.29) splice form HPR1,
NCBI Description
                  microbody - cucurbit >gi 1304042 dbj BAA08410 (D49432)
                   hydroxypyruvate reductase [Cucurbita sp.]
                   118407
Seq. No.
                   1509 6.R1010
Contig ID
5'-most EST
                   LIB24-077-Q1-E1-G10
Method
                   BLASTX
                   g2055273
NCBI GI
BLAST score
                   428
                   3.0e-42
E value
Match length
                   80
                   100
% identity
                   (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]
NCBI Description
                   118408
Seq. No.
                   1510 1.R1010
Contig ID
                   PLN g2443328
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2443329
BLAST score
                   4060
                   0.0e + 00
E value
Match length
                   884
% identity
                   88
                   (D86122) Mei2-like protein [Arabidopsis thaliana]
NCBI Description
                   118409
Seq. No.
                 · 1513 1.R1010
Contig ID
                   LIB23-054-Q1-E1-E4
5'-most EST
                   BLASTX
Method
                   g2852447
NCBI GI
BLAST score
                   2076
                   0.0e + 00
E value
Match length
                   426
% identity
                   (D88206) protein kinase [Arabidopsis thaliana]
NCBI Description
```

118410

Seq. No.

```
1514_1.R1010
Contig ID
5'-most EST
                  PLN_g2852448
                  BLASTX
Method
NCBI GI
                  g2852449
BLAST score
                  2009
E value
                  0.0e + 00
Match length
                  426
% identity
                  (D88207) protein kinase [Arabidopsis thaliana] >gi 2947061
NCBI Description
                  (AC002521) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  118411
                  1515 1.R1010
Contig ID
                  jC-atXLIB327404P2f11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q461729
BLAST score
                  498
E value
                  4.0e-50
Match length
                  98
% identity
                  100
                  10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES)
NCBI Description
                  >gi_2146744_pir__S65597 probable chaperonin, 10K -
                  Arabidopsis thaliana >gi 166662 (L02843) 10 kDa chaperonin
                  [Arabidopsis thaliana]
Seq. No.
                  118412
                  1516 1.R1010
Contig ID
                  jC-a\overline{t}XLIB327408P3f10b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3334123
BLAST score
                  1385
E value
                  1.0e-154
Match length
                  325
% identity
                  89
                  ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi 1655480 dbj BAA13599 (D88374) gamma subunit of
                  mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787
                  (AC002334) mitochondrial F1-ATPase, gamma subunit
                  [Arabidopsis thaliana]
                  118413
Seq. No.
                  1516 3.R1010
Contig ID
                  jC-aTXP96C249I11T7b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3334123
BLAST score
                  416
                  1.0e-50
E value
Match length
                  135
                  84
% identity
NCBI Description
                  ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi 1655480 dbj BAA13599 (D88374) gamma subunit of
                  mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787
                  (AC002334) mitochondrial F1-ATPase, gamma subunit
                  [Arabidopsis thaliana]
Seq. No.
                  118414
                  1517 1.R1010
Contig ID
```

```
5'-most EST
                  jC-atXLIB327412P4d07b1
Method
                  BLASTX
NCBI GI
                  g3334124
BLAST score
                   1160
E value
                   1.0e-127
                  238
Match length
% identity
                  100
                  ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                  >gi 1655482 dbj BAA13600 (D88375) delta subunit of
                  mitochondrial Fl-ATPase [Arabidopsis thaliana]
                  118415
Seq. No.
                  1517 4.R1010
Contig ID
5'-most EST
                   jC-atXLIB327426P4a12a1
                  BLASTN
Method
NCBI GI
                  q1655481
BLAST score
                   215
E value
                   1.0e-117
Match length
                   363
                  92
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for delta subunit of
                  mitochondrial F1-ATPase, complete cds
                   118416
Seq. No.
                   1518 1.R1010
Contig ID
                  jC-atXLIB327416P4d02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2493045
BLAST score
                   905
                   1.0e-97
E value
Match length
                   201
% identity
                   90
                  ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi 1655484_dbj_BAA13601_ (D88376) delta-prime subunit of
                  mitochondrial F1-ATPase [Arabidopsis thaliana]
                   118417
Seq. No.
Contia ID
                   1519 1.R1010
5'-most EST
                   jC-atXLIB327413P2g02b1
Method
                  BLASTX
NCBI GI
                   g2493052
BLAST score
                   373
E value
                   2.0e-35
Match length
                   70
                   100
% identity
                  ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL
NCBI Description
                  >gi 1655486 dbj_BAA13602_ (D88377) epsilon subunit of
                  mitochondrial F1-ATPase [Arabidopsis thaliana]
                   118418
Seq. No.
                   1520 1.R1010
Contig ID
5'-most EST
                  LIB25-089-Q1-E1-A6
                  BLASTX
Method
NCBI GI
                   g2970034
BLAST score
                  1585
E value
                   1.0e-177
```

Contig ID

```
305
Match length
% identity
                  94
                  (D88536) delta 9 desaturase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118419
                  1521 1.R1010
Contig ID
                  LIB3234-059-P1-K1-F2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2970036
BLAST score
                  1416
E value
                  1.0e-157
Match length
                  307
% identity
                  86
                  (D88537) delta 9 desaturase [Arabidopsis thaliana]
NCBI Description
                  118420
Seq. No.
Contig ID
                  1522 1.R1010
                  PLN g4165371
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3914996
BLAST score
                  2141
E value
                  0.0e + 00
Match length
                  430
% identity
                  PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)
NCBI Description
                  >gi 1665831 dbj BAA13640_ (D88541) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
                  >gi 2804260 dbj BAA24441 (AB010408) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
                  >gi_3367581_emb_CAA20033 (AL031135) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
Seq. No.
                  118421
                  1522 2.R1010
Contig ID
                  LIB23-073-Q1-E1-E10
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4165371
BLAST score
                  301
E value
                  1.0e-169
Match length
                  313
                  99
% identity
                  Arabidopsis thaliana mRNA for phosphoserine
NCBI Description
                  aminotransferase, complete cds
                  118422
Seq. No.
Contig ID
                  1524 1.R1010
5'-most EST
                  LIB24-125-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  q1669597
BLAST score
                  1067
E value
                  1.0e-116
Match length
                  273
% identity
                  79
NCBI Description
                  (D88745) AR192 [Arabidopsis thaliana]
                  118423
Seq. No.
```

1525 1.R1010

Method

BLASTX

```
LIB3168-037-P1-K1-B6
5'-most EST
Method
                   BLASTX
                   g1669599
NCBI GI
BLAST score
                   2622
E value
                   0.0e+00
Match length
                   565
                   92
% identity
                   (D88746) AR791 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118424
                   1527_1.R1010
PLN_g1669602
Contig ID
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1669603
BLAST score
                   932
E value
                   1.0e-101
Match length
                   242
                   76
% identity
NCBI Description
                   (D88748) AR411 [Arabidopsis thaliana]
                   118425
Seq. No.
Contig ID
                   1528 1.R1010
5'-most EST
                   LIB24-019-Q1-E1-C6
                   BLASTX
Method
                                                                      A . .
                   q3123712
NCBI GI
BLAST score
                   2551
                   0.0e + 00
E value
Match length
                   496
                   100
% identity
                   (D89051) ERD6 protein [Arabidopsis thaliana]
NCBI Description
                   118426
Seq. No.
Contig ID
                   1529 1.R1010
5'-most EST
                   LIB23-028-Q1-E1-E4
Method
                   BLASTX
NCBI GI
                   q3068717
BLAST score
                   3350
E value
                   0.0e + 00
Match length
                   683
                   97
% identity
NCBI Description
                   (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                   118427
                   1530 1.R1010
Contig ID
5'-most EST
                   LIB3175-060-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   q2723477
BLAST score
                   939
E value
                   1.0e-101
Match length
                   210
% identity
                   89
                   (D89824) GTP-binding protein [Arabidopsis thaliana]
NCBI Description
                   118428
Seq. No.
                   1531 1.R1010
Contig ID
                   PLN_{g}^{2}668491
5'-most EST
```

. . . .

```
NCBI GI
                          q2668492
     BLAST score
                          4301
                          0.0e+00
     E value
     Match length
                          949
                          90
     % identity
                          (D89981) metal-transporting P-type ATPase [Arabidopsis
     NCBI Description
.....
                          thaliana]
                          118429
     Seq. No.
                          1534 1.R1010
     Contig ID
     5'-most EST
                          PLN g2292916
     Method
                          BLASTX
     NCBI GI
                          q2292917
     BLAST score
                          1598
     E value
                          0.0e + 00
     Match length
                          497
     % identity
                          94
                          (X99851) galactokinase [Arabidopsis thaliana]
     NCBI Description
                          118430
     Seq. No.
                          1537_1.R1010
     Contig ID
     5'-most EST
                          q315\overline{6}23
     Method
                          BLASTX
                          q81624
     NCBI GI
                          523
     BLAST score
                          7.0e-53
     E value
     Match length
                          200
     % identity
                          qlycine-rich protein 2 - Arabidopsis thaliana
     NCBI Description
                          >gi_259445_bbs_117608 (S47408) glycine-rich protein, atGRP {clone atGRP-2} [Arabidopsis thaliana, C24, Peptide, 203 aa] [Arabidopsis thaliana] >gi_4467155_emb_CAB37524_
                          (AL035540) glycine-rich protein 2 (GRPZ) [Arabidopsis
                          thaliana]
     Seq. No.
                          118431
                          1537 3.R1010
     Contia ID
     5'-most EST
                          iC-atXLIB327414P4e02b2
     Method
                          BLASTN
     NCBI GI
                          q4490324
     BLAST score
                          274
     E value
                          1.0e-152
     Match length
                          385
     % identity
                          93
                          Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14
     NCBI Description
                          (ESSA project)
     Seq. No.
                          118432
     Contig ID
                          1538 1.R1010
     5'-most EST
                          jC-atXP37C157K18T7d2
     Method
                          BLASTN
     NCBI GI
                          q4581161
     BLAST score
                          481
     E value
                          0.0e + 00
     Match length
                          569
     % identity
                          72
     NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic
```

sequence, complete sequence Seq. No. 118433

Contig ID 1538_2.R1010 5'-most EST LIB35-036-Q1-E2-A2

Method BLASTN
NCBI GI g4581161
BLAST score 380
E value 0.0e+00

E value 0.00 Match length 596 % identity 50

NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic

sequence, complete sequence

Seq. No. 118434

Contig ID 1538_8.R1010

5'-most EST jC-atXP40C162J6T7d1

Method BLASTN
NCBI GI g259446
BLAST score 139
E value 4.0e-72
Match length 336
% identity 97

NCBI Description glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana,

C24, mRNA, 680 nt]

Seq. No. 118435 Contig ID 1538 9.R1010

5'-most EST jC-atXLIB327428P1e02b2

Method BLASTN
NCBI GI g259446
BLAST score 125
E value 9.0e-64
Match length 193
% identity 92

NCBI Description glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana,

C24, mRNA, 680 nt]

Seq. No. 118436

Contig ID 1538_10.R1010

5'-most EST g937360
Method BLASTN
NCBI GI g259446
BLAST score 158
E value 2.0e-83
Match length 222
% identity 98

NCBI Description glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana,

C24, mRNA, 680 nt]

 Seq. No.
 118437

 Contig ID
 1539_1.R1010

 5'-most EST
 g2759760

 Method
 BLASTX

 NCBI GI
 g99696

 BLAST score
 2158

 E value
 0.0e+00

Seq. No.

Contig ID

118441

1539_5.R1010

```
Match length
                  424
% identity
NCBI Description
                  glutamate--ammonia ligase (EC 6.3.1.2) precursor,
                  chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                  >gi 240070 bbs 69728 (S69727) light-regulated glutamine
                  synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                  aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln
                  synthetase [Arabidopsis thaliana]
Seq. No.
                  118438
Contig ID
                  1539 2.R1010
5'-most EST
                  LIB3176-065-P1-K1-E11
                  BLASTX
Method
NCBI GI
                  a99696
                  781
BLAST score
                  3.0e-83
E value
Match length
                  179
% identity
NCBI Description
                  glutamate--ammonia ligase (EC 6.3.1.2) precursor,
                  chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                  >gi_240070_bbs_69728 (S69727) light-regulated glutamine
                  synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                  aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln
                  synthetase [Arabidopsis thaliana]
                  118439
Seq. No.
                  1539 3.R1010
Contig ID
5'-most EST
                  LIB3177-022-P1-K2-C11
Method
                  BLASTX
NCBI GI
                  g121349
                  231
BLAST score
E value
                  7.0e-19
Match length
                  194
% identity
                  29
NCBI Description
                  GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA
                  LIGASE) (CLONE LAMBDA-GS28) >gi_20368_emb_CAA32461_
                  (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza
                  sativa]
Seq. No.
                  118440
                  1539 4.R1010
Contig ID
5'-most EST
                  LIB3177-098-P1-K1-H12
                  BLASTX
Method
NCBI GI
                  q99696
                  499
BLAST score
                  2.0e-50
E value
Match length
                  144
% identity
                  72
NCBI Description
                  glutamate--ammonia ligase (EC 6.3.1.2) precursor,
                  chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                  >gi_240070_bbs_69728 (S69727) light-regulated glutamine
                  synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                  aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln
                  synthetase [Arabidopsis thaliana]
```

Contig ID

```
5'-most EST
                   jC-atXLIB327427P2c07b1
Method
                   BLASTX
                   g99696
NCBI GI
BLAST score
                   366
E value
                   1.0e-87
Match length
                   172
% identity
                   93
                   glutamate--ammonia ligase (EC 6.3.1.2) precursor,
NCBI Description
                   chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                   >gi_240070_bbs_69728 (S69727) light-regulated glutamine
                   synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                   aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln
                   synthetase [Arabidopsis thaliana]
                   118442
Sea. No.
Contig ID
                   1540 1.R1010
5'-most EST
                   PLN g1617218
                   BLASTX
Method
NCBI GI
                   q1617219
BLAST score
                   2637
E value
                   0.0e + 00
Match length
                   496
% identity
                   100
                   (X99301) CPD photolyase [Arabidopsis thaliana] >qi 2984707
NCBI Description
                   (AF053365) type II CPD photolyase PHR1 [Arabidopsis
                   thalianal
Seq. No.
                   118443
Contig ID
                   1541 1.R1010
5'-most EST
                   jC-atXLIB327402P1c01b1
                   BLASTX
Method
NCBI GI
                   q4585882
BLAST score
                   586
E value
                   1.0e-124
Match length
                   255
% identity
NCBI Description
                   (AC005850) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
                   118444
Seq. No.
Contig ID
                   1541 4.R1010
5'-most EST
                   jC-atXP123C117C23T7091d1
Method
                   BLASTX
NCBI GI
                   g1172872
BLAST score
                   578
E value
                   2.0e-59
Match length
                   107
% identity
                   100
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
NCBI Description
                   precursor - Arabidopsis thaliana >gi 435618 dbj BAA02373
                   (D13042) thiol protease [Arabidopsis thaliana]
                   >qi 4539328 emb CAB38829.1 (AL035679) drought-inducible
                   cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                   118445
```

1541 5.R1010

% identity

NCBI Description

89

```
5'-most EST
                  LIB23-004-Q1-E1-B10
Method
                  BLASTX
NCBI GI
                  q1172872
BLAST score
                  1003
E value
                  1.0e-176
Match length
                  335
                  91
% identity
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
                  precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
                  (D13042) thiol protease [Arabidopsis thaliana]
                  >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                  cysteine proteinase RD19A precursor [Arabidopsis thaliana]
                  118446
Seq. No.
                  1541 10.R1010
Contig ID
5'-most EST
                  LIB35-040-Q1-E1-B8
Method
                  BLASTX
                  q1172872
NCBI GI
BLAST score
                  375
                  1.0e-95
E value
Match length
                  185
% identity
                  92
NCBI Description
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
                  precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
                  (D13042) thiol protease [Arabidopsis thaliana]
                  >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                  cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                  118447
                  1541 14.R1010
Contig ID
5'-most EST
                  g2758683
Method
                  BLASTX
NCBI GI
                  q1172872
BLAST score
                  404
                  2.0e-39
E value
Match length
                  80
% identity
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
                  precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
                  (D13042) thiol protease [Arabidopsis thaliana]
                  >gi 4539328 emb CAB38829.1 (AL035679) drought-inducible
                  cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                  118448
Contig ID
                  1542 1.R1010
                  jC-atXP91C245P5T7b1
5'-most EST
Method
                  BLASTX
                  a1170247
NCBI GI
                  1034
BLAST score
                  1.0e-113
E value
                  212
Match length
```

12855

HEVEIN-LIKE PROTEIN PRECURSOR >gi 407248 (U01880)

pre-hevein-like protein [Arabidopsis thaliana]

Match length

187

```
Seq. No.
                  118449
Contig ID
                  1542_2.R1010
                  jC-atXLIB327421P3h05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1170247
BLAST score
                  553
                  8.0e-57
E value
Match length
                  111
                  87
% identity
NCBI Description
                  HEVEIN-LIKE PROTEIN PRECURSOR >gi_407248 (U01880)
                  pre-hevein-like protein [Arabidopsis thaliana]
                  118450
Seq. No.
                  1544 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P2c06b1
                  BLASTX
Method
NCBI GI
                  g1172503
BLAST score
                  4140
                  0.0e + 00
E value
                  814
Match length
                  98
% identity
NCBI Description
                  PHOSPHATIDYLINOSITOL 3-KINASE (PI3-KINASE)
                  (PTDINS-3-KINASE) (PI3K) (ATVPS34) >gi 555700 (U10669)
                  phosphatidylinositol 3-kinase [Arabidopsis thaliana]
                  118451
Seq. No.
                  1548 1.R1010
Contig ID
5'-most EST
                  jC-atXP100C251M12T7b1
                  BLASTX
Method
NCBI GI
                  g4454036
BLAST score
                  822
                  5.0e-88
E value
Match length
                  151
                  100
% identity
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thaliana]
                  118452
Seq. No.
Contig ID
                  1548 2.R1010
5'-most EST
                  LIB35-022-Q1-E1-G2
Method
                  BLASTX
NCBI GI
                  g3153207
BLAST score
                  1075
E value
                  1.0e-117
Match length
                  235
                  86
% identity
NCBI Description (AF001949) ATHB-12 [Arabidopsis thaliana]
Seq. No.
                  118453
Contig ID
                  1548 3.R1010
5'-most EST
                  LIB24-013-Q1-E1-D2
Method
                  BLASTX
NCBI GI
                  g4454036
BLAST score
                  343
E value
                  1.0e-31
```

```
% identity
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  118454
                  1548 4.R1010
Contig ID
5'-most EST
                  LIB3176-064-P1-K1-D4
                  BLASTX
Method
NCBI GI
                  g4454036
BLAST score
                  657
E value
                  8.0e-69
Match length
                  150
% identity
                  85
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thaliana]
                  118455
Seq. No.
                  1548 6.R1010
Contig ID
5'-most EST
                  LIB3175-006-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q4454037
BLAST score
                  806
E value
                  3.0e-86
Match length
                  148
                  100
% identity
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thalianal
                   118456
Seq. No.
                  1548 7.R1010
Contig ID
5'-most EST
                  jC-atXLIB327431P1g01a1
Method
                  BLASTX
NCBI GI
                  g2244762
BLAST score
                   475
E value
                  2.0e-47
Match length
                  143
% identity
                   66
NCBI Description (Z97335) major latex protein [Arabidopsis thaliana]
                   118457
Seq. No.
                  1548 8.R1010
Contig ID
                  jC-aTXP60C198L15T7047d1
5'-most EST
Method
                  BLASTX
                  g4454036
NCBI GI
BLAST score
                   545
E value
                   6.0e-63
Match length
                  131
% identity
NCBI Description
                   (AL035394) putative major latex protein [Arabidopsis
                   thaliana]
Seq. No.
                   118458
                  1548 9.R1010
Contig ID
5'-most EST
                  jC-atXP102CE5E4T7063d1
Method
                  BLASTX
                  g3785981
NCBI GI
```

609

BLAST score

5'-most EST

```
E value
                   4.0e-63
 Match length
                   151
                   72
 % identity
                    (AC005560) putative major latex protein [Arabidopsis
 NCBI Description
                   thaliana]
                   118459
 Seq. No.
                   1548_10.R1010
 Contig ID
                   g1520739
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   g4454036
 BLAST score
                   45
 E value
                   6.0e-55
Match length
                   135
                   83
 % identity
                    (AL035394) putative major latex protein [Arabidopsis
 NCBI Description
                   thaliana]
                   118460
 Seq. No.
                   1548_11.R1010
 Contig ID
 5'-most EST
                   jC-atXLIB327415P3e02b1
 Method
                   BLASTX
 NCBI GI
                   g4454036
 BLAST score
                   343
 E value
                   9.0e-32
Match length
                   151
                   97
 % identity
                    (AL035394) putative major latex protein [Arabidopsis
 NCBI Description
                   thaliana]
                   118461
 Seq. No.
                   1548 14.R1010
 Contig ID
 5'-most EST
                   g3450564
 Method
                   BLASTX
                   g4454036
 NCBI GI
 BLAST score
                   189
                   3.0e-14
 E value
Match length
                   57
 % identity
                   61
 NCBI Description
                    (AL035394) putative major latex protein [Arabidopsis
                   thalianal
                   118462
 Seq. No.
 Contig ID
                   1548_15.R1010
 5'-most EST
                   jC-atXP90C246C6T7d2
 Method
                   BLASTX
                   q4454036
NCBI GI
 BLAST score
                   248
                   3.0e-21
 E value
Match length
                   91
 % identity
                   60
                   (AL035394) putative major latex protein [Arabidopsis
 NCBI Description
                   thaliana]
 Seq. No.
                   118463
                   1548 20.R1010
 Contig ID
```

jC-atXP63C204I22T7s2

```
Method
                   BLASTN
NCBI GI
                   a4454022
                   159
BLAST score
                   3.0e - 84
E value
                   289
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
NCBI Description
                   (ESSAII project)
                   118464
Seq. No.
Contig ID
                   1549_1.R1010
5'-most EST
                   PLN_g2522361
Method
                  BLASTX
NCBI GI
                   q3914056
                   4721
BLAST score
                   0.0e+00
E value
Match length
                   937
% identity
                   99
                  DNA MISMATCH REPAIR PROTEIN MSH2 >gi_2522362 (AF002706)
NCBI Description
                  MutS homolog 2 [Arabidopsis thaliana] >gi_2522364
                   (AF003005) MutS homolog 2 [Arabidopsis thaliana]
                   >gi_2547236 (AF026549) DNA mismatch repair protein MSH2
                   [Arabidopsis thaliana]
                  118465
Seq. No.
Contig ID
                  1552 1.R1010
5'-most EST
                  PLN g4101472
Method
                  BLASTX
NCBI GI
                   g4101473
BLAST score
                   2633
E value
                   0.0e + 00
Match length
                   618
% identity
                   87
NCBI Description
                  (AF003382) KEA1 [Arabidopsis thaliana]
                   118466
Seq. No.
                   1554_1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327425P1d03b1
Method
                  BLASTX
NCBI GI
                   q2224933
                   2919
BLAST score
E value
                   0.0e + 00
Match length
                   627
% identity
                   (AF004216) ethylene-insensitive3 [Arabidopsis thaliana]
NCBI Description
                  >gi 2224935 (AF004217) ethylene-insensitive3 [Arabidopsis
                   thaliana]
                   118467
Seq. No.
Contig ID
                   1554 2.R1010
                  LIB3176-011-P1-K1-C10
5'-most EST
                   BLASTX
Method
                   g2224927
NCBI GI
BLAST score
                  2777
E value
                   0.0e + 00
Match length
                   584
% identity
```

```
(AF004213) ethylene-insensitive3-like1 [Arabidopsis
NCBI Description
                   thaliana)
                   118468
Seq. No.
                   1556 1.R1010
Contig ID
                  LIB3175-015-P1-K1-C4
5'-most EST
                  BLASTX
Method
                   g2224931
NCBI GI
BLAST score
                   2723
E value
                   0.0e + 00
Match length
                   551
% identity
                  (AF004215) ethylene-insensitive3-like3 [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                   118469
                   1562 1.R1010
Contig ID
                   jC-a\(\bar{1}\)X24005Q1E1F05b1
5'-most EST
                   BLASTX
Method
                   q3169719
NCBI GI
                   1438
BLAST score
E value
                   1.0e-160
Match length
                   370
% identity
                  80
NCBI Description (AF007109) similar to yeast dcpl [Arabidopsis thaliana]
                   118470
Seq. No.
Contig ID
                  1564 1.R1010
                   PLN g2944179
5'-most EST
                   BLASTX
Method
                   g2944180
NCBI GI
                   1849
BLAST score
E value
                   0.0e + 00
                   374
Match length
% identity
                   97
NCBI Description
                   (AF007779) trehalose-6-phosphate phosphatase [Arabidopsis
                   thaliana!
Seq. No.
                   118471
                   1565_1.R1010
Contig ID
                   PLN_g2440014
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2909781
BLAST score
                   129
                   0.0e + 00
E value
                   1623
Match length
% identity
                   92
NCBI Description
                   (AF020288) MgATP-energized glutathione S-conjugate pump
                   [Arabidopsis thaliana]
                   118472
Seq. No.
                   1565 2.R1010
Contig ID
                   jC-atXLIB327427P3f03b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2340166
BLAST score
                   8048
                   0.0e + 00
E value
```

Method

BLASTX

```
Match length
                  1622
% identity
                  97
                   (AF008124) glutathione S-conjugate transporting ATPase
NCBI Description
                   [Arabidopsis thaliana] >gi 2459949 (AF008125) multidrug
                  resistance-associated protein homolog [Arabidopsis
                  thaliana]
                  118473
Seq. No.
Contig ID
                  1566_1.R1010
5'-most EST
                  jC-a\(\bar{1}\)XLIB327436P4g11b1
                  BLASTX
Method
                  g2352828
NCBI GI
BLAST score
                  776
                  1.0e-82
E value
                  149
Match length
                  100
% identity
                   (AF009228) NaCl-inducible Ca2+-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  118474
Seq. No.
                  1566 2.R1010
Contig ID
5'-most EST
                  jC-atXP26C126P22T7085a1
Method
                  BLASTX
                  g2352828
NCBI GI
                  465
BLAST score
                  8.0e-69
E value
                  146
Match length
                  95
% identity
                   (AF009228) NaCl-inducible Ca2+-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  118475
Seq. No.
                  1567 1.R1010
Contig ID
5'-most EST
                  LIB24-131-Q1-E1-C9
                  BLASTX
Method
NCBI GI
                  g2271477
BLAST score
                   2179
E value
                   0.0e + 00
Match length
                   438
                  96
% identity
NCBI Description
                   (AF009631) AP47/50p [Arabidopsis thaliana]
                  118476
Seq. No.
                  1567 3.R1010
Contig ID
                  g2758858
5'-most EST
Method
                  BLASTX
                  g2271477
NCBI GI
BLAST score
                   339
E value
                  7.0e-32
Match length
                  117
% identity
                  78
                  (AF009631) AP47/50p [Arabidopsis thaliana]
NCBI Description
                  118477
Seq. No.
Contig ID
                  1569 1.R1010
5'-most EST
                  jC-atXP94CH4G9T7020d1
```

Contig ID

Method

5'-most EST

```
NCBI GI
                   q2384671
BLAST score
                   3862
· E value
                   0.0e+00 ·
Match length
                   794
                   94
% identity
NCBI Description (AF012657) putative potassium transporter AtKT2p
                   [Arabidopsis thaliana]
Seq. No.
                   118478
                   1570 1.R1010
Contig ID
5'-most EST
                   LIB23-041-Q1-E1-A11
Method
                   BLASTX
NCBI GI
                   q2576411
BLAST score
                   3714
E value
                   0.0e + 00
                   809
Match length
% identity
                   91
                   (AF012833) similar to dynamin-like protein encoded by
NCBI Description
                   GenBank Accession Number X99669 [Arabidopsis thaliana]
                   118479
Seq. No.
Contig ID
                   1570 2.R1010
5'-most EST
                   jC-atXP95CG12D1T7066d1
Method
                   BLASTX
                   g4587686
NCBI GI
BLAST score
                   750
                   8.0e-80
E value
Match length
                   161
                   95
% identity
                   (AC007197) dynamin-like protein ADL2 [Arabidopsis thaliana]
NCBI Description
                   118480
Seq. No.
Contig ID
                   1571_1.R1010
5'-most EST
                   PLN_g4102597
Method
                   BLASTX
NCBI GI
                   g4102598
BLAST score
                   3776
                   0.0e + 00
E value
Match length
                   788
% identity
                   91
                   (AF013466) auxin response factor 4 [Arabidopsis thaliana]
NCBI Description
                   118481
Seq. No.
Contig ID
                   1572_1.R1010
                   PLN_{g}4102599
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4102600
BLAST score
                   4342
                   0.0e + 00
E value
Match length
                   933
% identity
                   89
NCBI Description
                   (AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.
                   118482
```

12862

1572 2.R1010

BLASTX

jC-atXP98CH7D8T7050d1

```
NCBI GI
                   q4102600
BLAST score
                   228
E value
                   4.0e-18
Match length
                   42
% identity
                   100
NCBI Description
                  (AF013467) ARF6 [Arabidopsis thaliana]
                   118483
Seq. No.
Contig ID
                   1572 4.R1010
                   q274\overline{9}193
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4102599
BLAST score
                   368
E value
                  .0.0e+00
Match length
                   424
                   97
% identity
NCBI Description
                   Arabidopsis thaliana ARF6 (ARF6) mRNA, complete cds
                   118484
Seq. No.
                   1573_1.R1010
Contig ID
                   PLN_{g}^{2}645970
5'-most EST
Method
                   BLASTX
                   g2645971
NCBI GI
                   1948
BLAST score
                   0.0e + 00
E value
Match length
                   360
                   100
% identity
                   (AF034255) reversibly glycosylated polypeptide-3
NCBI Description
                   [Arabidopsis thaliana]
                   118485
Seq. No.
                   1573_2.R1010
Contig ID
                   jC-a\overline{1}XLIB327436P1c04b1
5'-most EST
Method
                   BLASTX
                   q2317729
NCBI GI
BLAST score
                   1904
                   0.0e + 00
E value
                  352
Match length
% identity
                   99
NCBI Description
                   (AF013627) reversibly glycosylated polypeptide-1
                   [Arabidopsis thaliana]
                   118486
Seq. No.
                   1573 3.R1010
Contig ID
                   jC-atXLIB327429P4h02a2
5'-most EST
Method
                   BLASTX
                   q2645971
NCBI GI
BLAST score
                   1056
E value
                   1.0e-120
Match length
                   208
% identity
                   98
                   (AF034255) reversibly glycosylated polypeptide-3
NCBI Description
                   [Arabidopsis thaliana]
                   118487
Seq. No.
                   1573 5.R1010
Contig ID
```

12863

g2580661

5'-most EST

```
Method
                   BLASTX
NCBI GI
                   q2317729
BLAST score
                   468
E value
                   1.0e-46
Match length
                   114
% identity
                   82
NCBI Description
                   (AF013627) reversibly glycosylated polypeptide-1
                   [Arabidopsis thaliana]
Seq. No.
                   118488
                   1573_7.R1010
Contig ID
                  LIB3176-060-P1-K1-F1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q2317729
BLAST score
                   349
E value
                   4.0e-56
Match length
                   127
                   87
% identity
NCBI Description
                   (AF013627) reversibly glycosylated polypeptide-1
                   [Arabidopsis thaliana]
Seq. No.
                   118489
Contig ID
                   1573 8.R1010
5'-most EST
                  LIB3175-061-P1-K1-A7
                  BLASTX
Method
NCBI GI
                  a2130521
BLAST score
                   693
E value
                   3.0e~73
Match length
                  137
                   93
% identity
                   (U31565) reversibly glycosylatable polypeptide [Pisum
NCBI Description
                  sativum]
                  118490
Seq. No.
Contig ID
                  1573 10.R1010
5'-most EST
                  LIB23-013-Q1-E1-G3
Method
                  BLASTX
NCBI GI
                  q2317731
BLAST score
                   437
E value
                   4.0e-43
Match length
                   92
% identity
                  91
NCBI Description
                  (AF013628) reversibly glycosylated polypeptide-2
                   [Arabidopsis thaliana]
                  118491
Seq. No.
Contig ID
                  1575 1.R1010
5'-most EST
                  LIB22-029-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  q2058456
BLAST score
                  1975
E value
                  0.0e + 00
Match length
                  399
% identity
                  96
NCBI Description
                  (U66408) GTP-binding protein [Arabidopsis thaliana]
                  >gi_2345150_gb_AAB67830_ (AF014822) developmentally
                  regulated GTP binding protein [Arabidopsis thaliana]
```

```
118492
Seq. No.
Contig ID
                   1575 5.R1010
                   LIB2\overline{4}-043-Q1-E1-B7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2058456
BLAST score
                   408
E value
                   6.0e-40
Match length
                   81
% identity
                   100
NCBI Description
                   (U66408) GTP-binding protein [Arabidopsis thaliana]
                   >gi_2345150_gb_AAB67830_ (AF014822) developmentally
                   regulated GTP binding protein [Arabidopsis thaliana]
                   118493
Seq. No.
                   1576 1.R1010
Contig ID
                   jC-atXP94CG11C3T7078d1
5'-most EST
                   BLASTX
Method
                   q4467119
NCBI GI
                   2650
BLAST score
                   0.0e + 00
E value
Match length
                   501
% identity
                   98
NCBI Description
                   (AL035538) Histone deacetylase [Arabidopsis thaliana]
                   118494
Seq. No.
Contig ID
                   1578 1.R1010
                   jC-a\overline{t}XLIB327423P3f09b1
5'-most EST
Method
                   BLASTX
                   g4102703
NCBI GI
                   1355
BLAST score
                   1.0e-150
E value
Match length
                   268
% identity
                   100
NCBI Description
                   (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis
                   thaliana]
                   118495
Seq. No.
Contig ID
                   1578 2.R1010
                   jC-atXP37C157K5T7d2
5'-most EST
Method
                   BLASTX
                   q4102703
NCBI GI
BLAST score
                   226
E value
                   4.0e-18
                   89
Match length
% identity
                   65
                   (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   118496
                   1578 3.R1010
Contig ID
5'-most EST
                   q1054276
Method
                   BLASTX
NCBI GI
                   q4102703
BLAST score
                   593
                   2.0e-64
E value
Match length
                   214
```

```
% identity
                   63
                   (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                  118497
                  1578 4.R1010
Contig ID
5'-most EST
                   g1269278
                  BLASTN
Method
NCBI GI
                   g2760169
BLAST score
                   264
E value
                   1.0e-146
Match length
                   354
% identity
                   96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFB13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   118498
Contig ID
                   1583 1.R1010
5'-most EST
                   q906552
Method
                   BLASTX
NCBI GI
                   q3912988
BLAST score
                   1234
E value
                   1.0e-136
Match length
                   250
                   97
% identity
                  FLORAL HOMEOTIC PROTEIN AGL9 >qi 2345158 (AF015552) AGL9
NCBI Description
                   [Arabidopsis thaliana] >gi 2829878 (AC002396) AGL9
                   [Arabidopsis thaliana]
                   118499
Seq. No.
Contig ID
                   1584_1.R1010
5'-most EST
                   PLN_g3341716
Method
                   BLASTX
NCBI GI
                  q2781354
BLAST score
                   1545
E value
                   1.0e-172
Match length
                   314
% identity
                   94
NCBI Description
                  (AC003113) F2401.10 [Arabidopsis thaliana]
                  118500
Seq. No.
Contig ID
                   1584 2.R1010
5'-most EST
                   q2748931
Method
                   BLASTX
NCBI GI
                   q3341717
BLAST score
                   95
E value
                   6.0e-03
Match length
                   92
                   68
% identity
NCBI Description
                  (AF016100) ACC oxidase [Arabidopsis thaliana]
Seq. No.
                  118501
                   1584 3.R1010
Contig ID
5'-most EST
                   jC-atXP73CF2G8T7d2
Method
                  BLASTX
NCBI GI
                   g3341717
BLAST score
                   1090
```

Match length

```
E value
                   1.0e-119
Match length
                   280
% identity
                   68
                  (AF016100) ACC oxidase [Arabidopsis thaliana]
NCBI Description
                   118502
Seq. No.
                  1584 4.R1010
Contig ID
                  LIB3234-071-P1-K1-G12
5'-most EST
                  BLASTX
Method
NCBI GI
                   g2781354
BLAST score
                   376
E value
                  4.0e-36
                  104
Match length
% identity
                  75
                  (AC003113) F2401.10 [Arabidopsis thaliana]
NCBI Description
                  118503
Seq. No.
Contig ID
                  1584 5.R1010
                  LIB3176-023-P1-K1-C3
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2781354
BLAST score
                  114
E value
                   6.0e-05
Match length
                  207
% identity
                  83
                  (AC003113) F2401.10 [Arabidopsis thaliana]
NCBI Description
                  118504
Seq. No.
Contig ID
                  1584 6.R1010
                  LIB3177-016-P1-K2-D9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2781354
BLAST score
                   631
E value
                  7.0e-66
Match length
                  124
                  95
% identity
                  (AC003113) F2401.10 [Arabidopsis thaliana]
NCBI Description
                  118505
Seq. No.
Contig ID
                  1584_10.R1010
                  g241<u>2</u>872
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3341716
BLAST score
                  200
E value
                  1.0e-108
Match length
                  200
% identity
                  100
NCBI Description Arabidopsis thaliana ACC oxidase (ACO2) mRNA, complete cds
Seq. No.
                  118506
                  1586_1.R1010
Contig ID
5'-most EST
                  LIB3176-118-P2-K1-C8
                  BLASTX
Method
                 · q2760362
NCBI GI
BLAST score
                  700
                  8.0e-74
E value
```

5'-most EST

```
% identity
                  100
NCBI Description
                   (AF016511) 15.9 kDa subunit of RNA polymerase II
                   [Arabidopsis thaliana]
Seq. No.
                  118507
                  1587 1.R1010
Contig ID
                  jC-atXLIB327408P2c01b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2827888
BLAST score
                  1384
E value
                  1.0e-154
Match length
                  271
                  100
% identity
                   (AF016621) ATP-dependent Clp protease proteolytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  118508
                  1587 2.R1010
Contig ID
                  LIB3168-010-P1-K1-C8
5'-most EST
Method
                  BLASTN
                  g4760411
NCBI GI
BLAST score
                  406
E value
                  0.0e + 00
Match length
                  515
% identity
                  98
                  Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,
NCBI Description
                  complete sequence
                  118509
Seq. No.
                  1588 1.R1010
Contig ID
                  LIB3175-031-P1-K1-D12
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3122387
BLAST score
                  2229
E value
                  0.0e + 00
Match length
                  424
% identity
                  98
                  WD-40 REPEAT PROTEIN MSI1 >gi 2394229 (AF016846) WD-40
NCBI Description
                  repeat protein [Arabidopsis thaliana]
                  118510
Seq. No.
                  1589 1.R1010
Contig ID
                  jC-a\(\bar{1}\)XLIB327435P2h08b1
5'-most EST
Method
                  BLASTX
                  g3122388
NCBI GI
BLAST score
                  2154
E value
                  0.0e + 00
Match length
                  415
% identity
                  97
NCBI Description
                  WD-40 REPEAT PROTEIN MSI2 >gi_2394231 (AF016847) WD-40
                  repeat protein [Arabidopsis thaliana]
                  >gi_4581121_gb_AAD24611.1_AC005825_18 (AC005825) putative
                  WD-40 protein MSI2 [Arabidopsis thaliana]
Seq. No.
                  118511
                  1589 2.R1010
Contig ID
```

LIB25-102-Q1-E1-E8

```
Method
                   BLASTX
NCBI GI
                   q3122389
BLAST score
                   2205
E value
                   0.0e + 00
Match length
                   424
% identity
                   97
                  WD-40 REPEAT PROTEIN MSI3 >qi 2394233 (AF016848) WD-40
NCBI Description
                  repeat protein [Arabidopsis thaliana]
Seq. No.
                   118512
                   1591 1.R1010
Contig ID
5'-most EST
                   q1154964
Method
                   BLASTX
NCBI GI
                  q3372230
BLAST score
                   619
E value
                   2.0e-64
Match length
                   148
% identity
NCBI Description
                   (AF017074) RNA polymerase I, II and III 16.5 kDa subunit
                   [Arabidopsis thaliana] >gi_4585968_gb_AAD25604.1 AC005287 6
                   (AC005287) RNA polymerase I, II and III 16.5 kDa subunit
                   [Arabidopsis thaliana]
Seq. No.
                   118513
                   1591 2.R1010
Contig ID
5'-most EST
                  LIB3177-046-P1-K2-H11
                  BLASTX
Method
NCBI GI
                  q3372230
BLAST score
                   142
                  9.0e-46
E value
                   108
Match length
% identity
NCBI Description
                   (AF017074) RNA polymerase I, II and III 16.5 kDa subunit
                   [Arabidopsis thaliana] >gi_4585968_gb_AAD25604.1_AC005287_6
                   (AC005287) RNA polymerase I, II and III 16.5 kDa subunit
                   [Arabidopsis thaliana]
Seq. No.
                   118514
Contig ID
                  1593 1.R1010
5'-most EST
                   jC-atXLIB327420P1e03b1
Method
                  BLASTX
NCBI GI
                  q3372233
BLAST score
                   1037
E value
                   1.0e-113
Match length
                   205
% identity
                   100
NCBI Description
                   (AF019248) RNA polymerase I, II and III 24.3 kDa subunit
                   [Arabidopsis thaliana]
Seq. No.
                   118515
Contig ID
                  1595 1.R1010
5'-most EST
                  PLN g_{2444270}
Method
                  BLASTX
NCBI GI
                  g2444271
BLAST score
                  2507
E value
                  0.0e + 00
Match length
                  516
```

BLAST score

1719

```
95
% identity
                   (AF019637) putative amino acid or GABA permease
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   118516
                   1600 1.R1010
Contig ID
5'-most EST
                  LIB24-021-Q1-E1-G1
                                         . 45
Method
                  BLASTX
NCBI GI
                  q3659909
BLAST score
                   2171
E value
                  0.0e + 00
Match length
                   483
                  89
% identity
                  (AF020715) histidyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                  118517
Seq. No.
                  1600 2.R1010
Contig ID
                  g3449457
5'-most EST
                  BLASTN
Method
NCBI GI
                  q3659908
BLAST score
                  166
E value
                   4.0e-88
Match length
                  312
% identity
                  Arabidopsis thaliana histidyl-tRNA synthetase mRNA,
NCBI Description
                  complete cds
Seq. No.
                  118518
                  1600 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327403P3f09b2
                  BLASTN
Method
NCBI GI
                  q3659908
BLAST score
                  197
                  1.0e-106
E value
Match length
                  385
% identity
                  Arabidopsis thaliana histidyl-tRNA synthetase mRNA,
NCBI Description
                  complete cds
                  118519
Seq. No.
Contig ID
                  1600 4.R1010
5'-most EST
                  LIB3168-083-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  q3659908
BLAST score
                  186
E value
                  1.0e-100
Match length
                  423
% identity
                  Arabidopsis thaliana histidyl-tRNA synthetase mRNA,
NCBI Description
                  complete cds
                  118520
Seq. No.
Contig ID
                  1601 1.R1010
5'-most EST
                  PLN g2460202
Method
                  BLASTX
NCBI GI
                  q2460203
```

Contig ID

```
E value
                    0.0e + 00
                    324
 Match length
                    100
 % identity
                    (AF021244) coronatine-induced protein 1 [Arabidopsis
 NCBI Description
                    thaliana]
                    118521
Seq. No.
                    1602 1.R1010
 Contig ID
                    jC-atXLIB327408P1g05b1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q2736147
 BLAST score
                    449
                    1.0e-118
 E value
                    234
 Match length
                    83
 % identity
                    (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis
 NCBI Description
                    thaliana] >gi 3132481 (AC003096) fatty acid hydroxylase,
                    FAH1 [Arabidopsis thaliana]
                    118522
 Seq. No.
                    1602_2.R1010
 Contig ID
 5'-most EST
                    g397\overline{1}98
 Method
                    BLASTN
                    g3132469
 NCBI GI
 BLAST score
                    212
                    1.0e-115
 E value
 Match length
                    371
                    98
 % identity
                    Arabidopsis thaliana chromosome II BAC T29F13 genomic
 NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
                    118523
 Seq. No.
                    1603_1.R1010
 Contig ID
 5'-most EST
                    PLN_{g}^{2736154}
                    BLASTX
 Method
 NCBI GI
                    g2736155
 BLAST score
                    2341
 E value
                    0.0e + 00
 Match length
                    477
                    94
 % identity
                    (AF022082) sulfolipid biosynthesis protein [Arabidopsis
 NCBI Description
                    thaliana] >gi_3688184_emb_CAA21212_ (AL031804) sulfolipid
                    biosynthesis protein SQD1 [Arabidopsis thaliana]
 Seq. No.
                    118524
                    1604_1.R1010
 Contig ID
 5'-most EST
                    LIB25-088-Q1-E1-G4
 Method
                    BLASTX
 NCBI GI
                    q4103243
 BLAST score
                    2493
                    0.0e + 00
 E value
 Match length
                    1040
                    86
 % identity
                    (AF022368) BIPOSTO [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    118525
```

1605 1.R1010

Seq. No.

118530

```
5'-most EST
                   PLN g2511545
Method
                   BLASTX
NCBI GI
                   g2511546
BLAST score
                   876
E value
                   2.0e-94
Match length
                   238
% identity
                   72
                   (AF022658) putative c2h2 zinc finger transcription factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   118526
                   1606 1.R1010
Contig ID
                   LIB23-020-Q1-E1-F10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2921158
BLAST score
                   4325
E value
                   0.0e + 00
Match length
                   928
                   94
% identity
NCBI Description
                   (AF022909) ClpC [Arabidopsis thaliana]
Seq. No.
                   118527
Contig ID
                   1606_6.R1010
5'-most EST
                   jC-atXLIB327431P4d09a1
Method
                   BLASTX
NCBI GI
                   q2921158
BLAST score
                   628
E value
                   6.0e-89
Match length
                   194
                   96
% identity
NCBI Description
                   (AF022909) ClpC [Arabidopsis thaliana]
Seq. No.
                   118528
                   1610_1.R1010
Contig ID
5'-most EST
                   PLN_g2465922
Method
                   BLASTX
NCBI GI
                   q2465923
BLAST score
                   5105
E value
                   0.0e + 00
Match length
                   1020
                   96
% identity
NCBI Description
                   (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                   118529
                   1611 1.R1010
Contig ID
5'-most EST
                   PLN g2465924
Method
                   BLASTX
NCBI GI
                   q2465925
BLAST score
                   3080
E value
                   0.0e + 00
Match length
                   617
                   97
% identity
NCBI Description (AF024649) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
```

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```
1612 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327413P4b07b1
Method
                  BLASTX
NCBI GI
                  g1785621
BLAST score
                  3006
E value
                  0.0e + 00
Match length
                  617
% identity
NCBI Description
                  (Z84202) AtPK2324 [Arabidopsis thaliana] >gi 2465927
                  (AF024650) receptor-like serine/threonine kinase
                  [Arabidopsis thaliana] >gi_4249408 (AC006072) putative
                  serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.
                  118531
                  1613 1.R1010
Contig ID
                  LIB3168-014-P1-K1-A5
5'-most EST
Method
                  BLASTX
                  g3600031
NCBI GI
                  1562
BLAST score
                  1.0e-174
E value
                  344
Match length
% identity
                  89
NCBI Description
                  (AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic
                  acid aldolases [Arabidopsis thaliana]
                  118532
Seq. No.
                  1614 1.R1010
Contig ID
5'-most EST
                  PLN g4103356
Method
                  BLASTX
NCBI GI
                  g3858935
                  1017
BLAST score
E value
                  1.0e-110
Match length
                  219
% identity
                  91
NCBI Description
                  (AL021636) synaptobrevin-like protein [Arabidopsis
                  thaliana] >gi_4103357 (AF025332) vesicle-associated
                  membrane protein 7C; synaptobrevin 7C [Arabidopsis
                  thaliana]
Seq. No.
                  118533
Contig ID
                  1614 2.R1010
5'-most EST
                  jC-atXLIB327414P2e04a1
Method
                  BLASTX
NCBI GI
                  q3858935
BLAST score
                  400
E value
                  1.0e-38
Match length
                  102
% identity
                  75
NCBI Description
                  (AL021636) synaptobrevin-like protein [Arabidopsis
                  thaliana] >gi 4103357 (AF025332) vesicle-associated
                  membrane protein 7C; synaptobrevin 7C [Arabidopsis
                  thaliana]
                  118534
Seq. No.
Contig ID
                  1614 3.R1010
5'-most EST
                  LIB3175-025-P1-K1-A2
Method
                  BLASTX
```

Match length

1084

```
q3858935
NCBI GI
BLAST score
                   161
                   2.0e-52
E value
Match length
                  111
% identity
                   96
                   (AL021636) synaptobrevin-like protein (Arabidopsis
NCBI Description
                   thaliana] >gi 4103357 (AF025332) vesicle-associated
                  membrane protein 7C; synaptobrevin 7C [Arabidopsis
                   thaliana]
                   118535
Seq. No.
                  1614 4.R1010
Contig ID
                   jC-atXLIB327431P3d10a1
5'-most EST
Method
                   BLASTX
                   g3858935
NCBI GI
BLAST score
                   156
                   1.0e-26
E value
                   93
Match length
% identity
                   58
                   (AL021636) synaptobrevin-like protein [Arabidopsis
NCBI Description
                   thaliana] >gi 4103357 (AF025332) vesicle-associated
                  membrane protein 7C; synaptobrevin 7C [Arabidopsis
                   thaliana]
Seq. No.
                   118536
                   1616 1.R1010
Contig ID
5'-most EST
                   PLN g3335059
Method
                  BLASTX
NCBI GI
                   g3335060
BLAST score
                   5027
E value
                   0.0e+00
Match length
                   1014
% identity
                   98
NCBI Description
                   (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
                   thaliana] >gi 4468989 emb CAB38303 (AL035605) plasma
                  membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
                   118537
Seq. No.
                  1617 1.R1010
Contig ID
                  LIB3168-027-P1-K1-H10
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2605714
BLAST score
                   1206
                  1.0e-133
E value
Match length
                   267
% identity
NCBI Description
                   (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
                   thaliana]
Seq. No.
                   118538
                   1619 1.R1010
Contig ID
                   PLN \frac{1}{9}2827140
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2827141
BLAST score
                   5236
                   0.0e + 00
E value
```

```
% identity
                   (AF027173) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   118539
                   1619 2.R1010
 Contig ID
                   jC-atXP83CG3A4T7043d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3135611
BLAST score
                   694
E value
                   3.0e-73
Match length
                   147
                   90
 % identity
NCBI Description (AF062485) cellulose synthase [Arabidopsis thaliana]
                   118540
Seq. No.
                   1619 3.R1010
Contig ID
                   jC-atXP89CG6E2T7062d1
 5'-most EST
                   BLASTX
Method
NCBI GI
                   g3135611
BLAST score
                   632
E value
                   5.0e-66
Match length
                   155
 % identity
NCBI Description (AF062485) cellulose synthase [Arabidopsis thaliana]
                   118541
Seq. No.
                   1619 4.R1010
 Contig ID
                   jC-atXLIB327421P4c09b1
 5'-most EST
Method
                   BLASTX
                   g3135611
NCBI GI
BLAST score
                   762
E value
                   3.0e-81
Match length
                   147
 % identity
                   94
NCBI Description (AF062485) cellulose synthase [Arabidopsis thaliana]
Seq. No.
                   118542
                   1620 1.R1010
 Contig ID
                   PLN g2827142
 5'-most EST
Method
                   BLASTX
                   g2827143
NCBI GI
BLAST score
                   5515
                   0.0e + 00
 E value
                   1065
Match length
 % identity
                   97
                   (AF027174) cellulose synthase catalytic subunit
 NCBI Description
                   [Arabidopsis thaliana]
                   118543
 Seq. No.
                   1620 6.R1010
 Contig ID
                   jC-atXLIB327425P4e02b1
 5'-most EST
Method
                   BLASTN
NCBI GI
                   g2827142
 BLAST score
                   337
                   0.0e+00
 E value
Match length
                   451
```

```
% identity
                  Arabidopsis thaliana cellulose synthase catalytic subunit
NCBI Description
                   (Ath-B) mRNA, complete cds
                   118544
Seq. No.
                   1621_1.R1010
Contig ID
                   PLN_g2653884
5'-most EST
                   BLASTX
Method
                   g2653885
NCBI GI
BLAST score
                   4371
E value
                   0.0e + 00
Match length
                   855
                   97
% identity
                   (AF027408) phospholipase D-gamma; PLD-gamma [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   118545
                   1621 2.R1010
Contig ID
                   jC-atXLIB327419P3f02b2
5'-most EST
Method
                   BLASTX
                   g2653885
NCBI GI
BLAST score
                   1012
E value
                   1.0e-119
Match length
                   252
% identity
                   89
                   (AF027408) phospholipase D-gamma; PLD-gamma [Arabidopsis
NCBI Description
                   thaliana]
                   118546
Seq. No.
Contig ID
                   1621 3.R1010
                   g2048300
5'-most EST
Method
                   BLASTX
                   g2653885
NCBI GI
BLAST score
                   368
E value
                   4.0e-35
Match length
                   75
% identity
                   95
                   (AF027408) phospholipase D-gamma; PLD-gamma [Arabidopsis
NCBI Description
                   thaliana]
                   118547
Seq. No.
                   1622 1.R1010
Contig ID
                   PLN g_{2687354}
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2335192
BLAST score
                   2931
                   0.0e + 00
E value
Match length
                   596
% identity
                   96
NCBI Description
                  (AF013465) bHLH protein [Arabidopsis thaliana]
                  118548
Seq. No.
Contig ID
                  1623_1.R1010
5'-most EST
                  LIB3177-056-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2464941
BLAST score
                   765
```

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5'-most EST Method

```
E value
                  2.0e-81
Match length
                  153
                  90
% identity
                  (299708) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                  thaliana] >gi_2801446 (AF028340) ubiquitin-conjugating
                  enzyme 17 [Arabidopsis thaliana]
                  118549
Seq. No.
                  1624 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P3f07b1
Method
                  BLASTX
NCBI GI
                  g4191782
                  2504
BLAST score
                  0.0e + 00
E value
                  507
Match length
                  93
% identity
                  (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
NCBI Description
                  118550
Seq. No.
                  1625_1.R1010
Contig ID
                  jC-atXLIB327419P4c05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3108209
BLAST score
                  1192
E value
                  1.0e-131
Match length
                  221
% identity
                  100
                  (AF028809) eukaryotic cap-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  118551
Seq. No.
                  1626 1.R1010
Contig ID
5'-most EST
                  PLN_g2565435
Method
                  BLASTX
NCBI GI
                  g2565436
BLAST score
                  1797
                  0.0e + 00
E value
                  397
Match length
% identity
                  91 .
                  (AF028842) DegP protease precursor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118552
Contig ID
                  1626_3.R1010
5'-most EST
                  ARABL1-04-Q1-B1-H1
Method
                  BLASTN
NCBI GI
                  g2565435
BLAST score
                  181
E value
                  2.0e-97
                  277
Match length
% identity
                  Arabidopsis thaliana DegP protease mRNA, nuclear gene
NCBI Description
                  encoding chloroplast protein, complete cds
                  118553
Seq. No.
                  1628 1.R1010
Contig ID
```

12877:--

LIB3176-042-P1-K1-G6

BLASTX

Contig ID

```
g4103952
NCBI GI
BLAST score
                   1582
E value
                   1.0e-177
Match length
                   314
                   100
% identity
NCBI Description
                   (AF029980) A37 [Arabidopsis thaliana] >gi_4103954
                   (AF029981) A37 [Arabidopsis thaliana]
                   118554
Seq. No.
Contig ID
                   1628 2.R1010
5'-most EST
                   jC-atXP50C180G14T7050d1
Method
                   BLASTX
                  q4103952
NCBI GI
                   345
BLAST score
                   1.0e-37
E value
                   107
Match length
% identity
                   87
NCBI Description
                   (AF029980) A37 [Arabidopsis thaliana] >gi_4103954
                   (AF029981) A37 [Arabidopsis thaliana]
                  118555
Seq. No.
                   1630_1.R1010
Contig ID
                   jC-atXLIB327410P4b06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2772934
BLAST score
                   948
E value
                   1.0e-102
Match length
                   223
% identity
                   81
                   (AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis
NCBI Description
                   thaliana]
                   118556
Seq. No.
Contig ID
                   1630_2.R1010
5'-most EST
                   g2393258
Method
                   BLASTX
                   q2772934
NCBI GI
BLAST score
                   247
                  8.0e-21
E value
                  79
Match length
% identity
                  65
                   (AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis
NCBI Description
                   thaliana]
                  118557
Seq. No.
Contig ID
                   1631_1.R1010
                  LIB35-037-Q1-E1-C4
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2642215
BLAST score
                   332
E value
                   1.0e-30
                   79
Match length
                   78
% identity
                  (AF030386) NOI protein [Arabidopsis thaliana]
NCBI Description
                  118558
Seq. No.
```

1632_1.R1010

```
5'-most EST
                   iC-atXP92CH3G4T7046d1
Method
                   BLASTX
NCBI GI
                   g2832241
BLAST score
                   4884
E value
                   0.0e + 00
Match length
                   996
                   95
% identity .
                   (AF030864) nonphototropic hypocotyl 1 [Arabidopsis
NCBI Description
Seq. No.
                   118559
                   1632 2.R1010
Contig ID
                   jC-atX23018Q1E1F09b2
5'-most EST
                   BLASTX
Method
NCBI GI
                   a2832241
BLAST score
                   756
E value
                   2.0e-82
                   165
Match length
% identity
                   85
                   (AF030864) nonphototropic hypocotyl 1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   118560
Contig ID
                   1634_1.R1010
                   g937<u>2</u>53
5'-most EST
Method
                   BLASTX
                   q2500194
NCBI GI
BLAST score
                   937
                   1.0e-101
E value
                   196
Match length
                   93
% identity
                  RAC-LIKE GTP BINDING PROTEIN ARAC5 >gi 1293668 (U52350)
NCBI Description
                   GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                   118561
Contig ID
                   1634_2.R1010
                   PLN_g1304416
5'-most EST
                   BLASTX
Method
NCBI GI
                   a2500193
BLAST score
                   930
E value
                   1.0e-100
Match length
                   195
                   93
% identity
NCBI Description
                  RAC-LIKE GTP BINDING PROTEIN ARAC4 (GTP BINDING PROTEIN
                   ROP2) >gi_1304417 (U45236) Description: rac-like protein;
                   GTP binding protein; Method: conceptual translation
                   supplied by author. [Arabidopsis thaliana] >gi_1777764
                   (U49972) GTP binding protein Rop2At [Arabidopsis thaliana]
Seq. No.
                   118562
Contig ID
                   1634 3.R1010
5'-most EST
                   g1054214
Method
                  BLASTX
NCBI GI
                  g2500198
BLAST score
                   269
E value
                   6.0e-23
Match length
                   116
```

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```
% identity
                   45
NCBI Description RAC-LIKE GTP BINDING PROTEIN RAC2 >gi 1370201 emb CAA98190
                   (Z73962) RAC2 [Lotus japonicus]
                   118563
Seq. No.
Contig ID
                   1637 1.R1010
                  PLN \bar{g}3252867
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3252868
BLAST score
                   1566
                   1.0e-175
E value
Match length
                   353
% identity
                  88
                  (AF033536) putative zinc transporter [Arabidopsis thaliana]
NCBI Description
                  118564
Seq. No.
Contig ID
                  1643 1.R1010
5'-most EST
                   g259<del>6</del>825
Method
                  BLASTX
                   g4205079
NCBI GI
                   106
BLAST score
                   1.0e-03
E value
Match length
                   363
% identity
                   93
NCBI Description
                  (U70425) ankyrin repeat-containing protein 2 [Arabidopsis
                  thaliana]
                   118565
Seq. No.
Contig ID
                   1643 2.R1010
5'-most EST
                  jC-atXLIB327409P1a09b1
Method
                  BLASTX
                  q3478700
NCBI GI
BLAST score
                   1669
E value
                   0.0e + 00
                   367
Match length
% identity
                   90
NCBI Description
                  (AF034387) AFT protein [Arabidopsis thaliana]
                  118566
Seq. No.
                  1643 3.R1010
Contig ID
5'-most EST
                   jC-atXP123C119N10T7034a1
                   BLASTX
Method
                  q2262170
NCBI GI
BLAST score
                   493
E value
                  2.0e-49
                  101
Match length
% identity
                   95
                  (AC002329) predicted glycosyl hydrolase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  118567
                  1643 4.R1010
Contig ID
5'-most EST
                  jC-atxP11C97E11T7004d1
Method
                  BLASTX
                  g22621·70
NCBI GI
BLAST score
                  1064
E value
                  1.0e-116
```

12880

```
Match length
                  231
% identity
                  90
NCBI Description
                  (AC002329) predicted glycosyl hydrolase [Arabidopsis
                  thaliana]
Seq. No.
                  118568
                  1643_5.R1010
Contig ID
5'-most EST
                  LIB24-054-Q1-E1-E5
                  BLASTX
Method
NCBI GI
                  q2262170
BLAST score
                  630
E value
                  9.0e-67
Match length
                  175
                  79
% identity
                  (AC002329) predicted glycosyl hydrolase [Arabidopsis
NCBI Description
                  thaliana]
                  118569
Seq. No.
Contig ID
                  1643_6.R1010
                  jC-atXLIB327406P2h06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2262170
BLAST score
                  642
                  1.0e-131
E value
Match length
                  267
                  93
% identity
                  (AC002329) predicted glycosyl hydrolase [Arabidopsis
NCBI Description
                  thaliana]
                  118570
Seq. No.
                  1643_10.R1010
Contig ID
5'-most EST
                  LIB24-023-Q1-E1-A4
Method
                  BLASTX
                  q3478700
NCBI GI
BLAST score
                  291
E value
                  4.0e-26
                  87
Match length
                  72
% identity
NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]
Seq. No.
                  118571
                  1643 11.R1010
Contig ID
5'-most EST
                  LIB25-012-Q1-E1-E2
Method
                  BLASTX
NCBI GI
                  q3478700
BLAST score
                  146
                  4.0e-09
E value
Match length
                  89
% identity
                  56
NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]
                  118572
Seq. No.
Contig ID
                  1643 12.R1010
5'-most EST
                  LIB24-129-Q1-E1-B5
Method
                  BLASTX
NCBI GI
                  g3478700
BLAST score
                  151
```

```
4.0e-10
E value
Match length
                   68
                   72
% identity
                  (AF034387) AFT protein [Arabidopsis thaliana]
NCBI Description
                   118573
Seq. No.
                   1644_1.R1010
Contig ID
5'-most EST
                  PLN_g3132890
Method
                  BLASTX
                   g3132891
NCBI GI
                   2392
BLAST score
                   0.0e + 00
E value
Match length
                   462
                   97
% identity
                   (AF034573) endo-1,4-beta glucanase; ATCEL2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   118574
                   1645_1.R1010
Contig ID
5'-most EST
                  LIB2\overline{4}-113-Q1-E1-E8
Method
                  BLASTX
                   g3355475
NCBI GI
BLAST score
                   525
E value
                   3.0e~53
Match length
                   154
% identity
                  70
                  (AC004218) ribosomal protein L23a [Arabidopsis thaliana]
NCBI Description
                   118575
Seq. No.
                  1646 1.R1010
Contig ID
5'-most EST
                  PLN_g3056724
                   BLASTX
Method
                   g3056725
NCBI GI
BLAST score
                   3984
                   0.0e+00
E value
                  785
Match length
% identity
                  98
                  (AF034774) ent-kaurene synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118576
Contig ID
                  1647_1.R1010
5'-most EST
                  PLN g2921405
Method
                  BLASTX
NCBI GI
                   g2921406
BLAST score
                   2815
E value
                   0.0e+00
Match length
                   569
                   98
% identity
NCBI Description
                   (AF036234) vacuolar protein sorting homolog [Arabidopsis
                  thaliana]
Seq. No.
                  118577
                  1648 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327407P2h05b1
Method
                  BLASTX
                  g2674203
NCBI GI
BLAST score
                   2443
```

NCBI GI

```
E value
                   0.0e + 00
Match length
                   568
% identity
                   87
                   (AF036328) CLP protease regulatory subunit CLPX
NCBI Description
                   [Arabidopsis thaliana]
                   118578
Seq. No.
                   1649 1.R1010
Contig ID
                   PLN_g3158393
5'-most EST
                   BLASTX
Method
                   g2088647
NCBI GI
BLAST score
                   3007
E value
                   0.0e + 00
                   592
Match length
                   97
% identity
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
                   118579
Seq. No.
Contig ID
                   1650 1.R1010
5'-most EST
                   jC-atXmonuni27De07b1
                  BLASTX
Method
NCBI GI
                  g2708624
BLAST score
                   3699
                   0.0e + 00
E value
Match length
                   693
                   100
% identity
                   (AF036618) acetyl-CoA synthetase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118580
                   1651 1.R1010
Contig ID
                   PLN_g2689719
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2689720
BLAST score
                   1213
E value
                   1.0e-133
Match length
                   274
% identity
                   89
NCBI Description
                  (AF037168) DnaJ homologue [Arabidopsis thaliana]
                   118581
Seq. No.
                   1652 1.R1010
Contig ID
5'-most EST
                  PLN g^{2982221}
Method
                  BLASTX
NCBI GI
                  g2982222
BLAST score
                   4589
E value
                   0.0e + 00
Match length
                   902
% identity
                   97
                   (AF037229) transcription factor [Arabidopsis thaliana]
NCBI Description
                  118582
Seq. No.
                  1653 1.R1010
Contig ID
                  PLN_{g}^{-2}2708812
5'-most EST
                  BLASTN
Method
```

g2708812

BLAST score

2242

```
BLAST score
                   1781
                   0.0e+00
E value
Match length
                   1789
                   100
% identity
NCBI Description Arabidopsis thaliana ATA20 mRNA, complete cds
                                                 ė.
                   118583
Seq. No.
                   1653 2.R1010
Contig ID
                   g344\overline{9}416
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4159707
                   362
BLAST score
                   0.0e + 00
E value
Match length
                   418
% identity
                   97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJK13, complete sequence
                   118584
Seq. No.
                   1654 1.R1010
Contig ID
5'-most EST
                   PLN g2707335
Method
                   BLASTX
NCBI GI
                   g2707336
BLAST score
                   1942
E value
                   0.0e + 00
Match length
                   407
% identity
                   92
NCBI Description (AF037442) histone acetyltransferase [Arabidopsis thaliana]
Seq. No.
                   118585
                   1655 1.R1010
Contig ID
5'-most EST
                   PLN g2746338
Method
                  BLASTX
NCBI GI
                   g2746339
BLAST score
                   749
                   2.0e-79
E value
Match length
                   140
% identity
                   100
NCBI Description (AF037589) ATA7 [Arabidopsis thaliana]
                   118586
Seq. No.
                   1656 1.R1010
Contig ID
5'-most EST
                  LIB24-110-Q1-E1-G9
Method
                  BLASTX
                   g2746341
NCBI GI
BLAST score
                   2716
E value
                   0.0e + 00
Match length
                   522
% identity
                   95
NCBI Description (AF037590) ATA27 [Arabidopsis thaliana]
                   118587
Seq. No.
                   1657 1.R1010
Contig ID
5'-most EST
                   jC-atXP74C226A9T7048d1
                  BLASTX
Method
                  g3138972
NCBI GI
```

5'-most EST

```
E value
                  0.0e + 00
Match length
                  483
                  92
% identity
                  (AF038505) dihydrolipoylacyltransferase subunit of the
NCBI Description
                  branched-chain alpha-keto acid dehydrogenase complex
                   [Arabidopsis thaliana]
                  118588
Seq. No.
                  1657_3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327439P2h04b2
                  BLASTN
Method
NCBI GI
                  g3138971
BLAST score
                  327
                  0.0e + 00
E value
Match length
                  454
                  95
% identity
                  Arabidopsis thaliana dihydrolipoylacyltransferase subunit
NCBI Description
                  of the branched-chain alpha-keto acid dehydrogenase complex
                  (LTA1) mRNA, complete cds
                  118589
Seq. No.
                  1658_1.R1010
Contig ID
5'-most EST
                  PLN g4185739
Method
                  BLASTX
                  g4185740
NCBI GI
BLAST score
                   4614
                  0.0e + 00
E value
                  951
Match length
% identity
                  95
NCBI Description
                   (AF079999) putative glutamate receptor [Arabidopsis
                  thaliana]
                  118590
Seq. No.
Contig ID
                  1663_1.R1010
5'-most EST
                  PLN g2789659
                  BLASTX
Method
NCBI GI
                   g2789660
BLAST score
                   3628
E value
                  0.0e + 00
Match length
                  900
                  81
% identity
                  (AF040102) p105 [Arabidopsis thaliana]
NCBI Description
                  118591
Seq. No.
                  1663 2.R1010
Contig ID
                  LIB24-027-Q1-E1-E7
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2789659
BLAST score
                   385
E value
                  0.0e + 00
Match length
                  552
                  93
% identity
                  Arabidopsis thaliana p105 mRNA, complete cds
NCBI Description
Seq. No.
                  118592
                  1665 1.R1010
Contig ID
```

 $PLN_{g}4104930$

```
Method
                  BLASTX
NCBI GI
                  q4104931
BLAST score
                  4004
                  0.0e + 00
E value
Match length
                  811
% identity
                  94
                  (AF042196) auxin response factor 8 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118593
                  1666 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327409P1g04b1
Method
                  BLASTX
                  q2462824
NCBI GI
BLAST score
                  1766
                  0.0e + 00
E value
Match length
                  351
% identity
                  97
                   (AF000657) similar to Jun activation domain binding protein
NCBI Description
                   [Arabidopsis thaliana] >gi 2791885 (AF042334) JAB1
                   [Arabidopsis thaliana]
Seq. No.
                  118594
                  1667 1.R1010
Contig ID
                  LIB3175-027-P1-K1-G9
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2811226
BLAST score
                  3298
E value
                  0.0e + 00
Match length
                  654
% identity
                  98
                  (AF042669) fimbrin 2 [Arabidopsis thaliana] >gi 2811232
NCBI Description
                   (AF042671) fimbrin 2 [Arabidopsis thaliana]
                  118595
Seq. No.
Contig ID
                  1668 1.R1010
                  jC-atXLIB327439P2h11b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2829133
BLAST score
                  1531
E value
                  1.0e-171
Match length
                  293
% identity
                  100
NCBI Description
                  (AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis
                  thaliana] >gi 4490745 emb CAB38907.1 (AL035708)
                  adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana]
Seq. No.
                  118596
                  1668 2.R1010
Contig ID
5'-most EST
                  q2048478
Method
                  BLASTN
NCBI GI
                  q2829132
BLAST score
                  296
E value
                  1.0e-165
Match length
                  419
% identity
                  94
                  Arabidopsis thaliana adenosine-5'-phosphosulfate-kinase
NCBI Description
```

(akn2) mRNA, complete cds

```
Seq. No.
                   118597
                   1668 3.R1010
Contig ID
                   g2749600
5'-most EST
                   118598
Seq. No.
                   1668 6.R1010
Contig ID
                   LIB3176-033-P1-K1-D5
5'-most EST
Seq. No.
                   118599
Contig ID
                   1668 9.R1010
                   LIB2\overline{3}-069-Q1-E1-D9
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4490734
BLAST score
                   403
E value
                   0.0e + 00
Match length
                   503
                   95
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
NCBI Description
                   project)
                   118600
Seq. No.
Contig ID
                   1669 1.R1010
5'-most EST
                   jC-atXLIB327404P4b05b1
Method
                   BLASTX
                   q2511588
NCBI GI
                   1251
BLAST score
E value
                   1.0e-138
                   245
Match length
                   100
% identity
                   (Y13691) multicatalytic endopeptidase complex, proteasome
NCBI Description
                   component, alpha subunit [Arabidopsis thaliana]
                   118601
Seq. No.
                   1669 2.R1010
Contig ID
                   jC-atXP79C238C1T7b1
5'-most EST
                   BLASTX
Method
                   q3421072
NCBI GI
BLAST score
                   1255
                   1.0e-138
E value
Match length
                   246
                   100
% identity
                   (AF043519) 20S proteasome subunit PAA2 [Arabidopsis
NCBI Description
                   thaliana] >gi 4006819 (AC005970) 20S proteasome subunit
                   PAA2 [Arabidopsis thaliana]
                   118602
Seq. No.
                   1669 3.R1010
Contig ID
5'-most EST
                   jC-atX25001Q1E2H08b1
Method
                   BLASTX
NCBI GI
                   q3935145
BLAST score
                   328
E value
                   2.0e-30
Match length
                   62
% identity
                   100
```

NCBI Description (AC005106) T25N20.9 [Arabidopsis thaliana]

E value

```
Seq. No.
                  118603
Contig ID
                  1671 1.R1010
5'-most EST
                  jC-atX23020Q1E1D08b1
Method
                  BLASTX
NCBI GI
                  g2511574
BLAST score
                  1182
E value
                  1.0e-130
Match length
                  235
% identity
                  100
                  (Y13176) multicatalytic endopeptidase [Arabidopsis
NCBI Description
                  thaliana] >gi_3421075 (AF043520) 20S proteasome subunit
                  PAB1 [Arabidopsis thaliana]
                  118604
Seq. No.
Contig ID
                  1671 2.R1010
                  jC-atXLIB327406P4b11b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2511574
BLAST score
                  538
E value
                  5.0e-55
Match length
                  109
                  99
% identity
NCBI Description
                  (Y13176) multicatalytic endopeptidase [Arabidopsis
                  thaliana] >gi 3421075 (AF043520) 20S proteasome subunit
                  PAB1 [Arabidopsis thaliana]
                  118605
Seq. No.
Contig ID
                  1672 1.R1010
5'-most EST
                  jC-atXLIB327411P1b01b1
Method
                  BLASTX
NCBI GI
                  g3421077
BLAST score
                  1214
E value
                  1.0e-134
Match length
                  250
                  95
% identity
                  (AF043521) 20S proteasome subunit PAC1 [Arabidopsis
NCBI Description
                  thaliana]
                  118606
Seq. No.
Contig ID
                  1674 1.R1010
5'-most EST
                  g2757926
Method
                  BLASTX
NCBI GI
                  q3421082
BLAST score
                  1109
E value
                  1.0e-121
Match length
                  247
                  90
% identity
                  (AF043523) 20S proteasome subunit PAD2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  118607
                  1674 3.R1010
Contig ID
5'-most EST
                  g1158661
Method
                  BLASTX
NCBI GI
                  g3421082
BLAST score
                  582
```

4.0e-60

```
Match length
                    164
 % identity
                    77
                    (AF043523) 20S proteasome subunit PAD2 (Amabidopsis
 NCBI Description
                    thalianal
                    118608
 Seq. No.
 Contig ID
                    1675 1.R1010
                    PLN_g3421086
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q3421087
 BLAST score
                    1198
 E value
                    1.0e-132
                    236
 Match length
 % identity
                    100
 NCBI Description
                    (AF043524) 20S proteasome subunit PAE1 [Arabidopsis
                    thaliana]
 Seq. No.
                    118609
                    1676 1.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327420P3d12b1
 Method
                    BLASTX
 NCBI GI
                    g3421090
- BLAST score
                    1203
 E value
                    1.0e-132
 Match length
                    237
 % identity
                    100
 NCBI Description
                    (AF043525) 20S proteasome subunit PAE2 [Arabidopsis
                    thaliana]
                    118610
 Seq. No.
                    1679 1.R1010
 Contig ID
                    LIB3176-004-P1-K1-H10
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g3421096
 BLAST score
                    1129
 E value
                    1.0e-124
 Match length
                    246
 % identity
                    89
 NCBI Description
                    (AF043528) 20S proteasome subunit PAG1 [Arabidopsis
                    thaliana] >gi_3885332 (AC005623) proteasome component
                    [Arabidopsis thaliana]
                    118611
 Seq. No.
 Contig ID
                    1680 1.R1010
                    jC-atXLIB327408P1f11b1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g2511594
 BLAST score
                    1176
                    1.0e-129
 E value
 Match length
                    233
                    97
 % identity
                    (Y13694) multicatalytic endopeptidase complex, proteasome
 NCBI Description
                    precursor, beta subunit [Arabidopsis thaliana]
                    >gi 2827525 emb CAA16533 (AL021633) multicatalytic
                    endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S
                    proteasome subunit PBA1 [Arabidopsis thaliana]
```

```
Seq. No.
                  118612
Contig ID
                  1681 1.R1010
5'-most EST
                  jC-alXLIB327434P4e03b1
Method
                  BLASTX
NCBI GI
                  g3421102
BLAST score
                  1411
E value
                  1.0e-157
Match length
                  273
% identity
                  100
NCBI Description
                 (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis
                  thaliana]
Seq. No.
                  118613
Contig ID
                  1681 2.R1010
5'-most EST
                  LIB3176-071-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q3421104
BLAST score
                  1415
                  1.0e-157
E value
Match length
                  274
% identity
                  100
NCBI Description
                  (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis
                  thaliana]
                  118614
Seq. No.
                  1681_3.R1010
Contig ID
                  LIB3234-004-P1-K1-B12
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3421102
BLAST score
                  77
E value
                  4.0e-42
Match length
                  89
                  94
% identity
NCBI Description
                 (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis
                  thaliana]
                  118615
Seq. No.
Contig ID
                  1681 4.R1010
5'-most EST
                  LIB3234-090-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q3421102
BLAST score
                  494
E value
                  6.0e-50
Match length
                  116
% identity
NCBI Description
                  (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis
                  thaliana]
Seq. No.
                  118616
Contig ID
                  1683 1.R1010
5'-most EST
                  PLN g3421106
Method
                  BLASTX
NCBI GI
                  q3421109
BLAST score
                  201
E value
                  1.0e-105
Match length
                  203 -
```

```
% identity
NCBI Description
                    (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
                    thaliana]
                    118617
Seq. No.
Contig ID
                    1685 1.R1010
                    PLN_g3421110
5'-most EST
                    BLASTX
Method
                    g2511590
NCBI GI
BLAST score
                    1033
E value
                    1.0e-113
Match length
                    202
                    100
% identity
                    (Y13692) multicatalytic endopeptidase complex, proteasome
NCBI Description
                    component, beta subunit [Arabidopsis thaliana] >gi 3421111
                     (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis
                    thaliana]
                    118618
Seq. No.
                    1686_1.R1010
Contig ID
                    LIB3175-021-P1-K1-E12
5'-most EST
Method
                    BLASTX
NCBI GI
                    q2244837
BLAST score
                    1017
                    1.0e-111
E value
                    199
Match length
                    100
% identity
NCBI Description
                    (Z97337) proteasome chain protein [Arabidopsis thaliana]
                    >gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic
endopeptidase [Arabidopsis thaliana] >gi_3421114 (AF043535)
                    20S proteasome beta subunit PBD2 [Arabidopsis thaliana]
Seq. No.
                    118619
                    1687 1.R1010
Contig ID
5'-most EST
                    LIB3177-046-P1-K2-D3
Method
                    BLASTX
NCBI GI
                    q3914425
BLAST score
                    1432
E value
                    1.0e-159
Match length
                    274
% identity
                    100
                    PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
NCBI Description
                    CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                    >gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic
                    endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi 3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana]
Seq. No.
                    118620
Contiq ID
                    1689 1.R1010
5'-most EST
                    jC-atXLIB327415P4b08b1
Method
                    BLASTX
NCBI GI
                    g3421123
BLAST score
                    1291
                    1.0e-143
E value
Match length
                    246
```

100

% identity

Contig ID

```
NCBI Description (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis
                   thalianal
Seq. No.
                   118621
Contig ID
                   1690 1.R1010
5'-most EST
                   jC-atXLIB327405P1d06b2
Method
                   BLASTX
NCBI GI
                   g2829275
BLAST score
                   1057
E value
                   1.0e-115
Match length
                   238
% identity
                   87
NCBI Description
                   (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis
                   thaliana] >gi_3513740 (AF080118) contains similarity to
                   nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_
                   (AL049525) nucleoside diphosphate kinase 3 (ndpk3)
                   [Arabidopsis thaliana]
                   118622
Seq. No.
                   1692 1.R1010
Contig ID
                   jC-a\overline{1}XLIB327434P2f07b1
5'-most EST
Method
                   BLASTX
                   g2854070
NCBI GI
                   781
BLAST score
                   5.0e-83
E value
                   263
Match length
% identity
                   (AF044914) putative histone deacetylase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   118623
Contig ID
                   1692_3.R1010
                   jC-atXLIB327404P1e02b1
5'-most EST
Method
                   BLASTN
                   g2854069
NCBI GI
                   363
BLAST score
                   0.0e+00
E value
Match length
                   484
% identity
                   Arabidopsis thaliana putative histone deacetylase (HD2)
NCBI Description
                   mRNA, complete cds
Seq. No.
                   118624
                   1693 1.R1010
Contig ID
5'-most EST
                   LIB146-003-Q1-E1-F1
Method
                   BLASTX
                   q3342249
NCBI GI
                   2515
BLAST score
E value
                   0.0e + 00
                   509
Match length
% identity
                   95
                   (AF047719) GA3 [Arabidopsis thaliana] >gi_3342251
NCBI Description
                   (AF047720) GA3 [Arabidopsis thaliana]
                   118625
Seq. No.
```

1695 1.R1010

```
5'-most EST
                   LIB146-008-01-E1-B9
Method
                   BLASTX
NCBI GI
                   g2961542
BLAST score
                   1366
E value
                   1.0e-151
Match length
                   245
% identity
                   100
NCBI Description
                   (AF050463) zinc finger transcription factor [Arabidopsis
Seq. No.
                   118626
Contig ID
                   1696 1.R1010
                   jC-atXP91C247D7T7b1
5'-most EST
                   BLASTX
Method
                   a2952433
NCBI GI
BLAST score
                   2292
E value
                   0.0e + 00
                   454
Match length
                   96
% identity
                   (AF051135) putative ubiquitin activating enzyme E1
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   118627
                  1696_2.R1010
Contig ID
                  LIB3234-059-P1-K1-G6
5'-most EST
                  BLASTN
Method
NCBI GI
                  a2952432
BLAST score
                   388
                  0.0e + 00
E value
Match length
                   475
                   97
% identity
                  Arabidopsis thaliana putative ubiquitin activating enzyme
NCBI Description
                  E1 (ECR1) mRNA, complete cds
Seq. No.
                   118628
Contig ID
                  1700_1.R1010
5'-most EST
                  LIB3168-010-P1-K1-G4
                  BLASTX
Method
NCBI GI
                  q2981439
BLAST score
                   1451
E value
                  1.0e-161
Match length
                   319
                   93
% identity
NCBI Description
                  (AF051853) t-SNARE SED5 [Arabidopsis thaliana]
                  118629
Seq. No.
Contig ID
                  1701_1.R1010 ·
5'-most EST
                  PLN_g2997683
Method
                  BLASTX
NCBI GI
                  g2997684
BLAST score
                  526
E value
                  2.0e-53
Match length
                  102
% identity
NCBI Description
                   (AF053302) putative transcriptional co-activator
```

[Arabidopsis thaliana]

```
Seq. No.
                   118630
                   1702 1.R1010
Contig ID
                   jC-atXP112C132F7T7a1
5'-most EST
                   BLASTX
Method
                   q2997686
NCBI GI
BLAST score
                   504
                   9.0e-51
E value
                   119
Match length
% identity
NCBI Description
                   (AF053303) putative transcriptional co-activator
                   [Arabidopsis thaliana] >gi_3513735 (AF080118) contains
                   similarity to RNA polymerase II transcription cofactor p15
                   [Arabidopsis thaliana] >gi_4539366_emb_CAB40060.1
                   (AL049525) putative protein [Arabidopsis thaliana]
Seq. No.
                   118631
Contig ID
                   1702 2.R1010
                   jC-a\overline{1}XLIB327436P4a04b1
5'-most EST
Method
                  BLASTX
                   q2997686
NCBI GI
BLAST score
                   681
E value
                   2.0e-71
Match length
                   162
% identity
NCBI Description
                   (AF053303) putative transcriptional co-activator
                   [Arabidopsis thaliana] >gi_3513735 (AF080118) contains
                   similarity to RNA polymerase II transcription cofactor p15
                   [Arabidopsis thaliana] >gi_4539366_emb_CAB40060.1
                   (AL049525) putative protein [Arabidopsis thaliana]
                   118632
Seq. No.
                   1702 5.R1010
Contig ID
5'-most EST
                  LIB3177-090-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   q2541876
BLAST score
                   214
                   6.0e-17
E value
                   98
Match length
% identity
                   54
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
                   118633
Seq. No.
Contig ID
                   1704_1.R1010
                   PLN_g3319287
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2529668
BLAST score
                   2019
E value
                   0.0e + 00
Match length
                   435
% identity
                   90
NCBI Description
                   (AC002535) putative photolyase/blue-light receptor
                   [Arabidopsis thaliana] >gi_3319288 (AF053366)
                  photolyase/blue light photoreceptor PHR2 [Arabidopsis
                  thaliana]
```

118634

Seq. No.

```
Contig ID
                   1706 1.R1010
5'-most EST
                   PLN g3335515
Method
                   BLASTX
NCBI GI
                   q3335516
BLAST score
                   4694
E value
                   0.0e + 00
Match length
                   914
                   99
% identity
NCBI Description
                   (AF053941) nonphototropic hypocotyl 2 [Arabidopsis
                   thaliana]
Seq. No.
                   118635
                   1707 1.R1010
Contig ID
5'-most EST
                   q2722216
                   BLASTN
Method
                   g3283056
NCBI GI
BLAST score
                   387
                   0.0e + 00
E value
                   403
Match length
% identity
                   100
NCBI Description
                  Arabidopsis thaliana one helix protein (OHP) mRNA, complete
Seq. No.
                   118636
Contig ID
                   1708 1.R1010
                  LIB24-002-Q1-E1-H6
5'-most EST
Method
                  BLASTX
NCBI GI
                   q2997767
                   2370
BLAST score
E value
                   0.0e + 00
Match length
                   462
% identity
NCBI Description
                   (AF054906) myrosinase-binding protein homolog [Arabidopsis
                   thaliana]
Seq. No.
                   118637
                   1708 2.R1010
Contig ID
5'-most EST
                   jC-a\(\bar{1}\)XLIB327435P2h09a1
Method
                   BLASTX
NCBI GI
                   q2373405
BLAST score
                   565
E value
                   5.0e-58
Match length
                   110
% identity
                   29
                   (D85194) no known genes showing a high homology to 4B-1
NCBI Description
                   clone sequence were found in the EMBL database. Orf was 640
                   amino acid long and contained a proline and alanine repeat
                   [Arabidopsis thaliana]
Seq. No.
                   118638
Contig ID
                   1708 4.R1010
5'-most EST
                   jC-atX25022Q1E1B07b1
Method
                  BLASTX
NCBI GI
                   g2373405
BLAST score
                   881
E value
                   4.0e-95
Match length
                   210
```

```
% identity
                    22
                    (D85194) no known genes showing a high homology to 4B-1
 NCBI Description
                    clone sequence were found in the EMBL database. Orf was 640
                    amino acid long and contained a proline and alanine repeat
                    [Arabidopsis thaliana]
 Seq. No.
                    118639
                    1708_5.R1010
 Contig ID
 5'-most EST
                   LIB24-079-Q1-E1-D12
 Method
                    BLASTX
 NCBI GI
                    q4220450
 BLAST score
                    695
                    2.0e-73
 E value
 Match length
                    148
                    23
 % identity
                    (AC006216) Identical to qb D85194 mRNA which is similar to
 NCBI Description
                    gb AF054906 myrosinase-binding protein homolog from
                   Arabidopsis thaliana. ESTs gb Z34045 and gb Z34877 come
                    from this gene. [Arabidopsis thaliana]
                    118640
 Seq. No.
 Contig ID
                    1708 6.R1010
 5'-most EST
                    LIB2\overline{4}-114-Q1-E1-H1
                    BLASTX
^Method
                   g4220450
 NCBI GI
 BLAST score
                    454
 E value
                    6.0e - 45
 Match length
                    238
 % identity
                    (ACO06216) Identical to gb D85194 mRNA which is similar to
 NCBI Description
                    gb AF054906 myrosinase-binding protein homolog from
                   Arabidopsis thaliana. ESTs gb_Z34045 and gb_Z34877 come
                    from this gene. [Arabidopsis thaliana]
 Seq. No.
                    118641
 Contig ID
                    1709 1.R1010
 5'-most EST
                   PLN g3242788
Method
                    BLASTX
 NCBI GI
                    q3242789
 BLAST score
                    4604
 E value
                    0.0e+00
 Match length
                    921
 % identity
 NCBI Description
                    (AF055357) respiratory burst oxidase protein D [Arabidopsis
                    thaliana]
 Seq. No.
                    118642
 Contig ID
                    1711 1.R1010
 5'-most EST
                   LIB3176-110-P1-K1-F7
 Method
                   BLASTX
 NCBI GI
                    q3170531
 BLAST score
                    1677
 E value
                    0.0e + 00
 Match length
                    338
 % identity
                    95
 NCBI Description
                   (AF055635) protein tyrosine phosphatase 1; PTP1;
```

tyrosine-specific protein phosphatase [Arabidopsis

thaliana]

118643 Seq. No. 1712 1.R1010 Contig ID PLN_g4206708 5'-most EST Method BLASTX NCBI GI q3377507 BLAST score 2890 0.0e + 00E value Match length 629 % identity 91 NCBI Description (AF056026) auxin transport protein EIR1 [Arabidopsis thaliana] >gi_3661620 (AF093241) putative auxin efflux carrier AGR [Arabidopsis thaliana] >gi_3746886 (AF087459)
polar-auxin-transport efflux component AGRAVITROPIC 1 [Arabidopsis thaliana] >gi_4206709 (AF086906) root gravitropism control protein [Arabidopsis thaliana] Seq. No. 118644 1713_1.R1010 Contig ID jC-aTX24111Q1E1E06b1 5'-most EST Method BLASTX q3044212 NCBI GI 3512 BLAST score 0.0e + 00E value 692 Match length % identity 98 NCBI Description (AF057043) acyl-CoA oxidase [Arabidopsis thaliana] 118645 Seq. No. 1714 1.R1010 Contig ID 5'-most EST LIB24-120-Q1-E1-A7 Method BLASTX g3044214 NCBI GI BLAST score 3426 E value 0.0e + 00654 Match length . 100 % identity NCBI Description (AF057044) acyl-CoA oxidase [Arabidopsis thaliana] 118646 Seq. No. 1716 1.R1010 Contig ID 5'-most EST jC-a1X25051Q1E1B03b1 Method BLASTX NCBI GI q3044218 BLAST score 865 4.0e-93 E value Match length 166 % identity NCBI Description (AF057144) signal peptidase [Arabidopsis thaliana] 118647 Seq. No. Contig ID 1719 1.R1010

5'-most EST jC-atXLIB327417P4b10b1

Method BLASTX
NCBI GI g3063661
BLAST score 162

```
E value
                  1.0e-43
Match length
                  115
% identity
                  89
                  (AF058391) nucleoside diphosphate kinase Ia [Arabidopsis
NCBI Description
                  118648
Seq. No.
                  1719 2.R1010
Contig ID
                  LIB25-115-Q1-E1-A8
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3914117
BLAST score
                  1030
                  1.0e-112
E value
                  230
Match length
                  87
% identity
NCBI Description
                  NUCLEOSIDE DIPHOSPHATE KINASE II PRECURSOR (NDK II) (NDP
                  KINASE II) >gi 3093480 (AF017640) nucleoside diphosphate
                  kinase type 2 [Arabidopsis thaliana]
                  118649
Seq. No.
                  1722_1.R1010
Contig ID
5'-most EST
                  LIB24-073-Q1-E1-C9
Method
                  BLASTX
                  g3719211
NCBI GI
BLAST score
                  728
E value
                  5.0e-77
Match length
                  172
% identity
                  83
NCBI Description
                  (U97021) UIP2 [Arabidopsis thaliana]
                  118650
Seq. No.
                  1725 1.R1010
Contig ID
5'-most EST
                  PLN_g3201679
Method
                  BLASTX
NCBI GI
                  g3201680
BLAST score
                  4234
E value
                  0.0e + 00
Match length
                  884
                  93
% identity
NCBI Description (AF060941) extra-large G-protein [Arabidopsis thaliana]
Seq. No.
                  118651
Contig ID
                  1726 1.R1010
5'-most EST
                  PLN g3372670
Method
                  BLASTX
                  g3372671
NCBI GI
BLAST score
                  4183
E value
                  0.0e + 00
                  876
Match length
% identity
                  95
                  (AF061286) gamma-adaptin 1 [Arabidopsis thaliana]
NCBI Description
                  >gi_4704741_gb_AAD28247.1_AF124524_1 (AF124524)
                  gamma-adaptin 1 [Arabidopsis thaliana]
Seq. No.
                  118652
                  1726_2.R1010
Contig ID
5'-most EST
                  jC-atxP62C203C19T7d2
```

Contig ID

```
Method
                  BLASTX
NCBI GI
                   q4538987
BLAST score
                   4177
                   0.0e + 00
E value
Match length
                   876
% identity
                   95
NCBI Description
                   (AJ133777) gamma-adaptin 2 [Arabidopsis thaliana]
                   118653
Seq. No.
                   1726 3.R1010
Contig ID
5'-most EST
                   jC-atXP91CH1E5T7b1
Method
                   BLASTX
                   q3372671
NCBI GI
BLAST score
                   853
                   1.0e-91
E value
                   168
Match length
% identity
                   99
                   (AF061286) gamma-adaptin 1 [Arabidopsis thaliana]
NCBI Description
                   >gi 4704741 gb AAD28247.1 AF124524 1 (AF124524)
                   gamma-adaptin 1 [Arabidopsis thaliana]
Seq. No.
                   118654
Contig ID
                   1727 1.R1010
5'-most EST
                   jC-atXLIB327431P2e12a1
Method
                   BLASTX
                  ...q3108347
NCBI GI
                   1325
BLAST score
E value
                   1.0e-147
                   256
Match length
% identity
                   100
                   (AF061517) putative copper/zinc superoxide dismutase copper
NCBI Description
                   chaperone [Arabidopsis thaliana]
                   118655
Seq. No.
                   1728 1.R1010
Contig ID
5'-most EST
                   LIB3176-095-P1-K1-H4
                   BLASTX
Method
                   q3319350
NCBI GI
BLAST score
                   1786
                   0.0e + 00
E value
                   340
Match length
% identity
                   100
                   (AF077407) No definition line found [Arabidopsis thaliana]
NCBI Description
                   118656
Seq. No.
                   1728 2.R1010
Contig ID
5'-most EST
                   LIB3177-055-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q3319347
BLAST score
                   1279
                   1.0e-141
E value
                   292
Match length
                   83
% identity
                   (AF077407) No definition line found [Arabidopsis thaliana]
NCBI Description
                   118657
Seq. No.
```

1728_3.R1010

Contig ID

```
5'-most EST
                   iC-atXLIB327417P3a09b1
                  BLASTX
Method
NCBI GI
                   q3273751
BLAST score
                   1111
                   1.0e-122
E value
Match length
                   231
                   93
% identity
                   (AF061518) manganese superoxide dismutase [Arabidopsis
NCBI Description
                  thalianal
                  118658
Seq. No.
Contig ID
                  1728_6.R1010
                  q471\overline{4}047
5'-most EST
Method
                  BLASTX
                  a3319350
NCBI GI
                  847
BLAST score
E value
                   5.0e-91
                  200
Match length
                  76
% identity
                  (AF077407) No definition line found [Arabidopsis thaliana]
NCBI Description
                  118659
Seq. No.
Contig ID
                   1728 8.R1010
5'-most EST
                   jC-atXP24C123C9T7011d1
Method
                  BLASTX
                  q4713948
NCBI GI
                  1463
BLAST score
                  1.0e-163
E value
                  293
Match length
% identity
                   94
                  (AC007293) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118660
                  1728 13.R1010
Contig ID
5'-most EST
                  LIB3177-012-P1-K2-F4
Method
                  BLASTX
                  q3319348
NCBI GI
BLAST score
                   509
E value
                   3.0e-59
Match length
                  164
                  76
% identity
                  (AF077407) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118661
Contig ID
                  1728 16.R1010
                  jC-atXLIB327427P4e02b2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3273751
BLAST score
                  615
E value
                  9.0e-64
Match length
                  149
% identity
                  85
                  (AF061518) manganese superoxide dismutase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  118662
```

1729_1.R1010

```
5'-most EST
                   jC-atXLIB327422P4d11b1
Method
                   BLASTX
                   g3273753
NCBI GI
                   906
BLAST score
E value
                   8.0e-98
Match length
                   191
% identity
                   90
NCBI Description
                   (AF061519) copper/zinc superoxide dismutase [Arabidopsis
Seq. No.
                   118663
                   1731 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327414P3f11b1
Method
                   BLASTX
                 ... g4204270
NCBI GI
BLAST score
                   1780
                   0.0e + 00
E value
Match length
                   352
% identity
                   97
NCBI Description
                   (AC005223) branched-chain alpha-keto acid decarboxylase E1
                  beta subunit [Arabidopsis thaliana]
Seq. No.
                   118664
                   1732_1.R1010
Contiq ID
                   PLN g3219354
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3219355
BLAST score
                   1381
E value
                   1.0e-153
Match length
                   322
% identity
                   86
NCBI Description (AF062371) ROOT HAIRLESS 1 [Arabidopsis thaliana]
Seq. No.
                   118665
                   1733 1.R1010
Contig ID
                  LIB3168-030-P1-K1-C10
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4106340 _
BLAST score
                   2490
E value
                   0.0e + 00
Match length
                   477
% identity
                   100
NCBI Description
                   (AF062396) protein phosphatase 2A regulatory subunit
                   isoform B' delta [Arabidopsis thaliana]
Seq. No.
                   118666
                   1734 1.R1010
Contig ID
5'-most EST
                   PLN g3220236
Method
                  BLASTX
                   q3169569
NCBI GI
BLAST score
                   2301
E value
                  0.0e + 00
Match length
                   457
% identity
                  100
                  (AF062589) 3-keto-acyl-CoA thiolase 2 [Arabidopsis
NCBI Description
                  thaliana] >gi_3220237 (AF062591) peroxisomal
                  3-keto-acyl-CoA thiolase 2 precursor [Arabidopsis thaliana]
```

```
Seq. No.
                 . 118667
                  1734 2.R1010
Contig ID
                  jC-atXP31C147C20T7d2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3169569
BLAST score
                  2140
                  0.0e + 00
E value
Match length
                  424
% identity
                  100
NCBI Description
                  (AF062589) 3-keto-acyl-CoA thiolase 2 [Arabidopsis
                  thaliana] >gi 3220237 (AF062591) peroxisomal
                  3-keto-acyl-CoA thiolase 2 precursor [Arabidopsis thaliana]
                  118668
Seq. No.
Contig ID
                  1736 1.R1010
5'-most EST
                  jC-atXLIB327415P2f06b2
                  BLASTX
Method
NCBI GI
                  g3128477
BLAST score
                  1771
E value
                  0.0e + 00
Match length
                  335
% identity
                  100
NCBI Description (AF062640) metalloproteinase [Arabidopsis thaliana]
                  118669
Seq. No.
Contig ID
                  1736 2.R1010
5'-most EST
                  jC-atXLIB327430P4d05b1
                  BLASTN
Method
NCBI GI
                  g3128476
BLAST score
                  115
E value
                  1.0e-57
Match length
                  119
                  99
% identity
NCBI Description Arabidopsis thaliana metalloproteinase mRNA, complete cds
Seq. No.
                  118670
                  1737 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327427P2e07b1
Method
                  BLASTX
NCBI GI
                  g3287694
BLAST score
                  1395
E value
                  1.0e-155
Match length
                  257
% identity
                  100
NCBI Description
                  (AC003979) Similar to myb-related transcription factor
                  (THM27) gb X95296 from Solanum lycopersicum. ESTs
                  gb T42000, gb T04118, gb AA598042, gb AA394757 and
                  gb AA598046 come from this gene. [Arabidopsis thaliana]
                  118671
Seq. No.
                  1738 1.R1010
Contig ID
5'-most EST
                  jC-atXP69C220A8T7056d1 -
Method
                  BLASTX
NCBI GI
                  g3941412
BLAST score
                  1512
```

1.0e-169

E value

Method

BLASTX -

```
282
Match length
% identity
                  100
                   (AF062860) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                  118672
Seq. No.
                  1738 2.R1010
Contig ID
                  LIB3168-029-P1-K1-D4
5'-most EST
Method
                  BLASTX
                  g3941412
NCBI GI
BLAST score
                  511
E value
                  9.0e-52
Match length
                  93
                  99
% identity
                  (AF062860) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                  118673
Seq. No.
                  1739 1.R1010
Contig ID
5'-most EST
                  PLN_g3941419
                  BLASTX
Method
                  g2529681
NCBI GI
BLAST score
                  1906
E value
                  0.0e + 00
Match length
                  371
% identity
                  95
                  (AC002535) putative MYB-related transcription factor
NCBI Description
                   (protein P) [Arabidopsis thaliana]
                  118674
Seq. No.
                  1740 1.R1010
Contig ID
5'-most EST
                  PLN g3941429
                  BLASTX
Method
                  g3941430
NCBI GI
BLAST score
                  1188
                  1.0e-131
E value
Match length
                  261
% identity
                  85
                  (AF062869) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                  118675
Seq. No.
                  1743 1.R1010
Contig ID
5'-most EST
                  jC-atX22031Q1E1H08b1
Method
                  BLASTX
NCBI GI
                  g3941448
BLAST score
                  1586
E value
                  1.0e-177
Match length
                  333
% identity
                  90
                  (AF062878) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                  118676
Seq. No.
                  1744 1.R1010
Contig ID
                  LIB24-110-Q1-E1-C2
5'-most EST
```

```
NCBI GI
                   q3941466
BLAST score
                   1598
E value
                   1.0e-178
Match length
                   352
                   86
% identity
NCBI Description
                   (AF062887) putative transcription factor [Arabidopsis
                  thaliana] 🚉
                   118677
Seq. No.
                   1747_1.R1010
Contig ID
5'-most EST
                  PLN_g3941479
Method
                  BLASTX
NCBI GI
                   q3941480
BLAST score
                   1157
                   1.0e-127
E value
                   234
Match length
% identity
                   91
                   (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                   118678
Seq. No.
Contig ID
                   1747_2.R1010
                  jC-atXLIB327411P3g02b1
5'-most EST
Method
                  BLASTX
                  g3941480
NCBI GI
BLAST score
                   226
E value
                   8.0e-51
Match length
                  101
% identity
                   97
                   (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                   118679
Seq. No.
Contig ID
                  1748_1.R1010
5'-most EST
                  LIB3\overline{5}-054-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                   q3941482
BLAST score
                  1368
E value
                   1.0e-152
Match length
                   279
                   92
% identity
                   (AF062895) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                   118680
Seq. No.
Contig ID
                   1749_1.R1010
                  jC-atXP17C113E20T7d3
5'-most EST
Method
                  BLASTX
                  g3941494
NCBI GI
BLAST score
                   1422
E value
                   1.0e-158
Match length
                   376
% identity
                  73
NCBI Description
                  (AF062901) putative transcription factor (Arabidopsis
                  thaliana]
                  118681
Seq. No.
```

```
1750 1.R1010
Contig ID
                   PLN g3941507
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3941508
BLAST score
                   1092
                   1.0e-119
E value
                   211
Match length
% identity
                   94
NCBI Description
                   (AF062908) putative transcription factor [Arabidopsis
                   thaliana]
                   118682
Seq. No.
                   1750 2.R1010
Contig ID
                   jC-atXLIB327421P3f12b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3941508
                   259
BLAST score
E value
                   3.0e-22
Match length
                   97
% identity
                   92
NCBI Description
                   (AF062908) putative transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                   118683
                   1751 1.R1010
Contig ID
                   PLN g_{3941521}
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3941522
BLAST score
                   1194
E value
                   1.0e-131
Match length
                   249
% identity
                   90
NCBI Description
                   (AF062915) putative transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                   118684
                   1752 1.R1010
Contig ID
5'-most EST
                   PLN q3941523
Method
                   BLASTX
NCBI GI
                   q3941524
BLAST score
                   1654
E value
                   0.0e + 00
Match length
                   334
% identity
                   93
NCBI Description
                   (AF062916) putative transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                   118685
Contig ID
                   1753 1.R1010
5'-most EST
                   PLN q3941527
Method
                  BLASTX
NCBI GI
                   g3941528
BLAST score
                   1644
E value
                   0.0e + 00
Match length
                   333
% identity
                   92
NCBI Description
                   (AF062918) putative transcription factor [Arabidopsis
```

Seq. No.

Contig ID

118690

1756 1.R1010

```
thaliana]
                   118686
 Seq. No.
                   1754_1.R1010
 Contig ID
                   PLN_g3288822
 5'-most EST
                   BLASTX
Method
NCBI GI
                    g3288823 ...
BLAST score
                    1082
                   1.0e-118
E value
Match length
                   225
                   95
 % identity
NCBI Description
                   (AF063852) FUS5 [Arabidopsis thaliana]
                   118687
Seq. No.
                   1755 1.R1010
 Contig ID
 5'-most EST
                   906\overline{3}04
                   BLASTX
Method
                   g3288821
NCBI GI
BLAST score
                   2007
                   0.0e + 00
E value
Match length
                    401
                   96
 % identity
                    (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                   transaminase [Arabidopsis thaliana]
                   >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
                   alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
                   118688
Seq. No.
Contig ID
                   1755 2.R1010
 5'-most EST
                   jC-atXLIB327423P1b12b1
Method
                   BLASTX
NCBI GI
                   g3288821
BLAST score
                   882
E value
                   1.0e-102
Match length
                   205
% identity
                   87
NCBI Description
                   (AF063901) alanine:glyoxylate aminotransferase;
                   transaminase [Arabidopsis thaliana]
                   >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
                   alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
                   118689
Seq. No.
Contig ID
                   1755 7.R1010
 5'-most EST
                   jC-atXLIB327421P2b08b1
Method
                   BLASTX
NCBI GI
                   g3288821
BLAST score
                   159
E value
                   1.0e-10
Match length
                   28
 % identity
                   100
NCBI Description
                   (AF063901) alanine:glyoxylate aminotransferase;
                   transaminase [Arabidopsis thaliana]
                   >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
```

12906

alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

```
PLN g3142697
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3142698
BLAST score
                   1611
                   1.0e-180
E value
Match length
                   326
% identity
                   93
                   (AF064542) protein farnesyltransferase subunit A
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   118691
                   1757 1.R1010
Contig ID
                   jC-alXLIB327435P2d03a1
5'-most EST
Method
                   BLASTX
                   g3834325
NCBI GI
BLAST score
                   1681
E value
                   0.0e + 00
Match length
                   325
% identity
                   99
NCBI Description
                   (AC005679) Strong similarity to gb AF067141 gamma-glutamyl
                   hydrolase from Arabidopsis thaliana. ESTs gb R83955,
                   gb T45062, gb T22220, gb AA586207, gb AI09985\overline{1} and
                   gb AI00672 come from this gene. [Arabidopsis thaliana]
                   118692
Seq. No.
                   1757 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327410P1a10a1
Method
                   BLASTX
NCBI GI
                   g3834327
BLAST score
                   493
E value
                   2.0e-49
Match length
                   91
% identity
                   100
NCBI Description
                   (AC005679) Similar to gb AF067141 gamma-glutamyl hydrolase
                   from Arabidopsis thaliana; the beginning of this gene is
                   cut off. ESTs gb H76503 and gb AA712367 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                   118693
                   1759 1.R1010
Contig ID
                   jC-atXLIB327408P3f11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3435196
BLAST score
                   2854
E value
                   0.0e + 00
Match length
                   719
% identity
                   97
NCBI Description
                   (AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.
                   118694
                   1760 1.R1010
Contig ID
5'-most EST
                  PLN g3172537
Method
                  BLASTX
NCBI GI
                  g3172538
BLAST score
                  1334
E value
                  1.0e-148
Match length
                  303
```

```
% identity
                   89
                   (AF067789) tSNARE AtTLG2p [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118695
                   1763 1.R1010
Contig ID
                   PLN_g3493610
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3493611
BLAST score
                   1256
                   1.0e-138
E value
Match length
                   276
% identity
                   85
                   (AF068318) regulatory subunit of protein kinase CK2; CK2
NCBI Description
                   beta-subunit [Arabidopsis thaliana]
Seq. No.
                   118696
                   1764 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327433P1g11b1
Method
                   BLASTX
NCBI GI
                   q3941543
BLAST score
                   1832
E value
                   0.0e + 00
Match length
                   378
% identity
                   (AF069497) pelota [Arabidopsis thaliana]
NCBI Description
                   >gi 4469016 emb CAB38277 (AL035602) pelota (PEL1)
                   [Arabidopsis thaliana]
Seq. No.
                   118697
Contig ID
                   1765 1.R1010
                   jC-atXLIB327425P3f03b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3511223
BLAST score
                   1759
E value
                   0.0e + 00
Match length
                   353
% identity
                   96
NCBI Description
                   (AF069528) plant adhesion molecule 1 [Arabidopsis thaliana]
Seq. No.
                   118698
                   1767 1.R1010
Contig ID
                   LIB3168-051-P1-K1-B9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3264805
BLAST score
                   4862
E value
                   0.0e + 00
Match length
                   968
% identity
                   97
NCBI Description
                   (AF071788) phosphoenolpyruvate carboxylase [Arabidopsis
                   thaliana] >gi 4079630 emb CAA10486 (AJ131710) phospho
                   enole pyruvate carboxylase [Arabidopsis thaliana]
Seq. No.
                   118699
Contig ID
                  1767 2.R1010
5'-most EST
                   jC-atXP112C129F23T7d2
                   BLASTX
Method
NCBI GI
                   q3264805
```

5'-most EST

```
BLAST score
                   981
E value
                   1.0e-122
Match length
                   254
% identity
                   89
NCBI Description
                   (AF071788) phosphoenolpyruvate carboxylase [Arabidopsis
                   thaliana] >gi_4079630_emb_CAA10486_ (AJ131710) phospho
                   enole pyruvate carboxylase [Arabidopsis thaliana]
                   118700
Seq. No.
                   1767_7.R1010
LIB23-014-Q1-E1-D10
Contig ID
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4033349
BLAST score
                   656
E value
                   7.0e-69
Match length
                   137
% identity
                   96
                   (AJ223496) phosphoenolpyrovate carboxylase [Brassica
NCBI Description
                   juncea]
                   118701
Seq. No.
Contig ID
                   1768 1.R1010
5'-most EST
                   g2733629
Method
                   BLASTX
                   q3243274
NCBI GI
                   1634
BLAST score
                   0.0e + 00
E value
Match length
                   364
                   88
% identity
                   (AF072134) TCP3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118702
Contig ID
                   1769_1.R1010
5'-most EST
                   PLN_g3264777
Method
                   BLASTX
NCBI GI
                   q3264778
BLAST score
                   3041
                   0.0e + 00
E value
Match length
                   640
% identity
                   92
                   (AF072536) H-protein promoter binding factor-1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   118703
Contig ID
                   1770_1.R1010
5'-most EST
                   PLN_g4206639
                   BLASTX
Method
                   q4206640
NCBI GI
BLAST score
                   1785
E value
                   0.0e + 00
                   398
Match length
% identity
                   90
                   (AF072858) zinc transporter ZAT [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118704
                   1770_3.R1010
Contig ID
```

LIB22-085-Q1-E2-E10

```
Method
                  BLASTX
                  q3510254
NCBI GI
BLAST score
                  473
                  2.0e-47
E value
Match length
                  94
% identity
                  100
                  (AC005310) putative zinc transporter [Arabidopsis thaliana]
NCBI Description
                  118705
Seq. No.
Contig ID
                  1771 1.R1010
5'-most EST
                  jC-atXLIB327409P4h12b1
Method
                  BLASTX
                  q3377517
NCBI GI
                  2466
BLAST score
                  0.0e + 00
E value
                  578
Match length
% identity
                  85
NCBI Description
                  (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
                  118706
Seq. No.
Contig ID
                  1771 2.R1010
5'-most EST
                  q241\overline{3}793
Method
                  BLASTX
                  g548655
NCBI GI
BLAST score
                  488
E value
                  2.0e-55
Match length
                  186
                  71
% identity
                  50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C)
NCBI Description
                  >gi_541897_pir__C53394 ribosomal protein L12.C, chloroplast
                  - Arabidopsis thaliana >gi 468773 emb CAA48183 (X68046)
                  ribosomal protein L12 [Arabidopsis thaliana]
Seq. No.
                  118707
Contig ID
                  1771 4.R1010
                  jC-atXLIB327429P4a09a2
5'-most EST
Method
                  BLASTX
                  g548653
NCBI GI
BLAST score
                  729
                  4.0e-77
E value
Match length
                  191
% identity
                  82
                  50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A)
NCBI Description
                  >gi 541895 pir A53394 ribosomal protein L12.A, chloroplast
                   - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046)
                  ribosomal protein L12 [Arabidopsis thaliana]
                  118708
Seq. No.
                  1771 5.R1010
Contig ID
5'-most EST
                  q906467
Method
                  BLASTX
                  a548655
NCBI GI
BLAST score
                  451
                  1.0e-44
E value
Match length
                  112
                  86
% identity
NCBI Description 50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C)
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- Arabidopsis thaliana >gi 468773 emb CAA48183 (X68046)
                    ribosomal protein L12 [Arabidopsis thaliana]
                    118709
Seq. No.
                    1771 7.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327440P1g04a1
                    BLASTX
 Method
 NCBI GI
                    q3377517
 BLAST score
                    647
 E value
                    1.0e-67
 Match length
                    140
                    89
 % identity
                    (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
 NCBI Description
                    118710
 Seq. No.
 Contig ID
                    1771 9.R1010
                    jC-atXLIB327427P3f10a2
 5'-most EST
 Method
                    BLASTX
                   g548655
 NCBI GI
 BLAST score
                    692
 E value
                    9.0e-73
 Match length
                    187
 % identity
                    81
                    50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C)
 NCBI Description
                    >gi_541897_pir__C53394 ribosomal protein L12.C, chloroplast
                    - Arabidopsis thaliana >gi_468773_emb_CAA48183_ (X68046)
                    ribosomal protein L12 [Arabidopsis thaliana]
                    118711
 Seq. No.
                    1771 10.R1010
 Contig ID
                    g906<del>5</del>86
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g548653
 BLAST score
                    497
 E value
                    5.0e-50
 Match length
                    133
 % identity
                    73
 NCBI Description
                    50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A)
                    >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast
                    - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046)
                    ribosomal protein L12 [Arabidopsis thaliana]
 Seq. No.
                    118712
 Contig ID
                   1771 11.R1010
 5'-most EST
                    g2413867
 Method
                    BLASTX
 NCBI GI
                    q548655
 BLAST score
                    162
 E value
                    7.0e-11
                    55
 Match length
                    71
 % identity
                   50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C)
 NCBI Description
                   >gi_541897_pir__C53394 ribosomal protein L12.C, chloroplast
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>gi 541897 pir C53394 ribosomal protein L12.C, chloroplast

ribosomal protein L12 [Arabidopsis thaliana]

- Arabidopsis thaliana >gi_468773_emb_CAA48183_ (X68046)

Seq. No.

118717

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Seq. No.
                    118713
                    1771 13.R1010
Contig ID
5'-most EST
                    jC-atXP62C201N16T7004a1
                    BLASTX
Method
NCBI GI
                    q548653
BLAST score
                    498
                    5.0e-50
E value
Match length
                    183
                    65
% identity
NCBI Description
                    50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A)
                    >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast
                    - Arabidopsis thaliana >gi 468771_emb CAA48181_ (X68046)
                    ribosomal protein L12 [Arabidopsis thaliana]
Seq. No.
                    118714
                    1771 16.R1010
Contig ID
5'-most EST
                   LIB3177-004-P1-K2-F1
                   BLASTX
Method
                    q548653
NCBI GI
BLAST score
                    344
                    1.0e-32
E value
Match length
                    96
% identity
                    74
                   50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A)
NCBI Description
                   >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast
                    - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046)
                   ribosomal protein L12 [Arabidopsis thaliana]
Seq. No.
                    118715
                    1772 1.R1010
Contig ID
                    jC-atXLIB327418P1g02b1
5'-most EST
                    BLASTX
Method
NCBI GI
                   q2129559
BLAST score
                    2823
                    0.0e + 00
E value
Match length
                    605
% identity
                   cellulase homolog OR16pep - Arabidopsis thaliana
NCBI Description
                   >gi_1022807 (U37702) cellulase [Arabidopsis thaliana]
                   >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana]
>gi_3598956 (AF074375) cellulase [Arabidopsis thaliana]
>gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
                    [Arabidopsis thaliana]
                    118716
Seq. No.
Contig ID
                    1772 2.R1010
                    jC-atXP73CF2G6T7d2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3941492
BLAST score
                    364
E value
                    8.0e-61
Match length
                    126
                    87
% identity
NCBI Description
                    (AF062900) putative transcription factor [Arabidopsis
                    thaliana]
```

```
Contig ID
                  1772 6.R1010
5'-most EST
                  g2393327
Method
                  BLASTN
                  g1022806
NCBI GI
BLAST score
                  362
                  0.0e + 00
E value
                  427
Match length
% identity
                  Arabidopsis thaliana cellulase (OR16pep) mRNA, complete cds
NCBI Description
                  118718
Seq. No.
                  1775 1.R1010
Contig ID
                  LIB3176-006-P1-K1-B1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3603353
BLAST score
                  3622
                  0.0e + 00
E value
                  728
Match length
% identity
                  95
                  (AF074843) peroxisomal targeting signal type 1 receptor
NCBI Description
                   [Arabidopsis thaliana]
                  118719
Seq. No.
                  1776_1.R1010
Contig ID .
5'-most EST
                  LIB3234-097-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g2583135
BLAST score
                  1139
                  1.0e-125
E value
                  218
Match length
% identity
                  (AC002387) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3822216 (AF074948) FIL [Arabidopsis thaliana]
                  >gi 4322477 gb AAD16053 (AF087015) abnormal floral organs
                  protein [Arabidopsis thaliana]
                  118720
Seq. No.
                  1777_1.R1010
Contig ID
                  LIB23-016-Q1-E1-H10
5'-most EST
Method
                  BLASTX
                  g3309082
NCBI GI
BLAST score
                  1090
                  1.0e-119
E value
Match length
                   213
% identity
                  100
                   (AF076251) calcineurin B-like protein 1 [Arabidopsis
NCBI Description
                   thaliana]
                  118721
Seq. No.
                  1778 1.R1010
Contig ID
5'-most EST
                  LIB24-115-Q1-E1-H10
Method
                  BLASTX
NCBI GI
                  g3309084
BLAST score
                  1163
                  1.0e-128
E value
                   226
Match length
                  100
% identity
```

```
NCBI Description
                   (AF076252) calcineurin B-like protein 2 [Arabidopsis
                   thalianal
                   118722
Seq. No.
Contig ID
                   1779 1.R1010
5'-most EST
                   LIB3176-115-P2-K1-D5
                   BLASTX
Method
                   q3309086
NCBI GI
BLAST score
                   1161
E value
                   1.0e-127
Match length
                   226
% identity
                   100
                   (AF076253) calcineurin B-like protein 3 [Arabidopsis
NCBI Description
                   thaliana]
                   118723
Seq. No.
Contig ID
                   1781 1.R1010
                   jC-atXLIB327405P2b03b2
5'-most EST
Method
                   BLASTX
                   g2642159
NCBI GI
                   1855
BLAST score
E value
                   0.0e + 00
Match length
                   361
% identity
                   100
                   (AC003000) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose
                   pyrophosphorylase [Arabidopsis thaliana] >gi 4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
                   118724
Seq. No.
                   1781 4.R1010
Contig ID
5'-most EST
                   g275\overline{7}199
Method
                   BLASTX
                   g2642159
NCBI GI
BLAST score
                   259
E value
                   2.0e-22
                   68
Match length
% identity
                   85
NCBI Description
                   (AC003000) putative mannose-1-phosphate guanyltransferase
                   [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose
                   pyrophosphorylase [Arabidopsis thaliana] >gi 4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
Seq. No.
                   118725
Contig ID
                   1782 1.R1010
5'-most EST
                   LIB3175-041-P1-K1-H9
                   BLASTX
Method .
NCBI GI
                   q3395938
BLAST score
                   2164
E value
                   0.0e + 00
Match length
                   417
                   100
% identity
NCBI Description
                   (AF076924) polypyrimidine tract-binding protein homolog
                   [Arabidopsis thaliana]
Seq. No.
                   118726
```

1784 1.R1010

Contig ID

```
5'-most EST
                  LIB3177-086-P1-K1-G3
                  BLASTX
Method
                g3348077
NCBI GI
BLAST score
                  2424
                  0.0e+00
E value
Match length
                  503
% identity
                  95
NCBI Description (AF078080) isochorismate synthase [Arabidopsis thaliana]
                  118727
Seq. No.
Contig ID
                  1785_1.R1010
5'-most EST
                  PLN_g3790553
Method
                  BLASTX
                  g3790554
NCBI GI
BLAST score
                  870
                  8.0e-94
E value
Match length
                  158
% identity
                  98
                  (AF078683) RING-H2 finger protein RHAla [Arabidopsis
NCBI Description
                  thaliana]
                  118728
Seq. No.
Contig ID
                  1786 1.R1010
5'-most EST
                  jC-atXP69C217M8T7004d1
Method
                  BLASTX
NCBI GI
                  g3790567
BLAST score
                  836
                  1.0e-89
E value
Match length
                  157
                  96
% identity
                  (AF078821) RING-H2 finger protein RHA1b [Arabidopsis
NCBI Description
                  thaliana]
                  118729
Seq. No.
                  1787_1.R1010
Contig ID
5'-most EST
                  PLN_{g}3790568
Method
                  BLASTX
NCBI GI
                  q3790569.
BLAST score
                  759
E value
                  1.0e-80
Match length
                  155
                  95
% identity
                  (AF078822) RING-H2 finger protein RHA2a [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  118730
                  1787 3.R1010
Contig ID
5'-most EST
                  g2047543
Method
                  BLASTX
NCBI GI
                  g3790569
BLAST score
                  404
E value
                  3.0e-39
Match length
                  94
                  90
% identity
                  (AF078822) RING-H2 finger protein RHA2a [Arabidopsis
NCBI Description
                  thaliana]
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Match length

629

```
Seq. No.
                  118731
                  1788 1.R1010
Contig ID
                  iC-atXLIB327428P4d11b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4262223
BLAST score
                  397
E value
                  3.0e-38
Match length
                  147
% identity
                  86
NCBI Description
                  (AC006200) RING-H2 finger protein RHA2b [Arabidopsis
                  thaliana]
Seq. No.
                  118732
Contig ID
                  1788 2.R1010
5'-most EST
                  q315846
                  BLASTX
Method
NCBI GI
                  g4262223
BLAST score
                  412
                  2.0e-40
E value
Match length
                  86
% identity
                  98
NCBI Description
                  (AC006200) RING-H2 finger protein RHA2b [Arabidopsis
                  thaliana]
Seq. No.
                  118733
Contig ID
                  1789 1.R1010
5'-most EST
                  LIB24-095-Q1-E1-D7
Method
                  BLASTX
                  g2262176
NCBI GI
BLAST score
                  778
E value
                  7.0e-83
Match length
                  165
                  90
% identity
NCBI Description
                  (AC002329) putative RING zinc-finger protein [Arabidopsis
                  thaliana] >gi 3790573 (AF078824) RING-H2 finger protein
                  RHA3a [Arabidopsis thaliana]
                  118734
Seq. No.
Contig ID
                  1790 1.R1010
5'-most EST
                  PLN_g3790574
Method
                  BLASTX
NCBI GI
                  q3790575
BLAST score
                  863
E value
                  7.0e-93
Match length
                  200
% identity
                  81
NCBI Description
                  (AF078825) RING-H2 finger protein RHA3b [Arabidopsis
                  thaliana]
Seq. No.
                  118735
Contig ID
                  1791 1.R1010
5'-most EST
                  jC-atX24056Q1E2D01b1
Method
                  BLASTX
NCBI GI
                  q3806098
BLAST score
                  3138
E value
                  0.0e + 00
```

Method

BLASTX

```
% identity
                   96
NCBI Description
                   (AF079100) arginine-tRNA-protein transferase 1; Atelp
                   [Arabidopsis thaliana]
Seq. No.
                   118736
                   1791 4.R1010
Contig ID
5'-most EST
                  ARABLI-09-Q1-B1-E9
Method
                  BLASTX
NCBI GI
                   q3806098
BLAST score
                   345
E value
                   1.0e-32
Match length
                   92
% identity
                   78
NCBI Description
                   (AF079100) arginine-tRNA-protein transferase 1; Atelp
                   [Arabidopsis thaliana]
Seq. No.
                  118737
                   1792 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327410P2h09b1
                   BLASTX
Method
NCBI GI
                   q3790581
BLAST score
                   1030
E value
                   1.0e-112
Match length
                   190
                   100
%'identity
                   (AF079179) RING-H2 finger protein RHB1a [Arabidopsis
NCBI Description
                  thalianal
                   118738
Seq. No.
                   1793 1.R1010
Contig ID
5'-most EST
                   PLN g3790582
Method
                  BLASTX
NCBI GI
                  q2623297
BLAST score
                   1432
E value
                   1.0e-159
Match length
                   328
% identity
                   82
NCBI Description
                   (AC002409) unknown protein [Arabidopsis thaliana]
                  >gi 3790583 (AF079180) RING-H2 finger protein RHCla
                   [Arabidopsis thaliana]
                   118739
Seq. No.
Contig ID
                  1794 1.R1010
5'-most EST
                   jC-atXLIB327420P4g09b1
Method
                  BLASTX
NCBI GI
                  q3790587
BLAST score
                   1559
E value
                  1.0e-174
Match length
                   370
% identity
NCBI Description
                   (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
                  thalianal
Seq. No.
                  118740
                  1795 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1f01b1
```

....

```
NCBI GI
                   g2642154
BLAST score
                   1497
                   1.0e-167
E value
                   399
Match length
% identity
                  71
                   (AC003000) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3790595 (AF079186) RING-H2 finger protein RHC2a
                  [Arabidopsis thaliana]
                  118741
Seq. No.
                  1797 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327406P1e01b1
Method
                  BLASTX
NCBI GI
                  g3702964
BLAST score
                  1046
                  1.0e-114
E value
                  215
Match length
% identity
NCBI Description
                   (AF079485) rac GTP binding protein Aracl0 [Arabidopsis
                  thaliana]
                  118742
Seq. No.
                  1800 1.R1010
Contig ID
5'-most EST
                  PLN g3386545
Method
                  BLASTX
NCBI GI
                  g3386546
BLAST score
                  2008
                  0.0e + 00
E value
Match length
                   447
                  87
% identity
                   (AF079503) H-protein promoter binding factor-2a
NCBI Description
                   [Arabidopsis thaliana]
                  118743
Seq. No.
                  1801 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P4h02b1
Method
                  BLASTN
NCBI GI
                  g3386547
BLAST score
                   345
E value
                  0.0e + 00
Match length
                   435
                  99
% identity
NCBI Description
                  Arabidopsis thaliana H-protein promoter binding factor-2b
                  mRNA, complete cds
                  118744
Seq. No.
Contig ID
                  1803 1.R1010
5'-most EST
                  PLN g4185737
Method
                  BLASTX
NCBI GI
                  g4185738
BLAST score
                  3877
E value
                  0.0e + 00
Match length
                  808
% identity
NCBI Description
                   (AF079998) putative glutamate receptor [Arabidopsis
```

thaliana]

Seq. No.

118750

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Seq. No.
                   118745
Contig ID
                   1806 1.R1010
5'-most EST
                   PLN g3421377
                   BLASTX
Method
NCBI GI
                   q3421378
BLAST score
                   5044
E value
                   0.0e + 00
Match length
                   987
                   100
% identity
NCBI Description
                   (AF080249) kinesin-like heavy chain [Arabidopsis thaliana]
Seq. No.
                   118746
Contig ID
                   1807 1.R1010
5'-most EST
                   iC-atXLIB327419P4e10b1
Method
                   BLASTX
NCBI GI
                   g3415113
BLAST score
                   4314
E value
                   0.0e + 00
Match length
                   910
                   91
% identity
NCBI Description
                   (AF081201) villin 1 [Arabidopsis thaliana]
Seq. No.
                   118747
                   1808 1.R1010
Contig ID
                   jC-atXLIB327401P3b10b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   a3415117
BLAST score
                   4395
E value
                   0.0e + 00
Match length
                   953
                   89
% identity
                   (AF081203) villin 3 [Arabidopsis thaliana]
NCBI Description
                   118748
Seq. No.
Contig ID
                   1808 2.R1010
5'-most EST
                   jC-atXLIB327411P2d11b1
Method
                   BLASTX
NCBI GI
                   a3415115
BLAST score
                   4505
E value
                   0.0e+00
Match length
                   966
                   90
% identity
NCBI Description
                   (AF081202) villin 2 [Arabidopsis thaliana]
                   118749
Seq. No.
Contig ID
                   1808 4.R1010
5'-most EST
                   g152\overline{0}435
Method
                   BLASTN
NCBI GI
                   q2335089
BLAST score
                   302
E value
                   1.0e-169
Match length
                   402
% identity
                  Arabidopsis thaliana chromosome II BAC T11A7 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

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1808 5.R1010
Contig ID
5'-most EST
                   g1328081
Method
                   BLASTN
NCBI GI
                   g3415116
                   225
BLAST score
                   1.0e-123
E value
Match length
                   287
                   97
% identity
                  Arabidopsis thaliana villin 3 (VLN3) mRNA, complete cds
NCBI Description
Seq. No.
                   118751
                   1810 1.R1010
Contig ID
                   PLN g3420934
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3420935
BLAST score
                   2651
                   0.0e+00
E value
Match length
                   531
% identity
                   94
                   (AF082157) beta-glucosidase [Arabidopsis thaliana]
NCBI Description
                   >gi 3421390 (AF082158) beta-glucosidase homolog
                   [Arabidopsis thaliana]
Seq. No.
                   118752
                   1811 1.R1010
Contig ID
                   q2763396
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2618602
BLAST score
                   521
                   0.0e + 00
E value
                   542
Match length
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   118753
                   1812 1.R1010
Contig ID
5'-most EST
                   LIB3176-112-P1-K1-A9
Method
                   BLASTN
NCBI GI
                   q4544435
BLAST score
                   671
                   0.0e + 00
E value
Match length
                   671
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC F14M13 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   118754
                   1813 1.R1010
Contig ID
5'-most EST
                   LIB3176-064-P1-K1-E10
Method
                   BLASTN
NCBI GI
                   g3883123
BLAST score
                   478
E value
                   0.0e + 00
Match length
                   720
                   98
% identity
                  Arabidopsis thaliana arabinogalactan-protein (AGP3) mRNA,
NCBI Description
```

complete cds 118755 Seq. No. 1814 1.R1010 Contig ID 5'-most EST g2048793 · Method BLASTN g3883125 NCBI GI BLAST score 278 1.0e-155 E value 662 Match length % identity 99 Arabidopsis thaliana arabinogalactan-protein (AGP4) mRNA, NCBI Description complete cds 118756 Seq. No. 1814 2.R1010 Contig ID 5'-most EST g3450368 118757 Seq. No. 1814 4.R1010 Contig ID 5'-most EST $LIB2\overline{5}-097-Q1-E1-H9$ Seq. No. 118758 1815_1.R1010 PLN_g3883127 Contig ID 5'-most EST Method BLASTN NCBI GI q3883127 BLAST score 536 0.0e+00E value Match length 536 % identity 100 NCBI Description Arabidopsis thaliana arabinogalactan-protein (AGP5) mRNA, complete cds 118759 Seq. No. 1816 1.R1010 Contig ID

 Seq. No.
 118759

 Contig ID
 1816_1.R1010

 5'-most EST
 jC-atXLIB327427P2c06b1

 Method
 BLASTX

 NCBI GI
 g3746809

NCBI GI g3746809 BLAST score 1254 E value 1.0e-138 Match length 246 % identity 100

NCBI Description (AF082882) adenylate kinase [Arabidopsis thaliana]

Seq. No. 118760
Contig ID 1816_2.R1010

5'-most EST jC-atXmonuni27Bc06a1

Method BLASTX
NCBI GI g3746809
BLAST score 368
E value 5.0e-35
Match length 74
% identity 99

NCBI Description (AF082882) adenylate kinase [Arabidopsis thaliana]

Seq. No. 118761

Seq. No.

118766

```
1818 1.R1010
Contig ID
                  jC-atX22033Q1E1E07b1
5'-most EST
Method
                  BLASTX
                  g3450889
NCBI GI
BLAST score
                  1890
                  0.0e+00
E value
Match length
                  421
                  90
% identity
                  (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118762
                  1818 2.R1010
Contig ID
                  jC-atXLIB327402P4h02b1
5'-most EST
                  BLASTX
Method
                  q3450889
NCBI GI
BLAST score
                  672
E value
                  2.0e-70
                  223
Match length
                  53
% identity
                  (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
NCBI Description
                  118763
Seq. No.
                  1819 1.R1010
Contig ID
                  jC-alX24079Q1E1F03b1
5'-most EST
                  BLASTX
Method
                  q3859944
NCBI GI
                  1367
BLAST score
E value
                  1.0e-152
                  292
Match length
                  95
% identity
                  (AF084570) FKBP12 interacting protein [Arabidopsis
NCBI Description
                  thaliana]
                  118764
Seq. No.
                  1820 1.R1010
Contig ID
                  jC-atX24059Q1E1D03b1
5'-most EST
                  BLASTX
Method
                  q4322421
NCBI GI
BLAST score
                  2316
E value
                  0.0e + 00
                   485
Match length
% identity
                   (AF085230) cadmium resistance factor 1 [Arabidopsis
NCBI Description
                  thaliana]
                   118765
Seq. No.
                   1825 1.R1010
Contig ID
5'-most EST
                  LIB35-028-Q1-E1-H8
                  BLASTX
Method
NCBI GI
                  q3643192
BLAST score
                   1553
E value
                   1.0e-173
                   332
Match length
% identity
NCBI Description (AF087435) unknown [Arabidopsis thaliana]
```

```
Contig ID
                   1826 1.R1010
5'-most EST
                   jC-atXLIB327419P3g04b2
Method
                   BLASTX
NCBI GI
                   q3822403
BLAST score
                   2388
E value
                   0.0e + 00
Match length
                   485
% identity
NCBI Description
                   (AF087932) hydroperoxide lyase [Arabidopsis thaliana]
Seq. No.
                   118767
                   1827 1.R1010
Contig ID
                  LIB22-020-Q1-E1-H8
5'-most EST
                   BLASTX
Method
                   a4093157
NCBI GI
                   1512
BLAST score
E value
                   1.0e-168
                   305
Match length
% identity
                   95
                   (AF087936) phytochrome-associated protein 2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   118768
                   1828_1.R1010
Contig ID
                   g510767
5'-most EST
Method
                  BLASTX
                  q3482928
NCBI GI
BLAST score
                   2499
                  0.0e + 00
E value
Match length
                   524
% identity
                   93
                  (AC003970) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3929586 (AF100166) phytochrome interacting factor 3
                   [Arabidopsis thaliana]
                   118769
Seq. No.
                   1829 1.R1010
Contig ID
                   jC-atXLIB327414P4f10b2
5'-most EST
Method
                   BLASTX
                  a4093155
NCBI GI
                   1374
BLAST score
E value
                   1.0e-152
                   269
Match length
% identity
                   99
                   (AF088281) phytochrome-associated protein 1 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   118770
                   1829 2.R1010
Contig ID
5'-most EST
                   jC-atXP35C154B9T7d1
Method
                  BLASTN
                  q4093154
NCBI GI
BLAST score
                   248
E value
                  1.0e-137
Match length
                   296
                   97
% identity
NCBI Description Arabidopsis thaliana phytochrome-associated protein 1
```

NCBI GI

BLAST score

q3661595

738

Seq. No. 118771 1831_1.R1010 Contig ID PLN_g3608494 5'-most EST Method BLASTX q3608495 NCBI GI 1852 BLAST score 0.0e + 00E value Match length 397 % identity 95 NCBI Description (AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >gi_4510351_gb_AAD21440.1_ (AC006921) plastid division protein FtsZ [Arabidopsis thaliana] 118772 Seq. No. 1832_1.R1010 ' Contig ID $LIB2\overline{5}-071-Q1-E1-B1$ 5'-most EST Method BLASTX NCBI GI q4249662 BLAST score 2031 E value 0.0e + 00Match length 410 % identity NCBI Description (AF089810) Altered Response to Gravity [Arabidopsis thaliana] 118773 Seq. No. Contig ID 1833 1.R1010 LIB3175-004-P1-K1-C11 5'-most EST Method BLASTX NCBI GI q3661595 BLAST score 2089 E value 0.0e + 00Match length 389 % identity 100 (AF091844) aminoalcoholphosphotransferase [Arabidopsis NCBI Description thaliana] 118774 Seq. No. 1833 2.R1010 Contig ID 5'-most EST LIB25-096-Q1-E1-D3 Method BLASTX NCBI GI g3661593 BLAST score 2011 0.0e + 00E value 389 Match length % identity 97 (AF091843) aminoalcoholphosphotransferase [Arabidopsis NCBI Description thaliana] 118775 Seq. No. Contig ID 1833 3.R1010 5'-most EST jC-atXP19C111I10T7034a1 Method BLASTX

(PAP1) mRNA, complete cds

```
E value
                   3.0e-78
Match length
                   142
                   100
% identity
NCBI Description
                   (AF091844) aminoalcoholphosphotransferase [Arabidopsis
                   118776
Seq. No.
                   1837_1.R1010
Contig ID
                   PLN_g4218962
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4218963
BLAST score
                   1543
                   1.0e-172
E value
                   287
Match length
                   98
% identity
                   (AF093672) xyloglucan endotransglycosylase [Arabidopsis
NCBI Description
                   thaliana] >gi_4539300_emb_CAB39603.1_ (AL049480) putative
                   xyloglucan endo-1, 4-beta-D-glucanase [Arabidopsis
                   thaliana]
                   118777
Seq. No.
Contig ID
                   1839_1.R1010
                   jC-atXLIB327409P3d12b1
5'-most EST
Method
                   BLASTX
                   q3859536
NCBI GI
                   2861
BLAST score
                   0.0e + 00
E value
Match length
                   578
% identity
                   93
                   (AF095453) asparagine synthetase [Arabidopsis thaliana]
NCBI Description
                   118778
Seq. No.
Contig ID
                   1841_1.R1010
                   jC-atXLIB327406P2d03b1
5'-most EST
Method
                   BLASTX
                   q3885943
NCBI GI
BLAST score
                   984
                   1.0e-107
E value
Match length
                   196
                   100
% identity
                   (AF095455) PII protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4558559 gb AAD22652.1 AC007138 16 (AC007138) P II
                   nitrogen sensing protein GLB I [Arabidopsis thaliana]
                   118779
Seq. No.
                   1842_1.R1010
Contig ID
                   jC-a\overline{t}XLIB327420P3h05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3747111
BLAST score
                   1450
                   1.0e-161
E value
                   285
Match length
% identity
                   100
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
                   118780
Seq. No.
```

1842_2.R1010

Contig ID

```
jC-atXLIB327406P2h02b1
5'-most EST
Method
                  BLASTX
                  g3747111
NCBI GI
BLAST score
                   736
E value
                   5.0e-78
Match length
                  168
                   90
% identity
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118781
                  1842 3.R1010
Contiq ID
                  LIB25-053-Q1-E1-F8
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3747111
BLAST score
                   413
E value
                   2.0e-40
Match length
                   127
                  56
% identity
NCBI Description
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
                  118782
Seq. No.
Contig ID
                  1845 1.R1010
5'-most EST
                  jC-atXP79C239A1T7b1
                  BLASTX
Method
                  q3983125
NCBI GI
                   1869
BLAST score
                  0.0e + 00
E value
Match length
                   407
% identity
                   (AF097648) phosphate/triose-phosphate translocator
NCBI Description
                  precursor [Arabidopsis thaliana]
Seq. No.
                   118783
                   1845 2.R1010
Contig ID
                   jC-atXLIB327409P1c10b1
5'-most EST
Method
                   BLASTX
NCBI GI
                  q3983125
BLAST score
                   640
E value
                   4.0e-86
Match length
                   208
% identity
                  81
NCBI Description
                   (AF097648) phosphate/triose-phosphate translocator
                  precursor [Arabidopsis thaliana]
Seq. No.
                   118784
                   1845 4.R1010
Contig ID
5'-most EST
                   jC-atXLIB327423P4b12b1
Method
                   BLASTX
NCBI GI
                  q3983125
BLAST score
                   393
E value
                   6.0e-38
Match length
                   127
                   67
% identity
NCBI Description
                   (AF097648) phosphate/triose-phosphate translocator
                  precursor [Arabidopsis thaliana]
Seq. No.
                  118785
```

```
Contig ID
                   1845_5.R1010
5'-most EST
                   jC-atXP102CE3G12T7b1
Method
                   BLASTX
                   g3983125
NCBI GI
BLAST score
                   504
E value
                   2.0e-75
Match length
                   169
                   95
% identity
                   (AF097648) phosphate/triose-phosphate translocator
NCBI Description
                  precursor [Arabidopsis thaliana]
                   118786
Seq. No.
Contig ID
                   1847_1.R1010
5'-most EST
                   PLN g4164577
                   BLASTX
Method
NCBI GI
                   g4164578
BLAST score
                   2139
E value
                   0.0e + 00
Match length
                   428
                   97
% identity
                   (AF098947) CTF2B [Arabidopsis thaliana]
NCBI Description
                   118787
Seq. No.
Contig ID
                   1849 1.R1010
                   jC-a\overline{t}XLIB327416P2c03b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3851669
BLAST score
                   500
E value
                   0.0e + 00
Match length
                   539
                   99
% identity
NCBI Description
                  Arabidopsis thaliana J8 mRNA, nuclear gene encoding plastid
                  protein, complete cds
                   118788
Seq. No.
                   1849_3.R1010
Contig ID
5'-most EST
                   g2763009
Method
                   BLASTN
NCBI GI
                   g3851669
BLAST score
                   113
E value
                   2.0e-56
Match length
                   133
% identity
                   96
                  Arabidopsis thaliana J8 mRNA, nuclear gene encoding plastid
NCBI Description
                  protein, complete cds
                   118789
Seq. No.
                   1850_1.R1010
Contig ID
                   g17396
5'-most EST
Method
                   BLASTX
                   q3820620
NCBI GI
BLAST score
                   1670
E value
                   0.0e + 00
Match length
                   390
% identity
                   86
                   (AF099970) putative formamidopyrimidine-DNA glycosylase 1
NCBI Description
```

[Arabidopsis thaliana]

```
Seq. No.
                   118790
Contig ID
                  1850 3.R1010
5'-most EST
                  ARABL1-03-Q1-B1-D5
Method
                  BLASTN
NCBI GI
                   g3550981
BLAST score
                   148
E value
                   2.0e-77
Match length
                   537
                   99
% identity
NCBI Description
                  Arabidopsis thaliana mutM homologue gene, complete cds
                  118791
Seq. No.
                  1852 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327408P2f07b1
Method
                   BLASTX
NCBI GI
                   g4185507
BLAST score
                   4157
E value
                   0.0e+00
                  856
Match length
                  92
% identity
                  (AF100163) EZA1 [Arabidopsis thaliana]
NCBI Description
                  118792
Seq. No.
Contig ID
                  1854 1.R1010
5'-most EST
                  LIB3175-037-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q3983260
BLAST score
                   1845
E value
                   0.0e + 00
                   419
Match length
% identity
                  89
                  (AF101075) sigma-like factor [Arabidopsis thaliana]
NCBI Description
                  118793
Seq. No.
                  1855 1.R1010
Contig ID
5'-most EST
                   jC-atXP12C103G2T7d2
Method
                  BLASTX
NCBI GI
                  g4185509
BLAST score
                  ·713
E value
                  3.0e-75
Match length
                  139
% identity
                  100
                   (AF102821) actin depolymerizing factor 3 [Arabidopsis
NCBI Description
                  thaliana]
                  118794
Seq. No.
                  1855 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327426P2f12b1
Method
                  BLASTX
NCBI GI
                  g4185509
BLAST score
                  183
                   4.0e-13
E value
                  90
Match length
                  82
% identity
                  (AF102821) actin depolymerizing factor 3 [Arabidopsis
NCBI Description
                  thaliana]
```

Match length

```
Seq. No.
                  118795
Contig ID
                  1855 3.R1010
5'-most EST
                  jC-atX24056Q1E2E02b1
Method
                  BLASTX
NCBI GI
                  g4185511
                  687
BLAST score
                  3.0e-72
E value
Match length
                  139
                  96
% identity
NCBI Description
                  (AF102822) actin depolymerizing factor 4 [Arabidopsis
                  thaliana]
                  118796
Seq. No.
                  1855 4.R1010
Contig ID
                  LIB35-005-Q1-E1-G9
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4185509
BLAST score
                  374
                  2.0e-49
E value
Match length
                  101
% identity
                  (AF102821) actin depolymerizing factor 3 [Arabidopsis
NCBI Description
                  thaliana]
                  118797
Seq. No.
Contig ID
                  1858 1.R1010
5'-most EST
                  LIB3175-018-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q4185515
BLAST score
                  753
                  8.0e-80
E value
Match length
                  146
% identity
                  100
NCBI Description
                  (AF102824) actin depolymerizing factor 6 [Arabidopsis
                  thaliana]
                  118798
Seq. No.
Contig ID
                  1858 2.R1010
5'-most EST
                  LIB3175-041-P1-K1-E12
Method
                  BLASTX
                  q4185515
NCBI GI
                  190
BLAST score
E value
                  9.0e-53
Match length
                  142
% identity
                  80
                  (AF102824) actin depolymerizing factor 6 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  118799
                  1859_1.R1010
Contig ID
5'-most EST
                  PLN_g4106537
Method
                  BLASTX
                  q4106538
NCBI GI
BLAST score
                  1545
                  1.0e-172
E value
```

```
% identity
                     (AF104220) gamma-tocopherol methyltransferase [Arabidopsis
NCBI Description
                     thalianal
Seq. No.
                     118800
Contig ID
                     1860 1.R1010
                     jC-atXP115C248O14T7021d1
5'-most EST
                     BLASTX
Method
NCBI GI
                     q3157924
BLAST score
                     315
E value
                     1.0e-28
Match length
                     80
                     78
% identity
                     (AC002131) Contains homology to extensin-like protein
NCBI Description
                     gb D83227 from Populus nigra. ESTs gb H76425, gb T13883,
                     gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951
                    come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like
                    protein [Arabidopsis thaliana]
                    118801
Seq. No.
Contig ID
                    1860 2.R1010
                     jC-a\overline{t}XP92C249D15T7069d1
5'-most EST
Method
                    BLASTN
                    g2584827
NCBI GI
BLAST score
                     514
                     0.0e + 00
E value
Match length
                     719
% identity
                    Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
NCBI Description
                    complete sequence [Arabidopsis thaliana]
Seq. No.
                     118802
                     1860_3.R1010
Contig ID
5'-most EST
                    LIB3177-039-P1-K2-F3
Method
                    BLASTX
NCBI GI
                    q3157924
BLAST score
                    239
E value
                     3.0e-21
Match length
                     63
                    90
% identity
                     (AC002131) Contains homology to extensin-like protein
NCBI Description
                    gb D83227 from Populus nigra. ESTs gb H76425, gb T13883,
                    gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951 come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like
                    protein [Arabidopsis thaliana]
Seq. No.
                    118803
                    1860 6.R1010
Contig ID
5'-most EST
                    q906095
Method
                    BLASTN
NCBI GI
                    g4063706
BLAST score
                    341
E value
                    0.0e+00
Match length
                    425
                    97
% identity
```

BLAST score

1489

```
NCBI Description Arabidopsis thaliana extensin-like protein (ELP) mRNA,
                  complete cds
                   118804
Seq. No.
Contig ID
                   1860 8.R1010
5'-most EST
                  g957<del>5</del>27
Method
                  BLASTN
NCBI GI
                  g4063706
BLAST score
                   301
E value
                   1.0e-169
Match length
                   345
% identity
                   98
NCBI Description
                  Arabidopsis thaliana extensin-like protein (ELP) mRNA,
                   complete cds
                   118805
Seq. No.
Contig ID
                   1861 1.R1010
5'-most EST
                  LIB23-020-Q1-E1-C7
Method
                  BLASTX
NCBI GI
                   g4206763
BLAST score
                   463
E value
                   9.0e-46
Match length
                   87
% identity
                   100
NCBI Description
                   (AF104328) cell wall-plasma membrane linker protein homolog
                   [Arabidopsis thaliana]
Seq. No.
                   118806
Contig ID
                   1861 4.R1010
5'-most EST
                   g2581640
Method
                  BLASTX
                  g4206763
NCBI GI
BLAST score
                   55
E value
                   2.0e-33
Match length
                   81
% identity
                   90
NCBI Description
                   (AF104328) cell wall-plasma membrane linker protein homolog
                   [Arabidopsis thaliana]
Seq. No.
                   118807
                   1861_5.R1010
Contig ID
5'-most EST
                  LIB23-021-Q2-E1-D4
                  BLASTN
Method
NCBI GI
                  g4206762
BLAST score
                   249
                  1.0e-137
E value
Match length
                   550
% identity
                   63
                  Arabidopsis thaliana cell wall-plasma membrane linker
NCBI Description
                  protein homolog (CWLP) mRNA, complete cds
                  118808
Seq. No.
Contig ID
                  1862_1.R1010
5'-most EST
                  jC-atXLIB327430P4h05b1
Method
                  BLASTN
NCBI GI
                  g4206764
```

Method

BLASTX

```
0.0e + 00
E value
Match length
                   1489
                   100
% identity
                  Arabidopsis thaliana putative type 1 membrane protein (PMP)
NCBI Description
                  mRNA, complete cds
                   118809
Seq. No.
                   1863 1.R1010
Contig ID
                   jC-atXP25C122O2T7066a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4741952
BLAST score
                   577
E value
                   1.0e-152
Match length
                   265
                   70
% identity
                   (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
                   118810
Seq. No.
                  1863 3.R1010
Contig ID
                  LIB35-003-Q1-E1-C3
5'-most EST
                  BLASTX
Method
                   g3859606
NCBI GI
BLAST score
                   749
E value
                   2.0e-89
Match length
                   196
% identity
                  84
                   (AF104919) contains similarity to cysteine proteases (Pfam:
NCBI Description
                  PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]
                   118811
Seq. No.
Contig ID
                   1863_4.R1010
                   g937022
5'-most EST
                  BLASTX
Method
NCBI GI
                   g3859607
BLAST score
                   562
E value
                   1.0e-57
Match length
                  129
% identity
NCBI Description
                   (AF104919) contains similarity to cysteine proteases (Pfam:
                   PF00112, E=.21, N=1) [Arabidopsis thaliana]
                   118812
Seq. No.
                   1863 5.R1010
Contig ID
5'-most EST
                  LIB3168-069-P1-K1-B12
Method
                  BLASTX
NCBI GI
                   g3859606
BLAST score
                  864
E value
                  1.0e-136
Match length
                  359
% identity
                   63
NCBI Description
                   (AF104919) contains similarity to cysteine proteases (Pfam:
                  PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]
                  118813
Seq. No.
Contig ID
                  1863 7.R1010
5'-most EST
                   jC-atXLIB327401P4b11b2
```

```
NCBI GI
                  q3859606
BLAST score
                  155
E value
                  1.0e-131
Match length
                  250
                  92
% identity
                   (AF104919) contains similarity to cysteine proteases (Pfam:
NCBI Description
                  PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]
                  118814
Seq. No.
                  1863_8.R1010
Contig ID
5'-most EST
                  jC-atXLIB327408P3b08b1
Method
                  BLASTX
NCBI GI
                  g4206767
BLAST score
                  155
                   6.0e-10
E value
Match length
                  26
                  9.6
% identity
                   (AF104330) glycine-rich protein 3 short isoform
NCBI Description
                   [Arabidopsis thaliana]
                  118815
Seq. No.
                  1863 9.R1010
Contig ID
5'-most EST
                  jC-a\(\bar{1}\)XLIB327434P3a11b1
Method
                  BLASTX
                  g2317912
NCBI GI
BLAST score
                  588
                  1.0e-60
E value
                  118
Match length
                  92
% identity
                  (U89959) cathepsin B-like cysteine proteinase [Arabidopsis
NCBI Description
                  thaliana]
                  118816
Seq. No.
                  1863 10.R1010
Contig ID
5'-most EST
                   g1216982
Method
                  BLASTX
NCBI GI
                  g4206767
BLAST score
                   220
                  1.0e-17
E value
Match length
                  116
% identity
                   45
                   (AF104330) glycine-rich protein 3 short isoform
NCBI Description
                   [Arabidopsis thaliana]
                   118817
Seq. No.
                   1863 15.R1010
Contig ID
                   jC-atXP26C127K5T7d1
5'-most EST
Method
                  BLASTX
                   g2317912
NCBI GI
BLAST score
                   531
E value
                  3.0e-54
Match length
                  124
                  85
% identity
                  (U89959) cathepsin B-like cysteine proteinase [Arabidopsis
NCBI Description
                  thaliana]
```

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118818

Seq. No.

5'-most EST

g2747583

```
Contig ID
                  1863 19.R1010
                  LIB25-025-Q1-E1-F10
5'-most EST
Method
                   BLASTX
                   q4741952
NCBI GI
                   609
BLAST score
                   2.0e-63
E value
Match length
                   112
                   74
% identity
                   (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
                   118819
Seq. No.
Contig ID
                   1863 20.R1010
5'-most EST
                   jC-atXP102CE5F1T7b1
                   BLASTX
Method
NCBI GI
                   g4741952
BLAST score
                   528
                   1.0e-53
E value
Match length
                   193
                   97
% identity
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
                   118820
Seq. No.
Contig ID
                   1863 21.R1010
5'-most EST
                   g957464 ..
Method
                   BLASTX
                   g4741952
NCBI GI
BLAST score
                   952
                   1.0e-108
E value
Match length
                   214
% identity
                   67
                   (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
                   118821
Seq. No.
                   1863 23.R1010
Contig ID
5'-most EST
                   g914494
Method
                   BLASTX
                   g4741952
NCBI GI
BLAST score
                   502
                   8.0e-51
E value
Match length
                   114
                   88
% identity
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
                   118822
Seq. No.
Contig ID
                   1863 25.R1010
5'-most EST
                   jC-atXP102CE5F1T7008d1
Method
                   BLASTX
                   g4741952
NCBI GI
BLAST score
                   620
E value
                   2.0e-64
Match length
                   168
% identity
                   56
NCBI Description
                   (AF134126) Lhcb3 protein [Arabidopsis thaliana]
                   118823
Seq. No.
Contig ID
                   1863 26.R1010
```

```
Method
                  BLASTX
NCBI GI
                  a4741952
BLAST score
                  449
                  1.0e-44
E value
                  125
Match length
% identity
                  76
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
                  118824
Seq. No.
                  1863_29.R1010
Contig ID
5'-most EST
                  g1217315
Method
                  BLASTX
                  q4741952
NCBI GI
                  366
BLAST score
                  5.0e-35
E value
                  95
Match length
% identity
                  82
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
                  118825
Seq. No.
                  1863_34.R1010
Contig ID
5'-most EST
                  LIB3176-058-P1-K1-C5
Method
                  BLASTX
                  g515616
NCBI GI
BLAST score
                  64
                  3.0e-27
E value
Match length
                  73
                  76
% identity
                  (X61608) LHC II Type III chlorophyll a /b binding protein
NCBI Description
                  [Brassica napus]
                  118826
Seq. No.
Contig ID
                  1867_1.R1010
5'-most EST
                  PLN_g4324677
Method
                  BLASTX
NCBI GI
                  q3128220
                  1323
BLAST score
                  1.0e-146
E value
Match length
                  262
% identity
                  98
                  (AC004077) putative urease accessory protein [Arabidopsis
NCBI Description
                  thaliana] >gi_3337375 (AC004481) putative urease accessory
                  protein [Arabidopsis thaliana]
                  118827
Seq. No.
                  1867 2.R1010
Contig ID
                  jC-atXLIB327410P1h03b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3128220
BLAST score
                  1012
                  1.0e-110
E value
Match length
                  215
                  94
% identity
NCBI Description
                  (AC004077) putative urease accessory protein [Arabidopsis
                  thaliana] >gi_3337375 (AC004481) putative urease accessory
```

protein [Arabidopsis thaliana]

```
Seq. No.
                   118828
Contig ID
                   1868 1.R1010
5'-most EST
                   PLN g4324713
Method
                   BLASTX
NCBI GI
                   g4324714
BLAST score
                   2378
E value. -
                   0.0e+00
Match length
                   500
                   90
% identity
NCBI Description
                  (AF110771) ammonium transporter [Arabidopsis thaliana]
                   118829
Seq. No.
                   1869_1.R1010
Contig ID
                   g2758556
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4406384
BLAST score
                   1663
E value
                   0.0e + 00
Match length
                   323
                   100
% identity
                   (AF112303) serine acetyltransferase [Arabidopsis thaliana]
NCBI Description
                   118830
Seq. No.
Contig ID
                   1870_1.R1010
                   PLN_g4206788
5'-most EST
                   BLASTX
Method
                   g4206789
NCBI GI
BLAST score
                   1418
E value
                   1.0e-157
Match length
                   309
                   91
% identity
NCBI Description
                   (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis
                   thaliana]
                   118831
Seq. No.
                   1870 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327412P4d01b1
                   BLASTX
Method:
NCBI GI
                   g4206789
BLAST score
                   363
E value
                   2.0e-34
Match length
                   78
                   92
% identity
                   (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis
NCBI Description
                   thaliana]
                   118832
Seq. No.
                   1870 4.R1010
Contig ID
5'-most EST
                  LIB3234-018-P1-K1-F4
Method
                  BLASTX
NCBI GI
                   g4206789
BLAST score
                   490
                   2.0e-49
E value
Match length
                  97
                  99
% identity
NCBI Description
                  (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis
                   thaliana]
```

```
Seq. No.
                  118833
                  1871_1.R1010
Contig ID
                  PLN_g4469407
5'-most EST
                  BLASTX
Method
                  g4469408
NCBI GI
                  796
BLAST score
                  6.0e-85
E value
                  187
Match length
% identity
                  89
                  (AF116527) MADS box protein FLOWERING LOCUS F [Arabidopsis
NCBI Description
                  thaliana] >gi_4469410_gb_AAD21249_ (AF116528) MADS box
                  protein FLOWERING LOCUS F [Arabidopsis thaliana]
                  118834
Seq. No.
                  1872_1.R1010
Contig ID
5'-most EST
                  PLN g4204694
Method
                  BLASTX
NCBI GI
                  g4204695
BLAST score
                  3024
                  0.0e + 00
E value
Match length
                  590
% identity
                  97
NCBI Description
                  (AF117062) putative inositol polyphosphate 5-phosphatase
                  At5P1 [Arabidopsis thaliana]
Seq. No.
                  118835
                  1873 1.R1010
Contig ID
5'-most EST
                  PLN g4204696
Method
                  BLASTX
NCBI GI
                  g4204697
BLAST score
                  3269
E value
                  0.0e + 00
Match length
                  646
% identity
                  (AF117063) putative inositol polyphosphate 5-phosphatase
NCBI Description
                  At5P2 [Arabidopsis thaliana]
                  118836
Seq. No.
Contig ID
                  1874 1.R1010
5'-most EST
                  PLN g4337010
Method
                  BLASTX
                  g4337011
NCBI GI
BLAST score
                  1879
                  0.0e+00
E value
Match length
                  381
% identity
                  93
                  (AF119572) zinc-binding peroxisomal integral membrane
NCBI Description
                  protein [Arabidopsis thaliana]
                  118837
Seq. No.
                  1876_1.R1010
Contig ID
                  g2757301
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4039152
BLAST score
                  265
```

4.0e-23

E value

5'-most EST

```
Match length
                   54
% identity
                   96
NCBI Description
                   (AF104221) low temperature and salt responsive protein
                   LTI6B [Arabidopsis thaliana] >gi 4325219 gb AAD17303
                   (AF122006) hydrophobic protein [Arabidopsis thaliana]
Seq. No.
                   118838
                   1876 2.R1010
Contig ID
5'-most EST
                   q930<del>6</del>50
Method
                   BLASTX
NCBI GI
                   q4039152
BLAST score
                   279
                   1.0e-24
E value
Match length
                   54
                   100
% identity
                   (AF104221) low temperature and salt responsive protein
NCBI Description
                   LTI6B [Arabidopsis thaliana] >gi 4325219 gb AAD17303
                   (AF122006) hydrophobic protein [Arabidopsis thaliana]
Seq. No.
                   118839
                   1877 1.R1010
Contig ID
5'-most EST
                   LIB3176-001-Q1-K1-H2
Method
                   BLASTX
                   q4337027
NCBI GI
                   3595
BLAST score
                   0.0e + 00
E value
                   725
Match length
% identity
                   (AF123254) MFP2 [Arabidopsis thaliana]
NCBI Description
                   118840
Seq. No.
                   1877 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327418P3g10b1
Method
                   BLASTX
NCBI GI
                   q4337027
BLAST score
                   463
                   5.0e-46
E value
                   98
Match length
% identity
                   95
                   (AF123254) MFP2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118841
Contig ID
                   1879 1.R1010
5'-most EST
                   PLN_g4337039
Method
                   BLASTX
NCBI GI
                   q4337040
BLAST score
                   2338
E value
                   0.0e + 00
Match length
                   464
% identity
                   (AF124159) molybdopterin synthase sulphurylase [Arabidopsis
NCBI Description
                   thaliana] >gi_4337042_gb_AAD18051_ (AF124160) molybdopterin
                   synthase sulphurylase [Arabidopsis thaliana]
Seq. No.
                   118842
                   1880 1.R1010
Contig ID
```

PLN g4325323

```
Method
                   BLASTX
                   g4325324
NCBI GI
BLAST score
                   2939
                   0.0e + 00
E value
Match length
                   626 ...
 % identity
                   91
NCBI Description
                   (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
                   thaliana]
                   118843
Seq. No.
                   1880 4.R1010
Contig ID
 5'-most EST
                   g1216895
Method
                   BLASTX
NCBI GI
                   g4325324
BLAST score
                   468
                   2.0e-77
E value
Match length
                   153
                   96
 % identity
NCBI Description
                   (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
                   thaliana]
                   118844
Seq. No.
                   1881_1.R1010
Contig ID
5'-most EST
                   g17343 .
Method
                   BLASTX
NCBI GI
                   g4427003
BLAST score
                   1273
E value [
                   1.0e-141
Match length
                   282
                   89
% identity
                   (AF127664) NBD-like protein [Arabidopsis thaliana]
NCBI Description
                   118845
Seq. No.
                   1882_1.R1010
Contig ID
5'-most EST
                   PLN g4512121
Method
                   BLASTX
                   g4512122
NCBI GI
BLAST score
                   1477
-E value
                   1.0e-164
                   316
Match length
% identity
                   91
                   (AF131219) chorismate mutase 3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118846
                   1883 1.R1010
Contig ID
 5'-most EST
                   PLN g2121272
Method
                   BLASTX ·
NCBI GI
                   g2500036
BLAST score
                   1953
E value
                   0.0e+00
Match length
                   377
% identity
                   100
                   DIHYDROOROTASE PRECURSOR (DHOASE) >gi 2121273 (AF000146)
NCBI Description
                   dihydroorotase [Arabidopsis thaliana]
                   >gi 3292818 emb CAA19808 (AL031018) dihydroorotase
```

[Arabidopsis thaliana]

BLAST score

2006

```
Seq. No.
                   118847
Contig ID
                   1884_1.R1010
5'-most EST
                   PLN_{g}^{2}2121274
                   BLASTX
Method
NCBI GI
                   q2497486
BLAST score
                   1002
E value
                   1.0e-109
                   195
Match length
                   100
% identity
NCBI Description
                   URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
                   KINASE) >gi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis
                   thalianal
                   118848
Seq. No.
                   1884 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327405P2b11b2
Method
                   BLASTX
                   q2497486
NCBI GI
BLAST score
                   57
E value
                   1.0e-70
Match length
                   174
% identity
                   82
                  URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
NCBI Description
                   KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis
                   thaliana]
                   118849
Seq. No.
Contig ID
                   1887 2.R1010
5'-most EST
                   jC-atXP41C163H5T7s1
Method
                   BLASTN
NCBI GI
                   g2351066
BLAST score
                   326
E value
                   0.0e + 00
Match length
                   409
% identity
                   96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MOP9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   118850
                   1887 3.R1010
Contig ID
5'-most EST
                   jC-atXP41C163H5T7d1
Method
                   BLASTX
NCBI GI
                   g3309575
BLAST score
                   211
                   9.0e-17
E value
Match length
                   60
% identity
                   72
NCBI Description
                   (AF060553) calcium sensor homolog [Arabidopsis thaliana]
                   >gi_4538989_emb_CAB39731.1_ (Y18870) CBL4 protein
                   [Arabidopsis thaliana]
Seq. No.
                   118851
Contig ID
                   1889 1.R1010
5'-most EST
                   LIB2\overline{2}-021-Q1-E1-C1
Method
                   BLASTX
NCBI GI
                   g2641638
```

Method

...

BLASTX

```
0.0e + 00
E value
Match length
                   420
% identity
                   92
NCBI Description
                   (AF032883) AtJ3 [Arabidopsis thaliana]
Seq. No.
                   118852
                   1889 2.R1010
Contig ID
5'-most EST
                   q936<del>6</del>63
Method
                   BLASTX
                   q1169383
NCBI GI
BLAST score
                   1830
E value
                   0.0e + 00
Match length
                   414
% identity
                   86
                   DNAJ PROTEIN HOMOLOG ATJ >gi_535588 (L36113) putative
NCBI Description
                   [Arabidopsis thaliana] >gi_1582356_prf__2118338A AtJ2
                   protein [Arabidopsis thaliana]
Seq. No.
                   118853
Contig ID
                   1889 4.R1010
5'-most EST
                   jC-atXLIB327426P1h09b1
Method
                   BLASTN
NCBI GI
                   q4587641
BLAST score
                   224
E value
                   1.0e-122
Match length
                   490
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F20D21 genomic
                   sequence, complete sequence
Seq. No.
                   118854
Contig ID
                   1889 5.R1010
5'-most EST
                   q105\overline{3}443
Method
                   BLASTX
NCBI GI
                   q2641638
BLAST score
                   544
E value
                   2.0e-55
Match length
                   201
% identity
                   92
NCBI Description
                   (AF032883) AtJ3 [Arabidopsis thaliana]
Seq. No.
                   118855
Contig ID
                   1889 6.R1010
5'-most EST
                   jC-atXP89C242M5T7026d1
Method
                   BLASTN
NCBI GI
                   q4587641
BLAST score
                   206
E value
                   1.0e-112
Match length
                   210
% identity
                   100
                   Arabidopsis thaliana chromosome I BAC F20D21 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   118856
                   1889_7.R1010
LIB3175-039-P1-K1-A10
Contig ID
5'-most EST
```

```
NCBI GI
                   g2245006
BLAST score
                   224
E value
                   3.0e-18
Match length
                   87
                   51
% identity
                  (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  118857
Seq. No.
Contig ID
                   1889 8.R1010
                   jC-a\overline{t}XP12C99I5T7d2
5'-most EST
Method
                  BLASTN
NCBI GI
                   g4587641
BLAST score
                   204
                   1.0e-111
E value
Match length
                   210
                   99
% identity
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
NCBI Description
                  sequence, complete sequence
                  118858
Seq. No.
                  1889 9.R1010
Contig ID
5'-most EST
                  g2723255
Method
                  BLASTN
                  g4587641
NCBI GI
BLAST score
                   253
                  1.0e-140
E value
Match length
                   469.
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
                  118859
Seq. No.
Contig ID
                  1890_1.R1010
5'-most EST
                  PLN_g166626
Method
                  BLASTX
NCBI GI
                   g137465
BLAST score
                   2510
E value
                  0.0e + 00
Match length
                   492
% identity
                  100
                  VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)
NCBI Description
                   (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886
                  H+-transporting ATPase (EC 3.6.1.35) 57K chain -
                  Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding
                   subunit of vacuolar ATPase [Arabidopsis thaliana]
                  118860
Seq. No.
Contig ID
                  1890 2.R1010
                  jC-atXLIB327438P4d04a2
5'-most EST
Method
                  BLASTX
                  q137465
NCBI GI
BLAST score
                   1094
                  1.0e-120
E value
                  216
Match length
% identity
                  99
                  VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)
NCBI Description
                   (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886
```

H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No. 118861

Contig ID 1890_3.R1010

5'-most EST jC-atXP86CG4F10T7d2

Method BLASTX
NCBI GI g137465
BLAST score 792
E value 1.0e-84
Match length 229
% identity 75

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)

(V-ATPASE 57 KD SUBUNIT) >gi_81637_pir_A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain -

Arabidopsis thaliana >gi 166627 (J04185) nucleotide-binding

subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No. 118862

Contig ID 1890_5.R1010

5'-most EST jC-aTXLIB327418P1d07b1

Method BLASTX
NCBI GI g137465
BLAST score 615
E value 1.0e-79
Match length 172
% identity 92

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)

(V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain -

Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding

subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No. 118863

Contig ID 1890_6.R1010

5'-most EST LIB23-027-Q1-E1-H1

Method BLASTX
NCBI GI g137465
BLAST score 625
E value 5.0e-65
Match length 152
% identity 85

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)

(V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain -

Arabidopsis thaliana >gi 166627 (J04185) nucleotide-binding

subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No. 118864

Contig ID 1890 8.R1010

5'-most EST LIB25-049-Q1-E1-C5

Method BLASTX
NCBI GI g137465
BLAST score 360
E value 3.0e-34
Match length 81



90 % identity

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)

(V-ATPASE 57 KD SUBUNIT) >gi 81637 pir A31886 H+-transporting ATPase (EC $3.6.1.3\overline{5}$) $57\overline{K}$ chain -

Arabidopsis thaliana >gi 166627 (J04185) nucleotide-binding

subunit of vacuolar ATPase [Arabidopsis thaliana]

118865 Seq. No.

1890 9.R1010 Contig ID

5'-most EST $LIB2\overline{5}-071-Q1-E1-D5$

BLASTX Method NCBI GI g137465 BLAST score 463 3.0e-46E value 100 Match length 93 % identity

VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) NCBI Description

> (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain -

Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding

subunit of vacuolar ATPase [Arabidopsis thaliana]

118866 Seq. No.

Contig ID 1891 1.R1010

5'-most EST jC-atXLIB327416P3e04b1

Method BLASTX q1168609 NCBI GI BLAST score 1818 E value 0.0e + 00564 Match length 95 % identity

AUXIN-RESISTANCE PROTEIN AXR1 >gi 479664 pir S35071 NCBI Description

> auxin-resistance protein AXR1 - Arabidopsis thaliana >gi 304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to Arabidopsis AXR1 (gb ATHAXR1122). [Arabidopsis thaliana] >gi 448755 prf 1917337A ubiquitin-activating enzyme E1

[Arabidopsis thaliana]

Seq. No. 118867

1897 1.R1010 Contig ID

5'-most EST LIB3175-079-P1-K1-B1

Method BLASTX NCBI GI g1237102 BLAST score 5885 E value 0.0e + 00Match length 1261 93 % identity

NCBI Description (L40358) calmodulin-binding protein [Arabidopsis thaliana]

>gi 1589171 prf 2210340A calmodulin-binding protein

[Arabidopsis thaliana]

118868 Seq. No.

1899 1.R1010 Contig ID

5'-most EST jC-alxLIB327434P1f03b1

Method BLASTX NCBI GI q1703091

```
BLAST score
                   617
                   4.0e-64
E value .
                  122
Match length
                  100
% identity
                  ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR (ACP)
NCBI Description
                   (NADH-UBIQUINONE OXIDOREDUCTASE 9.6 KD SUBUNIT) (MTACP-1)
                  >gi 903689 (L23574) acyl carrier protein precursor
                   [Arabidopsis thaliana] >gi_3341682 (AC003672) acyl carrier
                  protein [Arabidopsis thaliana]
                  118869
Seq. No.
Contig ID
                  1900 1.R1010
                  jC-a\overline{t}XLIB327429P3c08b2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q871780
BLAST score
                   439
                   4.0e-43
E value
Match length
                  85
                  100
% identity
                  (L43080) pEARLI 1 gene product [Arabidopsis thaliana]
NCBI Description
                  >gi 4725947_emb_CAB41718.1_ (AL049730) Phospholipase D
                   (pEARLI 1) [Arabidopsis thaliana]
Seq. No.
                  118870
Contig ID
                  1900_3.R1010
5'-most EST
                  LIB35-026-Q1-E1-H11
                  BLASTX
Method
                  g4725946
NCBI GI
BLAST score
                  461
                  1.0e-45
E value
                  90
Match length
                  100
% identity
                  (AL049730) putative Phospholipase D [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118871
                  1900 5.R1010
Contig ID
5'-most EST
                  jC-atXP67C213N9T7063a1
                  BLASTX
Method
                  g4725946
NCBI GI
BLAST score
                  234
                  2.0e-19
E value
                  52
Match length
                  87
% identity
                  (AL049730) putative Phospholipase D [Arabidopsis thaliana]
NCBI Description
                  118872
Seq. No.
                  1901 1.R1010
Contig ID
5'-most EST
                  PLN_g871781
Method
                  BLASTX
NCBI GI
                  g871782
BLAST score
                  3363
E value
                  0.0e + 00
Match length
                  766
% identity
NCBI Description
                  (L43081) pEARLI 4 gene product [Arabidopsis thaliana]
```

118873

Seq. No.

```
Contig ID
                   1902 1.R1010
5'-most EST
                   PLN_g675490
                   BLASTX
Method
                   g1172633
NCBI GI
                   3483
BLAST score
E value
                   0.0e + 00
                   716
Match length
% identity
                   PROLIFERA PROTEIN >gi_675491 (L39954) contains MCM2/3/5
NCBI Description
                   family signature; PROSITE; PS00847; disruption leads to
                   early lethal phenotype; similar to MCM2/3/5 family, most
                   similar to YBR1441 [Arabidopsis thaliana]
                   118874
Seq. No.
                   1903_1.R1010
Contig ID
                   g906<del>2</del>75
5'-most EST
Method
                   BLASTX
                   g1076413
NCBI GI
BLAST score
                   1637
                   0.0e + 00
E value
Match length
                   314
                   100
% identity
                   serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis
NCBI Description
                   thaliana >gi_2146776_pir__S67482 serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis thaliana >gi_608577 (L34076)
                   serine acetyltransferase [Arabidopsis thaliana]
                   >gi_608677_emb_CAA84371_ (Z34888) serine acetyltransferase
                    [Arabidopsis thaliana] >gi_1093493_prf__2104212A Ser
                   acetyltransferase [Arabidopsis thaliana]
                   118875
Seq. No.
Contig ID
                   1904 1.R1010
5'-most EST
                   LIB24-029-Q1-E1-G2
Method
                   BLASTX
NCBI GI
                   q1181531
BLAST score
                   661
E value
                   3.0e-69
Match length
                   134
                   92
% identity
NCBI Description
                   (L41244) thionin [Arabidopsis thaliana]
                   >gi 1586833 prf 2204399A thionin [Arabidopsis thaliana]
                   118876
Seq. No.
                   1904 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327412P4f01a1
                   118877
Seq. No.
                   1906_1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327417P3g08b1
Method
                   BLASTX
NCBI GI
                   q585536
BLAST score
                   2700
E value
                   0.0e + 00
Match length
                   542
% identity
                   92
                   MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
NCBI Description
```

>gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1)

5'-most EST

Method

NCBI GI

Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

```
118878
Seq. No.
                  1906 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327430P2d12b1
                  BLASTX
Method
                  g4218121
NCBI GI
BLAST score
                   689
                  2.0e-72
E value
Match length
                  141
% identity
                  95
                  (AL035353) putative protein [Arabidopsis thaliana]
NCBI Description
                  118879
Seq. No.
                  1906 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327420P1e09b1
Method
                  BLASTX
                  g1362007
NCBI GI
BLAST score
                  1242
                  1.0e-137
E value
Match length
                   327
% identity
                   62
NCBI Description
                  thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana
                  >gi_871992_emb_CAA55787_ (X79195) thioglucosidase
                   [Arabidopsis thaliana]
                  118880
Seq. No.
                  1906 5.R1010
Contig ID
5'-most EST
                   jC-atXLIB327406P3h05b2
                  BLASTX
Method
NCBI GI
                  g1362007
BLAST score
                  1098
                   1.0e-120
E value
                  202
Match length
% identity
                  100
NCBI Description
                  thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana
                  >gi_871992_emb_CAA55787_ (X79195) thioglucosidase
                   [Arabidopsis thaliana]
                  118881
Seq. No.
Contig ID
                  1906 6.R1010
5'-most EST
                  LIB2\overline{5}-052-Q1-E1-E3
Method
                  BLASTX
NCBI GI
                  g4218121
BLAST score
                   455
E value
                  7.0e-59
Match length
                  191
% identity
                   63
NCBI Description
                   (AL035353) putative protein [Arabidopsis thaliana]
                  118882
Seq. No.
                  1906 8.R1010
Contig ID
```

jC-alXLIB327435P3e09b1

BLASTX

q585536

```
BLAST score
                  1114
E value
                  1.0e-122
Match length
                  302
                  72
% identity
                  MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
NCBI Description
                  >gi 1362006 pir S56653 thioglucosidase (EC 3.2.3.1) -
                  Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase
                  [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194)
                  thioglucosidase [Arabidopsis thaliana]
                  118883
Seq. No.
                  1906 9.R1010
Contig ID
5'-most EST
                  jC-atXLIB327419P4g08b1
Method
                  BLASTX
                  g1362007
NCBI GI
BLAST score
                  892
                  2.0e-96
E value
Match length
                  164
                  100
% identity
                  thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana
NCBI Description
                  >gi_871992_emb_CAA55787_ (X79195) thioglucosidase
                  [Arabidopsis thaliana]
Seq. No.
                  118884
                  1906 10.R1010
Contig ID
                  jC-atXLIB327409P3b08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1362007
BLAST score
                  1328
                  1.0e-147
E value
                  259
Match length
                  95
% identity
                  thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana
NCBI Description
                  >gi_871992_emb_CAA55787_ (X79195) thioglucosidase
                   [Arabidopsis thaliana]
                  118885
Seq. No.
                  1906 11.R1010
Contig ID
5'-most EST
                  g2733709
Method
                  BLASTX
                  g127734
NCBI GI
BLAST score
                  104
E value
                  2.0e-18
Match length
                  96
% identity
                  52
                  MYROSINASE MB3 PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
NCBI Description
                  >gi_99850_pir__S19149 thioglucosidase (EC 3.2.3.1) - white
                  mustard >gi_21150_emb_CAA42534_ (X59879) thioglucoside
                  glucohydrolase (myrosinase) [Sinapis alba]
Seq. No.
                  118886
                  1906_12.R1010
Contig ID
5'-most EST
                  g906688
Method
                  BLASTX
                  g585536
NCBI "GI
BLAST score
                  458
E value
                  8.0e-46
```

```
Match length
                  104
% identity
                  85
                  MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
NCBI Description
                  >gi 1362006 pir S56653 thioglucosidase (EC 3.2.3.1) -
                  Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase
                  [Arabidopsis thaliana] >gi_871990_emb_CAA55786 (X79194)
                  thioglucosidase [Arabidopsis thaliana]
                  118887
Seq. No.
                  1908 1.R1010
Contig ID
                  jC-alXLIB327435P2c12a1
5'-most EST
                  BLASTX
Method
                  g1146165
NCBI GI
BLAST score
                  1634
                  0.0e + 00
E value
                  369
Match length
                  89
% identity
                  (L47479) urophorphyrin III methylase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118888
                  1909 1.R1010
Contig ID
                  LIB35-048-Q1-E1-A1
5'-most EST
                  BLASTX
Method
                  g1173103
NCBI GI
BLAST score
                  1052
                  1.0e-115
E value
Match length
                  187
% identity
                  100
NCBI Description
                  RIBONUCLEASE 1 PRECURSOR >gi 561998 (U05206) ribonuclease
                   [Arabidopsis thaliana] >gi_3461823 (AC004138) ribonuclease,
                  RNS1 [Arabidopsis thaliana]
                  118889
Seq. No.
                  1913 1.R1010
Contig ID
5'-most EST
                  LIB23-032-Q1-E1-A4
                  BLASTX
Method
                  g1351945
NCBI GI
BLAST score
                  1962
                  0.0e + 00
E value
                  432
Match length
% identity
                  FLORAL HOMEOTIC PROTEIN APETALA2 >gi 533709 (U12546)
NCBI Description
                  APETALA2 protein [Arabidopsis thaliana]
                  >gi 2464888_emb_CAB16765.1_ (Z99707) APETALA2 protein
                   [Arabidopsis thaliana]
                  118890
Seq. No.
                  1914 1.R1010
Contig ID
5'-most EST
                  PLN_g557879
                  BLASTX
Method
NCBI GI
                  g557880
BLAST score
                  2762
E value
                  0.0e + 00
                  533
Match length
% identity
                  (U13203) phosphoinositide-specific phospholipase C
NCBI Description
```

[Arabidopsis thaliana] >gi_1096531_prf__2111450A

Contig ID 5'-most EST

rie .

```
thaliana]
                  118891
Seq. No.
                  1915 1.R1010
Contig ID
5'-most EST
                  PLN g564029
Method ·
                  BLASTX
                  g2129539
NCBI GI
BLAST score
                   1942
                  0.0e + 00
E value
Match length
                   368
% identity
                  100
                  AtJ1 protein - Arabidopsis thaliana >gi_564030 (U16246)
NCBI Description
                  AtJ1 [Arabidopsis thaliana]
                   118892
Seq. No.
                   1916 1.R1010
Contig ID
5'-most EST
                   jC-alXLIB327436P3c05b1
Method
                   BLASTX
NCBI GI
                  g2501188
BLAST score
                   1564
E value
                   1.0e-175
Match length
                   349
% identity
                   90
                  THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir__S71191 TH14
NCBI Description
                  protein homolog - Arabidopsis thaliana >gi_1113783 (U17589)
                  Thil protein [Arabidopsis thaliana]
                   118893
Seq. No.
                   1916 2.R1010
Contig ID
                   g273\overline{3}748
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2501188
BLAST score
                   234
                   3.0e-19
E value
Match length
                   66
% identity
                   76
                  THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir__S71191 TH14
NCBI Description
                   protein homolog - Arabidopsis thaliana >gi 1113783 (U17589)
                   Thil protein [Arabidopsis thaliana]
                   118894
Seq. No.
                   1917 1.R1010
Contig ID
                   jC-aTXLIB327418P2d08b2
5'-most EST
Method
                   BLASTX
                   q862640
NCBI GI
BLAST score
                   1087
E value
                   1.0e-119
                   230
Match length
% identity
                   95
                   (U20182) MADS-box protein AGL11 [Arabidopsis thaliana]
NCBI Description
                   >gi 4538999 emb CAB39620.1 (AL049481) MADS-box protein
                   AGL11 [Arabidopsis thaliana]
                   118895
Seq. No.
                   1919 1.R1010
```

phosphoinositide-specific phospholipase C [Arabidopsis

LIB3177-043-P1-K2-C4

```
Method
                  BLASTX
                   q862650
NCBI GI
BLAST score
                   1011
E value
                  1.0e-110
Match length
                   211
                  94
% identity
                  (U20193) MADS-box protein AGL12 [Arabidopsis thaliana]
NCBI Description
                  118896
Seq. No.
                  1920 1.R1010
Contig ID
5'-most EST
                  LIB3175-063-P1-K1-G10
Method
                  BLASTX
NCBI GI
                   a1262171
BLAST score
                   2971
                  0.0e + 00
E value
                   587
Match length
                  100
% identity
                  (U21557) phosphoprotein phosphatase 2A, regulatory subunit
NCBI Description
                  A [Arabidopsis thaliana]
                  118897
Seq. No.
                  1922_1.R1010
Contig ID
                   jC-a\overline{t}XLIB327428P1e07b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3334128
BLAST score
                   1195
                   1.0e-131
E value
                   280
Match length
% identity
                   88
                  BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE
NCBI Description
                   PRECURSOR (BCCP) >gi 1066348 (U23155) acetyl-CoA
                   carboxylase biotin-containing subunit [Arabidopsis
                   thaliana]
                   118898
Seq. No.
                   1922_3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327438P4d11a2
Method
                   BLASTN
                   g2924733
NCBI GI
BLAST score
                   381
                   0.0e + 00
E value
Match length
                   478
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUF9, complete sequence [Arabidopsis thaliana]
                   118899
Seq. No.
                   1925_1.R1010
Contig ID
5'-most EST
                   PLN_g780813
Method
                   BLASTX
NCBI GI
                   g1706749
                   2360
BLAST score
                   0.0e + 00
E value
                   473
Match length
% identity
                   97
                  3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR
NCBI Description
                   (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi 780814 (U24177)
```

```
thaliana]
                   118900
 Seq. No.
                   1930 1.R1010
 Contig ID
 5'-most EST
                   PLN g1899024
                   BLASTX
 Method
 NCBI GI
                   g1899025
 BLAST score
                   2349
 E value
                   0.0e + 00
 Match length
                   502
 % identity
                   93
                    (U28215) hexokinase 2 [Arabidopsis thaliana] >gi 3687232
 NCBI Description
                    (AC005169) hexokinase [Arabidopsis thaliana]
                   118901
 Seq. No.
 Contig ID
                   1930 2.R1010
                   q2413868
 5'-most EST
                   BLASTN
 Method
 NCBI GI
                   g3687221
 BLAST score
                   264
 E value
                   1.0e-146
Match length
                   351
 % identity
                   93 :
                   Arabidopsis thaliana chromosome II BAC F6F22 genomic
. NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   118902
 Seq. No.
                   1932 1.R1010
 Contig ID
 5'-most EST
                   PLN g2098248
                   BLASTX
 Method
 NCBI GI
                   g2072393
 BLAST score
                   3576
 E value
                   0.0e+00
 Match length
                   755
 % identity
                   92
 NCBI Description
                   (U29168) similar to human Xeroderma pigmentosum group B DNA
                   repair protein, Swiss-Prot Accession Number P19447
                    [Arabidopsis thaliana]
                   118903
 Seq. No.
                   1933 1.R1010
 Contig ID
                   g276\overline{2}741
 5'-most EST
 Method
                   BLASTX
                   g968975
 NCBI GI
 BLAST score
                   1872
 E value
                   0.0e + 00
 Match length
                   405
 % identity
                   92
                   (U29699) NADPH:protochlorophyllide oxidoreductase A
 NCBI Description
                    [Arabidopsis thaliana] >gi_1583455_prf__2120441A
                   protochlorophyllide oxidoreductase [Arabidopsis thaliana]
                   118904
 Seq. No.
 Contig ID
                   1934 1.R1010
 5'-most EST
                   jC-atXP32C147H3T7d2
 Method
                   BLASTX
```

3-ketoacyl-acyl carrier protein synthase I [Arabidopsis

```
q2507092
NCBI GI
BLAST score
                   1781
                   0.0e + 00
E value
Match length
                   401
% identity
                   89
NCBI Description
                  PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR (PCR)
                   (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE) >qi 968977
                   (U29785) NADPH:protochlorophyllide oxidoreductase B
                   [Arabidopsis thaliana] >gi_1583456_prf__2120441B
                   protochlorophyllide oxidoreductase [Arabidopsis thaliana]
Seq. No.
                   118905
                   1936 1.R1010
Contig ID
5'-most EST
                   iC-atXLIB327418P3d06b1
                   BLASTX
Method
NCBI GI
                   q2146774
BLAST score
                   1242
                   1.0e-137
E value
                   312
Match length
                   78
% identity
                  serine acetyltransferase (EC 2.3.1.30) Sat-52 - Arabidopsis
NCBI Description
                   thaliana >gi_905391 (U30298) serine acetyltransferase
                   [Arabidopsis thaliana]
                   118906
Seq. No.
                   1938 1.R1010
Contig ID
                  PLN g1167915
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3024654
BLAST score
                   1484
E value
                   1.0e-165
Match length
                   382
% identity
                   75
                  HOMEOBOX PROTEIN SHOOTMERISTEMLESS >gi_2129615_pir__$68456
NCBI Description
                  homeotic protein shootmeristemless - Arabidopsis thaliana
                   >gi_1167916 (U32344) class I knotted-like homeodomain
                  containing protein; Method: conceptual translation supplied by author [Arabidopsis thaliana]
                   >gi 1586022 prf 2202329A homeo domain protein [Arabidopsis
                   thalianal
                   118907
Seq. No.
Contig ID
                   1940 1.R1010
5'-most EST
                  LIB25-027-Q1-E1-E6
Method
                  BLASTX
NCBI GI
                  q3639089
BLAST score
                   1849
E value
                   0.0e + 00
Match length
                   810
% identity
                   94
NCBI Description
                   (AF090445) phospholipase D1 [Brassica oleracea]
                  >gi_4324969_gb_AAD17208_ (AF113918) phospholipase D1
                   [Brassica oleracea var. capitata]
```

12953

118908

1940 7.R1010

jC-atXLIB327423P2c06b1

Seq. No.

Contig ID 5'-most EST

```
Method
                  BLASTX
NCBI GI
                  q2499706 .
BLAST score
                  341
                  2.0e-45
E value
                  168
Match length
                  62
% identity
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi_1297302 (U36381) phospholipase D [Arabidopsis thaliana]
                  118909
Seq. No.
                  1941_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P2a07b2
                  BLASTX
Method
                  q2494896
NCBI GI
BLAST score
                  1677
                  0.0e+00
E value
Match length
                  328
% identity
                  96
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT
NCBI Description
                  (EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING
                  PROTEIN 1) (TRIP-1) >gi 2129749 pir__S60256 TGF-beta
                  receptor interacting protein 1 homolog - Arabidopsis
                  thaliana >gi 1036803 (U36765) TGF-beta receptor interacting
                  protein 1 homolog [Arabidopsis thaliana]
                  118910
Seq. No.
                  1943 1.R1010
Contig ID
                  jC-a\overline{1}XLIB327435P2b03a1
5'-most EST
Method
                  BLASTX
                  g1049293
NCBI GI
BLAST score
                  2315
                  0.0e+00
E value
Match length
                  551
% identity
                  85
                  (U37247) SecY homolog; targetted to the thylakoid membrane;
NCBI Description
                  the protein has a chloroplast targetting signal, but the
                  processing site is not known [Arabidopsis thaliana]
                  118911
Seq. No.
                  1944 1.R1010
Contig ID
                  LIB3175-006-P1-K1-A6
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1705677
BLAST score
                  3836
E value
                  0.0e + 00
                  790
Match length
                  96
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG
NCBI Description
                  >gi 2118115 pir S60112 cell division control protein CDC48
                  homolog - Arabidopsis thaliana >gi 1019904 (U37587) cell
```

division cycle protein [Arabidopsis thaliana]

Seq. No. 118912

Contig ID 1944 2.R1010

5'-most EST jC-atXLIB327426P1f08b1

Method BLASTX

```
NCBI GI
                  q3337433
BLAST score
                   111
                               , to
                   9.0e-26
E value
                  117
Match length
                   42
% identity
                   (AF047037) transitional endoplasmic reticulum ATPase TER94
NCBI Description
                   [Drosophila melanogaster]
                   118913
Seq. No.
                  1944_3.R1010
Contig ID
                  jC-atXP50C180L9T7078d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2492504
BLAST score
                  100
                  2.0e-03
E value
                  169
Match length
                  16
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG
NCBI Description
                 ..>gi 1669660 emb CAA70565 (Y09396) protein of AAA family
                   [Capsicum annuum]
                   118914
Seq. No.
                   1945 1.R1010
Contig ID
5'-most EST
                  PLN g1173829
                  BLASTX
Method
                  g2129662
NCBI GI
BLAST score
                  3328
                   0.0e + 00
E value
                   718
Match length
% identity
                   91
                  ovule-specific homeotic protein homolog A20 - Arabidopsis
NCBI Description
                  thaliana >gi 1881536 (U37589) A20 [Arabidopsis thaliana]
                   118915
Seq. No.
Contig ID
                   1946 1.R1010
                  LIB25-056-Q1-E1-E10
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1346194
BLAST score
                  2558
E value
                   0.0e + 00
                   499
Match length
                   100
% identity
                  GLUTATHIONE REDUCTASE, CYTOSOLIC (GR) (GRASE) (OBP29)
NCBI Description
                  >qi 1022797 (U37697) glutathione reductase [Arabidopsis
                  thaliana]
                   118916
Seq. No.
                   1950 1.R1010
Contig ID
5'-most EST
                   PLN_g3869252
Method
                  BLASTX
NCBI GI
                   g3869253
BLAST score
                   8282
                   0.0e + 00
E value
                   1629
Match length
                   99
% identity
                   (U39288) ferredoxin-dependent glutamate synthase precursor
NCBI Description
                   [Arabidopsis thaliana]
```

```
Seq. No.
                  118917
Contig ID
                  1951 1.R1010
5'-most EST
                  PLN_g1184166
                  BLASTX
Method
NCBI GI
                  g2501102
BLAST score
                  1428
E value
                  1.0e-158
Match length
                  310
                  94
% identity
NCBI Description
                  SYNTAXIN-RELATED PROTEIN KNOLLE >gi_1184165 (U39451)
                  syntaxin-related [Arabidopsis thaliana] >gi_1184167
                  (U39452) syntaxin-related [Arabidopsis thaliana]
                  >gi 3063443 (AC003981) F22013.4 [Arabidopsis thaliana]
                  >gi 1587182_prf 2206310A syntaxin-related protein
                  [Arabidopsis thaliana]
                  118918
Seq. No.
                  1951 2.R1010
Contig ID
5'-most EST
                  PLN_g1465734
Method
                  BLASTX
NCBI GI
                  q1465735
BLAST score
                  2197
E value
                  0.0e + 00
Match length
                  462
                  92
% identity
NCBI Description
                  (U44133) violaxanthin de-epoxidase precursor [Arabidopsis
                  thaliana] >gi 3063441 (AC003981) F22013.3 [Arabidopsis
                  thaliana]
                  118919
Seq. No.
                  1951 3.R1010
Contig ID
5'-most EST
                  PLN_g1184164
Method
                  BLASTX
NCBI GI
                  g2501102
BLAST score
                  1446
E value
                  1.0e-161
Match length
                  310
% identity
NCBI Description
                  SYNTAXÎN-RELATED PROTEIN KNOLLE >gi_1184165 (U39451)
                  syntaxin-related [Arabidopsis thaliana] >gi 1184167
                  (U39452) syntaxin-related [Arabidopsis thaliana]
                  >gi 3063443 (AC003981) F22013.4 [Arabidopsis thaliana]
                  >gi 1587182 prf 2206310A syntaxin-related protein
                  [Arabidopsis thaliana]
                  118920
Seq. No.
                  1951_5.R1010
Contig ID
5'-most EST
                  jC-atXLIB327405P2d11b2
Method
                  BLASTX
NCBI GI
                  q1465735
BLAST score
                  624
E value
                  4.0e-65
Match length
                  144
% identity
                  (U44133) violaxanthin de-epoxidase precursor [Arabidopsis
NCBI Description
```

thaliana] >gi 3063441 (AC003981) F22013.3 [Arabidopsis

thaliana] 118921 Seq. No. 1953 1.R1010 Contig ID $g276\overline{2}176$ 5'-most EST BLASTX Method NCBI GI g1145697 BLAST score 1176 1.0e-129 E value 250 Match length 94 % identity (U39485) delta tonoplast integral protein [Arabidopsis NCBI Description thaliana] 118922 Seq. No. 1953 3.R1010 Contig ID jC-atXLIB327408P1c02b1 5'-most EST BLASTX Method g1145697 NCBI GI BLAST score 439 4.0e-46 E value 122 Match length 89 % identity NCBI Description (U39485) delta tonoplast integral protein [Arabidopsis thaliana] 118923 Seq. No. 1953 4.R1010 Contig ID g937401 5'-most EST Method -BLASTX g1145697 NCBI GI BLAST score 506 1.0e-51 E value Match length 129 % identity 88 (U39485) delta tonoplast integral protein [Arabidopsis NCBI Description thaliana] 118924 Seq. No. 1953 5.R1010 Contig ID g2413834 5'-most EST Method BLASTX NCBI GI g1145697 BLAST score 407 2.0e-39 E value Match length 125 76 % identity (U39485) delta tonoplast integral protein [Arabidopsis NCBI Description thaliana] Seq. No. 118925 1953_7.R1010 Contig ID 5'-most EST g2708406 Method BLASTX NCBI GI g1145697 BLAST score 198

2.0e-15

E value

Contig ID

```
Match length
                  55
% identity
                  69
NCBI Description
                  (U39485) delta tonoplast integral protein [Arabidopsis
                  thaliana]
                 ~118926
Seq. No.
                  1954 1.R1010
Contig ID
                  jC-aTXLIB327406P1c01b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1912286
BLAST score
                  1667
E value
                  0.0e + 00
                  307
Match length
                  100
% identity
                  (U39568) type 2A serine/threonine protein phosphatase
NCBI Description
                  [Arabidopsis thaliana] >gi_2194141 (AC002062) Match to
                  Arabidopsis protein phosphatase PP2A (gb U39568). EST
                  gb T41959 comes from this gene. [Arabidopsis thaliana]
                  118927
Seq. No.
                  1955 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P4a07b1
Method
                  BLASTX
                  q2576361
NCBI GI
                  2262
BLAST score
                  0.0e + 00
E value
                  446
Match length
% identity
                  96
NCBI Description
                  (U39782) lysine and histidine specific transporter
                  [Arabidopsis thaliana]
                  118928
Seq. No.
Contig ID
                  1956_1.R1010
                  PLN_g2576362
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2576363
                  2164
BLAST score
                  0.0e + 00
E value
Match length
                  432
% identity
                  (U39783) amino acid transport protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  118929
                  1957_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327431P2b12a1
Method
                  BLASTX
NCBI GI
                  q1408460
                  2639
BLAST score
                  0.0e+00
E value
Match length
                  501
% identity
                  100
                  (U40161) type 2A protein serine/threonine phosphatase 55
NCBI Description
                  kDa B regulatory subunit [Arabidopsis thaliana]
                  118930
Seq. No.
                  1958 1.R1010
```

5'-most EST

Method

```
5'-most EST
                  PLN g1113102
Method
                  BLASTX
NCBI GI
                  q2498706
BLAST score
                  1817
                  0.0e + 00
E value
Match length
                  363
% identity
                  97
                  ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi 1113103
NCBI Description
                  (U40269) atOrc2p [Arabidopsis thaliana] >gi_3236239
                   (AC004684) origin recognition complex protein [Arabidopsis
                  thaliana]
                  118931
Seq. No.
                  1959 1.R1010
Contig ID
5'-most EST
                  LIB23-021-Q2-E1-H8
                  BLASTX
Method
NCBI GI
                  q1477480
BLAST score
                  5939
                  0.0e + 00
E value
                  1181
Match length
% identity
                  98
                  (U40341) carbamoyl phosphate synthetase large chain
NCBI Description
                  [Arabidopsis thaliana]
                  118932
Seq. No.
                  1960 1.R1010
Contig ID
5'-most EST
                  LIB23-061-Q1-E1-G8
                  118933
Seq. No.
                  1960 2.R1010
Contig ID
5'-most EST
                  LIB3175-065-P1-K1-D5
                  BLASTX
Method
NCBI GI
                  g2129569
BLAST score
                  842
                  2.0e-90
E value
                  173
Match length
% identity
                  93
                  cytosolic cyclophilin ROC3 - Arabidopsis thaliana
NCBI Description
                  >gi 1305455 (U40399) cytosolic cyclophilin [Arabidopsis
                  thaliana] >gi_4581104_gb_AAD24594.1_AC005825_1 (AC005825)
                  cytosolic cyclophilin (ROC3) [Arabidopsis thaliana]
                  118934
Seq. No.
                  1960 3.R1010
Contig ID
                  jC-atXLIB327426P1c05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4204266
BLAST score
                  765
E value
                  2.0e-81
Match length
                  185
% identity
                  86
                  (AC005223) 52263 [Arabidopsis thaliana]
NCBI Description
                  118935
Seq. No.
Contig ID
                  1960 4.R1010
```

jC-aIXLIB327435P3a10b1

BLASTX

```
NCBI GI
                  g134103
BLAST score
                   1554
                  1.0e-173
E value
                  332
Match length
                  95
% identity
                  RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60
NCBI Description
                  KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)
                  118936
Seq. No.
                  1961 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327410P4h09b1
                  BLASTX
Method
                  g3913518
NCBI GI
                  1459
BLAST score
                  1.0e-162
E value
                  332
Match length
                  88 -
% identity
NCBI Description 3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE
                   (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE)
                   (DPNPASE) >gi 1103921 (U40433) 3'(2'),5'-bisphosphate
                  nucleotidase [Arabidopsis thaliana]
                  118937
Seq. No.
                  1965 1.R1010
Contig ID
                  LIB23-051-Q1-E1-E4
5'-most EST
Method
                  BLASTX
                  g1703220
NCBI GI
BLAST score
                  794
                  8.0e-85
E value
Match length.
                  169
                  88
% identity
                  AIG2 PROTEIN >gi 1127806 (U40857) AIG2 [Arabidopsis
NCBI Description
                  thaliana]
                  118938
Seq. No.
                  1965 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327417P4a05b1
Method
                  BLASTX
                  g1703220
NCBI GI
BLAST score
                  352
                  1.0e-50
E value
Match length
                  116
                  93
% identity
                  AIG2 PROTEIN >gi 1127806 (U40857) AIG2 [Arabidopsis
NCBI Description
                  thaliana]
                  118939
Seq. No.
                  1965 3.R1010
Contig ID
5'-most EST
                  9403\overline{2}66
Method
                  BLASTX
                  g1703220
NCBI GI
BLAST score
                  357
                  8.0e-34
E value
Match length
                  80
% identity
                  80
NCBI Description AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis
                  thaliana]
```

```
Seq. No.
                  118940
Contig ID
                  1965 5.R1010
                  jC-a\overline{1}X25050Q1E1E03b1
5'-most EST
                  BLASTX
Method
                  g1703220
NCBI GĬ
BLAST score
                  291
                  3.0e-26
E value
                  94
Match length
                  61
% identity
                  AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis
NCBI Description
                  thaliana]
                  118941
Seq. No.
                  1967 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327431P4g01a1
Method
                  BLASTX
NCBI GI
                  q1688072
BLAST score
                  1813
                  0.0e + 00
E value
                  367
Match length
                  97
% identity
NCBI Description
                  (U41369) biotin holocarboxylase synthetase [Arabidopsis
                  thaliana]
                  118942
Seq. No.
                  1969 1.R1010
Contig ID
5'-most EST
                  LIB3176-008-P1-K4-H3
                  BLASTX
Method
                  g1151244
NCBI GI
                  1455
BLAST score
                  1.0e-162
E value
                  313
Match length
% identity .
                  93
NCBI Description (U43377) GTP-binding protein [Arabidopsis thaliana]
                  118943
Seq. No.
                  1969 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327401P4e01b2
Method
                  BLASTX.
NCBI GI
                  q1151244
BLAST score
                  562
E value
                  1.0e-63
Match length
                  135
% identity
                  94
                  (U43377) GTP-binding protein [Arabidopsis thaliana]
NCBI Description
                  118944
Seq. No.
Contig ID
                  1974 1.R1010
5'-most EST
                  PLN g1229163
Method
                  BLASTX
                  g2129674
NCBI GI
BLAST score
                  1625
E value
                  0.0e + 00
Match length
                  378
% identity
                  88
NCBI Description pregeranygeranyl pyrophosphate synthase GGPS2 - Arabidopsis
```

Method

NCBI GI BLAST score

E value

```
pyrophosphate synthase [Arabidopsis thaliana]
Seq. No.
                  118945
                  1976 1.R1010
Contig ID
5'-most EST
                  LIB22-080-Q1-E2-G12
Method
                  BLASTX
                  g2494175
NCBI GI
                  2489
BLAST score
E value
                  0.0e + 00
Match length
                  494
% identity
                  GLUTAMATE DECARBOXYLASE 2 (GAD 2) >gi_1184960 (U46665)
NCBI Description
                  glutamate decarboxylase 2 [Arabidopsis thaliana]
                  >gi_1236619 (U49937) glutamate decarboxylase [Arabidopsis
                  thalianal
                  118946
Seq. No.
                  1976 2.R1010
Contig ID
5'-most EST
                  g16861
Method
                  BLASTN
NCBI GI
                  g3869073
BLAST score
                  423
E value
                  0.0e + 00
Match length
                  427
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MKN22, complete sequence [Arabidopsis thaliana]
                  118947
Seq. No.
Contig ID
                  1976 3.R1010
                  g2393505
5'-most EST
```

thaliana >gi 1229164 (U44876) pregeranygeranyl

Match length 126
% identity 83
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No. 118948 Contig ID 1976 5.R1010

5'-most EST jC-aTXLIB327403Pld02b1

BLASTN g4539415

1.0e-10

36

Method BLASTN
NCBI GI g3659491
BLAST score 168
E value 2.0e-89
Match length 265
% identity 95

NCBI Description Sequence of BAC T22H22 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No. 118949
Contig ID 1977_1.R1010
5'-most EST LIB24-030-Q1-E1-G3
Method BLASTX

noa banoin

```
NCBI GI
                  q1345132
BLAST score
                   4825
E value
                  0.0e + 00
Match length
                   976
                   96
% identity
                  (U47029) ERECTA [Arabidopsis thaliana]
NCBI Description
                  >gi 1389566 dbj BAA11869 (D83257) receptor protein kinase
                   [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
                  protein kinase, ERECTA [Arabidopsis thaliana]
                  118950
Seq. No.
                  1979 1.R1010
Contig ID
5'-most EST
                  PLN g1216483
                  BLASTX
Method
                  q1076386
NCBI GI
BLAST score
                   1641
                  0.0e + 00
E value
                  319
Match length
                   97
% identity
                  protein kinase ADK1 - Arabidopsis thaliana >gi_1216484
NCBI Description
                   (U48779) dual specificity kinase 1 [Arabidopsis thaliana]
                   118951
Seq. No.
                  1980 1.R1010
Contig ID
                  jC-alXLIB327434P4c09b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2618721
BLAST score
                   1086
                   1.0e-119
E value
                   236
Match length
% identity
                   89
                  (U49072) IAA16 [Arabidopsis thaliana]
NCBI Description
                   118952
Seq. No.
                  1980 2.R1010
Contig ID
                   jC-alXLIB327434P3c09a1
5'-most EST
                  BLASTX
Method
                   q2618721
NCBI GI
BLAST score
                   143
                   7.0e-23
E value
Match length
                   58
% identity
                   97
                  (U49072) IAA16 [Arabidopsis thaliana]
NCBI Description
                   118953
Seq. No.
                   1982 1.R1010
Contig ID
                   jC-atXLIB327417P3d04b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2146741
BLAST score
                   1389
                   1.0e-154
E value
Match length
                   284
% identity
                   94
                  isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) -
NCBI Description
                   Arabidopsis thaliana >gi 1293565 (U49259) isopentenyl
                   diphosphate:dimethylallyl diphosphate isomerase
```

[Arabidopsis thaliana]

```
118954
Seq. No.
                  1982 2.R1010
Contig ID
                  jC-atXP46C173I16T7027d1
5'-most EST
                  BLASTX
Method
                  q2146741
NCBI GI
                  1323 -
BLAST score
                  1.0e-146
E value
                  256
Match length
% identity
                  isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) -
NCBI Description
                  Arabidopsis thaliana >gi_1293565 (U49259) isopentenyl
                  diphosphate:dimethylallyl diphosphate isomerase
                  [Arabidopsis thaliana]
                  118955
Seq. No.
                  1982 3.R1010
Contig ID
                  jC-atX25010Q1E1B10b1
5'-most EST
                  BLASTX
Method
                  g1213442
NCBI GI
                  710
BLAST score
                  3.0e-75
E value
                  137
Match length
                  100
% identity
                  (U48961) isopentenyl pyrophosphate isomerase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  118956
                  1982 4.R1010
Contig ID
5'-most EST
                  jC-atXLIB327406P3b12b2
Method
                  BLASTX
                  q1213442
NCBI GI
BLAST score
                  332
                  2.0e-34
E value
                  105
Match length
% identity
                  76
                  (U48961) isopentenyl pyrophosphate isomerase [Arabidopsis
NCBI Description
                  thaliana]
                  118957
Seq. No.
                  1983 1.R1010
Contig ID
5'-most EST
                  LIB22-039-Q1-E1-H10
                  BLASTX
Method
                  g1245182
NCBI GI
BLAST score
                  2341
E value
                  0.0e + 00
                  432
Match length
                  99
% identity
                  (U49398) sterol delta-7 reductase [Arabidopsis thaliana]
NCBI Description
                  118958
Seq. No.
Contig ID
                  1984 1.R1010
5'-most EST
                  jC-atXLIB327423P3c10b1
                  BLASTX
Method
                  g2146731
NCBI GI
BLAST score
                  2560
```

0.0e + 00

E value

NCBI GI

```
Match length
                  551
% identity
                  91
NCBI Description
                  FK506-binding protein - Arabidopsis thaliana >gi_1354207
                  (U49453) rof1 [Arabidopsis thaliana]
Seq. No.
                  118959
Contig ID
                  1985 1.R1010
5'-most EST
                  jC-atXP87CG8F12T7b1
Method
                  BLASTX
NCBI GI
                  q1762150
BLAST score
                  3709
E value
                  0.0e + 00
Match length
                  757
% identity
                  (U49919) lupeol synthase [Arabidopsis thaliana]
NCBI Description
                  118960
Seq. No.
                  1987 1.R1010
Contig ID.
                  LIB25-088-Q1-E1-E10
5'-most EST
                  BLASTX
Method
                  q2558666
NCBI GI
BLAST score
                  928
                  1.0e-100
E value
                  197
Match length
% identity
                  (U49971) GTP binding protein RoplAt [Arabidopsis thaliana]
NCBI Description
                  >qi 3603426 (AF085480) rac-like GTP binding protein Aracl1
                   [Arabidopsis thaliana]
                  118961
Seq. No.
                  1989_1.R1010
Contig ID
5'-most EST
                  PLN_g1399180
Method
                  BLASTX
NCBI GI
                  q1399181
                  2617
BLAST score
E value
                  0.0e + 00
                  524
Match length
                 96
% identity
                  (U50738) lycopene epsilon cyclase [Arabidopsis thaliana]
NCBI Description
                  118962
Seq. No.
                  1991 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327421P3c11b1
Method
                  BLASTX
NCBI GI
                  g2129622
BLAST score
                  701
E value
                  6.0e-74
Match length
                  143
                  94
% identity
                  immunophilin FKBP15-1 - Arabidopsis thaliana >qi 1272406
NCBI Description
                   (U52046) immunophilin [Arabidopsis thaliana]
                  118963
Seq. No.
                  1991 3.R1010
Contig ID
                  jC-atXLIB327421P2f12b1
5'-most EST
Method
                  BLASTX
```

g2129622

```
691
BLAST score
                  1.0e-72
E value
                  142
Match length
                  93
% identity
                  immunophilin FKBP15-1 - Arabidopsis thaliana >gi 1272406
NCBI Description
                  (U52046) immunophilin [Arabidopsis thaliana]
                  118964
Seq. No.
                  1992 1.R1010
Contig ID
                  jC-atXLIB327417P1a03b1
5'-most EST
                  BLASTX
Method
                  g2129623
NCBI GI
BLAST score
                  676
                  6.0e-71
E value
                  144
Match length
                  90
% identity
                  immunophilin FKBP15-2 - Arabidopsis thaliana >gi 1272408
NCBI Description
                  (U52047) immunophilin [Arabidopsis thaliana]
Seq. No.
                  118965
                  1994 1.R1010
Contig ID
                  LIB3168-067-P1-K1-F4
5'-most EST
                  BLASTX
Method
                  g1354466
NCBI GI
BLAST score
                  960
                  1.0e-103
E value
Match length
                  204
% identity
                  92
                   (U52910) U1 snRNP 70K truncated protein [Arabidopsis
NCBI Description
                  thaliana] >gi 1354468 (U52909) U1 snRNP 70K truncated
                  protein [Arabidopsis thaliana]
                  118966
Seq. No.
                  1994 5.R1010
Contig ID
                  LIB24-042-Q1-E1-H9
5'-most EST
Method
                  BLASTX
                  g2129740
NCBI GI
BLAST score
                  710
                   4.0e-75
E value
                  136
Match length
                  99
% identity
                  small nuclear ribonucleoprotein - Arabidopsis thaliana
NCBI Description
                  >gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis
                  thaliana >gi 12\overline{55}711 (M93439) small nuclear
                  ribonucleoprotein [Arabidopsis thaliana] >gi_1354469
                   (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]
                  118967
Seq. No.
                  1995 1.R1010
Contig ID
5'-most EST
                   jC-atXP41C164M18T7d1
Method
                  BLASTX
NCBI GI
                  g1280611
BLAST score
                  1370
                  1.0e-152
E value
Match length
                  262
                  95
% identity
                  (U53860) steroid reductase DET2 [Arabidopsis thaliana]
NCBI Description
```

BLAST score

2671

```
Seq. No.
                  118968
                  1999 1.R1010 ·
Contig ID
                  LIB3176-046-P1-K1-C3
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2351374
BLAST score
                  1354
                  1.0e-150
E value
                  308
Match length
                  89
% identity
                  (U54560) putative 26S proteasome subunit athMOV34
NCBI Description
                  [Arabidopsis thaliana]
                  118969
Seq. No.
                  2000 1.R1010
Contig ID
5'-most EST
                  g17107
Method
                  BLASTX
                  g2088652
NCBI GI
                  1318
BLAST score
                  1.0e-146
E value
                  293
Match length
                  89
% identity
                  (AF002109) 26S proteasome regulatory subunit S12 isolog
NCBI Description
                  [Arabidopsis thaliana] >gi_2351376 (U54561) translation
                  initiation factor eIF2 p47 subunit homolog [Arabidopsis
                  thaliana]
                  118970
Seq. No.
Contig ID
                  2000 2.R1010
5'-most EST
                  jC-alXLIB327436P3h04b1
Method
                  BLASTN
NCBI GI
                  g2351375
BLAST score
                  330
E value
                  0.0e+00
Match length
                  457
                  94
% identity
                  Arabidopsis thaliana translation initiation factor eIF2 p47
NCBI Description
                  subunit homolog mRNA, complete cds
Seq. No.
                  118971
                  2008 2.R1010
Contig ID
5'-most EST
                  jC-atXP62C202N18T7076a1
Method
                  BLASTX
NCBI GI
                  g3334133
BLAST score
                  450
E value
                  1.0e-44
Match length
                  90
                  97
% identity
NCBI Description
                  CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi 1432145
                  (U61231) cytochrome P450 [Arabidopsis thaliana]
                  118972
Seq. No.
                  2009_1.R1010
Contig ID
5'-most EST
                  LIB25-062-Q1-E1-F6
Method
                  BLASTX
NCBI GI
                  g2257743
```

```
0.0e+00
E value
Match length
                  544
% identity
                  98
                   (U62020) lysine-sensitive aspartate kinase [Arabidopsis
NCBI Description
                  thaliana]
                  118973
Seq. No.
                  2010_1.R1010
Contig ID
                  PLN g_{1589777}
5'-most EST
                  BLASTX
Method
                  g1589778
NCBI GI
                   4511
BLAST score
                  0.0e+00
E value
Match length
                  911
                   94
% identity
                  (U62135) SPINDLY [Arabidopsis thaliana]
NCBI Description
                  118974
Seq. No.
                  2011 1.R1010
Contig ID
                   jC-atX25051Q1E1H05b1
5'-most EST
Method
                  BLASTX
                   g4097557
NCBI GI
                  1059
BLAST score
                   1.0e-116
E value
                  205
Match length
                   100
% identity
                  (U64911) ATFP8 [Arabidopsis thaliana]
NCBI Description
                   118975
Seq. No.
                  2012 1.R1010
Contig ID
                  LIB2\overline{4}-025-Q1-E1-G7
5'-most EST
                   BLASTX
Method
                   g4097561
NCBI GI
BLAST score
                   1024
E value
                   1.0e-111
Match length
                   199
                   100
% identity
                  (U64918) ATGP1 [Arabidopsis thaliana]
NCBI Description
                   118976
Seq. No.
Contig ID
                   2015 1.R1010
5'-most EST
                   jC-atXLIB327421P1g12b1
Method
                   BLASTX
                   g4455242
NCBI GI
BLAST score
                   607
                   1.0e-62
E value
                   118
Match length
                   100
% identity
                   (AL035523) geranylgeranylated protein ATGP4 [Arabidopsis
NCBI Description
                   thaliana]
                   118977
Seq. No.
                   2016 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327411P2h01b1
Method
                   BLASTN
NCBI GI
                   g4220633
BLAST score
                   1035
```

Seq. No.

118982

```
E value
                  0.0e + 00
Match length
                  1188
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K7J8, complete sequence [Arabidopsis thaliana]
                  118978
Seq. No.
                  2016 2.R1010
Contig ID
                  g2413823
5'-most EST
                  BLASTN
Method
NCBI GI
                  g2737903
BLAST score
                  323
                  0.0e + 00
E value
Match length
                  424
% identity
                  95
                  Arabidopsis thaliana retrotransposon TSCL genomic sequence
NCBI Description
                  118979
Seq. No.
                  2017 1.R1010
Contig ID
5'-most EST
                  LIB23-011-Q1-E1-B3
Method
                  BLASTX
                  g3334404
NCBI GI
BLAST score
                  3160
E value
                  0.0e + 00
Match length
                  623
% identity
                  98
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                  SUBUNIT) >gi 2266990 (U65638) vacuolar type ATPase subunit
                  A [Arabidopsis thaliana] >gi 3834305 (AC005679) Identical
                  to gb U65638 Arabidopsis thaliana vacuolar type ATPase
                  subunit A mRNA. ESTs gb N96435, gb N96106, gb N96189,
                  qb N96091, qb AA042286, qb F14324, qb W43643, qb N96027,
                  gb N96299, gb R29943, gb T43460, gb T43544, gb T22472
                  118980
Seq. No.
Contig ID
                  2018 1.R1010
                  LIB3176-067-P1-K1-B4
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1498629
BLAST score
                  1318
E value
                  1.0e-146
Match length
                  280
% identity
                  91
                  (U66223) p40 protein homolog [Arabidopsis thaliana]
NCBI Description
                  118981
Seq. No.
Contig ID
                  2019 1.R1010
5'-most EST
                  LIB3177-021-P1-K2-E4
Method
                  BLASTX
                  g2052379
NCBI GI
BLAST score
                  1866
E value
                  0.0e + 00
Match length
                  354
% identity
                  97
                  (U66343) calreticulin [Arabidopsis thaliana]
NCBI Description
```

```
2019 2.R1010
Contig ID
5'-most EST
                  LIB3175-006-P1-K1-A3
Method
                  BLASTX
                  g3249100
NCBI GI
BLAST score
                  1781
                  0.0e + 00
E value
Match length
                  364
                  92
% identity
                  (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698
NCBI Description
                  and DNA gb_U66344. ESTs gb_T45719, gb_T22451, gb_H36323
                  and gb_AA042519 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  118983
                  2019 3.R1010
Contig ID
                  jC-atXP115C251K15T7007d1
5'-most EST
                  BLASTX
Method
                  g1009712
NCBI GI
BLAST score
                  634
                  5.0e-66
E value
                  189
Match length
                  68
% identity
                  (U27698) calreticulin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  118984
                  2019 6.R1010
Contig ID
5'-most EST
                  g3449601
Method
                  BLASTN
                  g1009711
NCBI GI
BLAST score
                  329
                  0.0e + 00
E value
                  349
Match length
                  99
% identity
                  Arabidopsis thaliana calreticulin (AtCRTL) mRNA, partial
NCBI Description
                  118985
Seq. No.
Contig ID
                  2020 1.R1010
5'-most EST
                  jC-atXLIB327438P3a07a2
                  BLASTX
Method
NCBI GI
                  g2052383
BLAST score
                  1944
E value
                  0.0e + 00
Match length
                  424
                  85
% identity
                  (U66345) calreticulin [Arabidopsis thaliana]
NCBI Description
                  118986
Seq. No.
                  2022_1.R1010
Contig ID
5'-most EST
                  LIB3175-076-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2905893
BLAST score
                  3141
E value
                  0.0e + 00
Match length
                  687
                  90
% identity
NCBI Description (U66424) fimbrin-like protein [Arabidopsis thaliana]
```

```
118987
Seq. No.
                   2023_1.R1010
Contig ID
                   PLN_g4097687
5'-most EST
                  BLASTX
Method
NCBI GI
                   g2842494
BLAST score
                   1284
E value
                   1.0e-142
Match length
                   288
% identity
                   91
                   (AL021749) prohibitin-like protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4097688 (U66591) prohibitin 1 [Arabidopsis thaliana]
                  >gi 4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]
                   118988
Seq. No.
                   2023 2.R1010
Contig ID
                   jC-a\overline{l}XLIB327435P3f07a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4586035
BLAST score
                   607
E value
                   5.0e-63
Match length
                   132
% identity
NCBI Description
                   (AC007109) putative prohibitin protein [Arabidopsis
                   thaliana]
                   118989
Seq. No.
Contig ID
                   2024 1.R1010
5'-most EST
                  LIB3176-085-P1-K1-G5
                  BLASTX
Method
NCBI GI
                   g4097690
BLAST score
                   1415
E value
                   1.0e-157
Match length
                   286
% identity
                   100
                   (U66592) prohibitin 2 [Arabidopsis thaliana] >gi_4099801
NCBI Description
                   (U89791) prohibitin-like protein [Arabidopsis thaliana]
                   >gi 4204301 (AC003027) prohibitin 2 [Arabidopsis thaliana]
Seq. No.
                   118990
Contig ID
                   2025_1.R1010
                   jC-atXLIB327439P2g12b2
5'-most EST
Method
                   BLASTX
                   q1946331
NCBI GI
BLAST score
                   1286
                   1.0e-142
E value
                   277
Match length
                   95
% identity
                   (U69155) prohibitin [Arabidopsis thaliana] >gi 4097692
NCBI Description
                   (U66593) prohibitin 3 [Arabidopsis thaliana]
                   118991
Seq. No.
Contig ID
                   2025 2.R1010
                   jC-atXLIB327402P1d06a1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q1946331
BLAST score
                   375
```

7.0e-36

E value

NCBI GI

```
Match length
                  82
                  95
% identity
NCBI Description
                  (U69155) prohibitin [Arabidopsis thaliana] >gi 4097692
                  (U66593) prohibitin 3 [Arabidopsis thaliana]
                  118992
Seq. No.
Contig ID
                  2025 3.R1010
5'-most EST
                  jC-atXLIB327414P1b11a1
Method
                  BLASTN
NCBI GI
                  g4097691
BLAST score
                  323
                  0.0e+00
E value
Match length
                  327
% identity
                  100
                  Arabidopsis thaliana prohibitin 3 (Atphb3) mRNA, complete
NCBI Description
                  cds
                  118993
Seq. No.
                  2026 1.R1010
Contig ID
5'-most EST
                  jC-atXP15C107F20T7047a1
Method
                  BLASTX
                  g2842744
NCBI GI
BLAST score
                  573
E value
                  6.0e-59
                  109
Match length
                  100
% identity
NCBI Description
                  ENHANCER OF RUDIMENTARY HOMOLOG >gi 1595812 (U67398)
                  enhancer of rudimentary homolog ATER [Arabidopsis thaliana]
                  118994
Seq. No.
                  2031 1.R1010
Contig ID
5'-most EST
                  LIB23-030-Q1-E1-E9
Method
                  BLASTX
NCBI GI
                  g2781394
BLAST score
                  1891
E value
                  0.0e + 00
Match length
                  363
% identity
                  100
                  (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
NCBI Description
                  118995
Seq. No.
                  2031 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327428P4c12b2
Method
                  BLASTN
NCBI GI
                  g2264307
BLAST score
                  147
E value
                  2.0e-76
Match length
                  425
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MED24, complete sequence [Arabidopsis thaliana]
                  118996
Seq. No.
                  2031 5.R1010
Contig ID
5'-most EST
                  g2597716
Method
                  BLASTX
```

g2781394

BLAST score

362

```
BLAST score
                   336
                   2.0e-31
E value
                   88
Match length
% identity
                   85
                  (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
NCBI Description
                   118997
Seq. No.
                   2031_6.R1010
Contig ID
                   jC-a\overline{t}XLIB327411P1d04b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2781394
BLAST score
                   701
                   5.0e-74
E value
Match length
                   130
                   100
% identity
                  (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
NCBI Description
                   118998
Seq. No.
                   2031 7.R1010
Contig ID
                   LIB3177-053-P1-K1-C6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2781394
BLAST score
                   212
E value
                   1.0e-114
Match length
                   273
% identity
                   85
                  (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   118999
                   2034 1.R1010
Contig ID
                   LIB3168-009-P1-K1-B1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2246456
BLAST score
                   1910
E value
                   0.0e + 00
Match length
                   359
% identity
                   100
                   (U71400) S-adenosyl-methionine-sterol-C-methyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   119000
Seq. No.
Contig ID
                   2037_1.R1010
                   PLN g4097949
5'-most EST
Method
                   BLASTX
                   g4097950
NCBI GI
                   1516
BLAST score
                   1.0e-169
E value
Match length
                   320
% identity
                   95
                  (U72393) plant IF-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   119001
                   2037 2.R1010
Contig ID
5'-most EST
                   jC-atXP20C115G24T7055a1
Method
                   BLASTN
                   q3695022
NCBI GI
```

NCBI GI

```
E value
                  0.0e + 00
Match length
                   501
                   99
% identity
                  Arabidopsis thaliana AIR12 mRNA, partial cds
NCBI Description
Seq. No.
                   119002
                   2037 5.R1010
Contig ID
5'-most EST
                   g4210240
                   BLASTN
Method
                  g4097949
NCBI GI
BLAST score
                   128
E value
                  6.0e-66
                   166
Match length
                   99
% identity
                  Arabidopsis thaliana plant IF-like protein mRNA, complete
NCBI Description
                  119003
Seq. No.
                  2038_1.R1010
Contig ID
                  jC-aTXP43C169A11T7048d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1710151
BLAST score
                  1779
                   0.0e+00
`E value
Match length
                   329
% identity
                  100
                  (U72711) proline iminopeptidase [Arabidopsis thaliana]
NCBI Description
                  119004
Seq. No.
                   2039 1.R1010
Contig ID
                  LIB24-052-Q1-E1-C2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2462781
BLAST score
                   2219
E value
                  0.0e + 00
Match length
                   420
% identity
                  100
                  (U73175) carbamoyl phosphate synthetase small subunit
NCBI Description
                   [Arabidopsis thaliana]
                   119005
Seq. No.
                   2040 1.R1010
Contig ID
5'-most EST
                  LIB23-044-Q1-E2-A5
Method
                  BLASTX
NCBI GI
                  g2160690
BLAST score
                  2428
                  0.0e + 00
E value
Match length
                   495
                   95
% identity
NCBI Description
                  (U73526) B' regulatory subunit of PP2A [Arabidopsis
                  thaliana]
                  119006
Seq. No.
Contig ID
                  2041 1.R1010
5'-most EST
                  jC-atXLIB327406P2b04b1
Method
                  BLASTX
```

g2160692

```
BLAST score
                   2303
E value
                   0.0e + 00
Match length
                   499
                   90
% identity
                   (U73527) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                   thaliana]
                   119007
Seq. No.
                   2042_1.R1010
Contig ID
5'-most EST
                   PLN_{g}^{2}160693
                   BLASTX
Method
NCBI GI
                   g2160694
BLAST score
                   2540
                   0.0e + 00
E value
Match length
                   522
                   95
% identity
                   (U73528) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   119008
                   2045 1.R1010
Contig ID
5'-most EST
                   g460372
Method
                   BLASTX
NCBI GI
                   g3024516
BLAST score
                   1087
E value
                   1.0e-119
Match length
                   217
                   100
% identity
NCBI Description
                   RAS-RELATED PROTEIN RAB11C >gi_2160157 (AC000132) Strong
                   similarity to A. thaliana ara-\overline{2} (gb ATHARA2). ESTs
                   gb_ATTS2483,gb_ATTS2484,gb_AA042159 come from this gene.
                    [Arabidopsis thaliana] >gi_2231303 (U74669) ras-related
                   small GTPase [Arabidopsis Thaliana]
                   119009
Seq. No.
                   2046 1.R1010
Contig ID
5'-most EST
                   PLN g1755151
                   BLASTX
Method
NCBI GI
                   g1755152
BLAST score
                   917
E value
                   3.0e-99
Match length
                   205
% identity
                   90
                   (U75187) germin-like protein [Arabidopsis thaliana]
NCBI Description
                   119010
Seq. No.
Contig ID
                   2050_1.R1010
5'-most EST
                   jC-atXP69C219H4T7038d1
Method
                   BLASTX
NCBI GI
                   g3482931
BLAST score
                   850
E value
                   1.0e-94
Match length
                   180
% identity
                   100
NCBI Description
                   (AC003970) germin-like protein [Arabidopsis thaliana]
```

119011

Seq. No.

```
2053 1.R1010
Contig ID
                  PLN q1755165
5'-most EST
Method
                  BLASTX
                  g1755166
NCBI GI
BLAST score
                  1138
                  1.0e-125
E value
Match length
                  222
% identity
                  100
NCBI Description
                  (U75194) germin-like protein [Arabidopsis thaliana]
Seq. No.
                  119012
                  2061 1.R1010
Contig ID
                  PLN q1755181
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1755182
BLAST score
                  692
E value
                  7.0e~73
Match length
                  147
                  92
% identity
                  (U75202) germin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119013
Contig ID
                  2065_1.R1010
5'-most EST
                  jC-alXLIB327435P4c02b1
                  BLASTX
Method
NCBI GI
                  q1755192
BLAST score
                  1075
E value
                  1.0e-117
Match length
                  209
                  100
% identity
NCBI Description
                  (U75207) germin-like protein [Arabidopsis thaliana]
Seq. No.
                  119014
                  2066_1.R1010
Contig ID
                  LIB3176-092-P1-K1-C11
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4128197
BLAST score
                  977
E value
                  1.0e-106
Match length
                  216
% identity
                  (U75273) acyl-CoA binding protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119015
Contig ID
                  2068 1.R1010
5'-most EST
                  LIB3177-091-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g2231312
BLAST score
                  998
E value
                  1.0e-108
Match length
                  200
% identity
                  97
NCBI Description
                  (U75603) AtRab18 [Arabidopsis thaliana]
Seq. No.
                  119016
Contig ID
                  2069 1.R1010
5'-most EST
                  PLN g3399766
```

```
Method
                   BLASTX
NCBI GI
                   a3399767
BLAST score
                   682
                   1.0e-71
E value
                   260
Match length
% identity
                   57
                   (U76298) uclacyanin I [Arabidopsis thaliana] >gi 3831466
NCBI Description
                   (AC005700) uclacyanin I [Arabidopsis thaliana]
Seq. No.
                   119017
Contig ID
                   2071 1.R1010
5'-most EST
                   PLN g3395757
                   BLASTN
Method
                   a3395757
NCBI GI
                   857
BLAST score
                   0.0e+00
E value
Match length
                   899
                   98
% identity
NCBI Description
                  Arabidopsis thaliana unknown mRNA
                   119018
Seq. No.
Contig ID
                   2074_1.R1010
                   jC-atXLIB327419P3f08b2
5'-most EST
Method
                   BLASTX
                   a2347098
NCBI GI
                   1856
BLAST score
                   0.0e + 00
E value
Match length
                   371
% identity
                   (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
NCBI Description
                   >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific
                  protease (AtUBP3) [Arabidopsis thaliana]
                   119019
Seq. No.
Contig ID
                   2076 1.R1010
5'-most EST
                   PLN_g3080737
                   BLASTX
Method
NCBI GI
                   q3080740
BLAST score
                   200
E value
                   0.0e + 00
Match length
                   622
% identity
NCBI Description
                   (U77366) pasticcino 1-D [Arabidopsis thaliana]
                   119020
Seq. No.
                   2079 1.R1010
Contig ID
5'-most EST
                  LIB3176-062-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   q3023848
BLAST score
                   1714
E value
                   0.0e + 00
Match length
                   327
                   100
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                   PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                   >gi 2289095 (U77381) WD-40 repeat protein [Arabidopsis
```

thaliana]

Seq. No. Contig ID

Method

5'-most EST

```
119021
Seq. No.
                   2079 2.R1010
Contig ID
                  jC-atXP29C137L4T7074d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3023848
                   221
BLAST score .
                   1.0e-84
E value
                   180
Match length
% identity
                   40
NCBI Description
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                  >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis
                  thaliana
                  119022
Seq. No.
Contig ID
                  2081 1.R1010
                  LIB2\overline{3}-032-Q1-E1-F11
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1699023
BLAST score
                  1284
E value
                  1.0e-142
Match length
                  251
% identity
                  100
NCBI Description
                   (U78866) putative arginine-aspartate-rich RNA binding
                  protein [Arabidopsis thaliana] >gi 1699051 (U78867)
                  putative aspartate-arginine-rich mRNA binding protein
                   [Arabidopsis thaliana]
                  119023
Seq. No.
Contig ID
                  2082 1.R1010
5'-most EST
                   jC-atXLIB327421P3d12b1
Method
                  BLASTX
NCBI GI
                  g1699024
BLAST score
                  1266
E value
                  1.0e-140
Match length
                  241
                  95
% identity
NCBI Description
                   (U78866) gene1000 [Arabidopsis thaliana] >gi 1699057
                   (U78870) unknown [Arabidopsis thaliana]
                  119024
Seq. No.
                  2087 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327411P1h01b1
Method
                  BLASTX
NCBI GI
                  q1737220
                   3297
BLAST score
E value
                  0.0e + 00
Match length
                  614
% identity
NCBI Description
                   (U79960) vacuolar sorting receptor homolog [Arabidopsis
                  thaliana]
                  119025
```

12978

2088_1.R1010

PLN $g_{2454181}$

BLASTX

```
NCBI GI
                   g2454182
BLAST score
                   2051
                   0.0e + 00
E value
Match length
                   428
% identity
                   93
                   (U80185) pyruvate dehydrogenase E1 alpha subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   119026
                   2088 3.R1010
Contig ID
5'-most EST
                   jC-alXLIB327434P2h09b1
Method
                   BLASTX
NCBI GI
                   q2454182
BLAST score
                   211
                   2.0e-16
E value
Match length
                   130
% identity
                   70
NCBI Description
                   (U80185) pyruvate dehydrogenase E1 alpha subunit
                   [Arabidopsis thaliana]
Seq. No.
                   119027
Contig ID
                   2088 4.R1010
5'-most EST
                   q2748387
Method
                   BLASTX
NCBI GI
                   q2454182
BLAST score
                   422
E value
                   4.0e-45
Match length
                   172
% identity
                   66
NCBI Description
                   (U80185) pyruvate dehydrogenase El alpha subunit
                   [Arabidopsis thaliana]
Seq. No.
                   119028
Contig ID
                   2089 1.R1010
5'-most EST
                   jC-alXLIB327435P2q11b1
Method
                   BLASTX
NCBI GI
                   q2454184
BLAST score
                   2016
E value
                   0.0e + 00
Match length
                   406
% identity
                   97
NCBI Description
                   (U80186) pyruvate dehydrogenase El beta subunit
                   [Arabidopsis thaliana]
                   119029
Seq. No.
Contig ID
                   2089 2.R1010
5'-most EST
                   g1158627
Method
                   BLASTX
NCBI GI
                   g3128205
BLAST score
                   696
E value
                   2.0e-73
Match length
                   171
% identity
                   83
NCBI Description
                   (AC004077) putative pyruvate dehydrogenase complex E1 beta
                   subunit [Arabidopsis thaliana]
```

119030

Seq. No.

```
2089 5.R1010
Contig ID
5'-most EST
                  LIB3175-038-P1-K1-A2
Method
                  BLASTX
                  g2454184
NCBI GI
BLAST score
                  771
                  5.0e-82
E value
                  232
Match length
% identity
                  73
NCBI Description
                  (U80186) pyruvate dehydrogenase El beta subunit
                   [Arabidopsis thaliana]
Seq. No.
                  119031
                  2089 6.R1010
Contig ID
5'-most EST
                  jC-atXLIB327416P2d05b1
Method
                  BLASTX
NCBI GI
                  g4220474
BLAST score
                  253
E value
                  1.0e-21
Match length
                  55
% identity
                  93
NCBI Description
                  (AC006069) putative myosin heavy chain [Arabidopsis
                  thaliana]
                  119032
Seq. No.
                  2089 7.R1010
Contig ID
5'-most EST
                  LIB23-046-Q1-E1-H9
Method
                  BLASTX
NCBI GI
                  q4220474
BLAST score
                  332
E value
                  9.0e-31
Match length
                  95
% identity
                  76
NCBI Description
                  (AC006069) putative myosin heavy chain [Arabidopsis
                  thaliana]
Seq. No.
                  119033
                  2091 1.R1010
Contig ID
5'-most EST
                  jC-alXLIB327434P1d07b1
Method
                  BLASTX
NCBI GI
                  q4098647
BLAST score
                  2437
E value
                  0.0e + 00
Match length
                  449
% identity
                  100
                  (U80668) homogentisate 1,2-dioxygenase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  119034
Contig ID
                  2093 1.R1010
                  LIB25-108-Q1-E1-A4
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2661179
BLAST score
                  3624
E value
                  0.0e+00
                  742
Match length
% identity
                  (U80984) AtZW10 [Arabidopsis thaliana]
NCBI Description
```

```
119035
Seq. No.
                   2094 1.R1010
Contig ID
5'-most EST
                   jC-atXP69C218L15T7058d1
Method
                  BLASTX
NCBI GI
                  q3643609
BLAST score
                   1518
                   1.0e-169
E value
                   315
Match length
% identity
                   90
NCBI Description
                   (AC005395) putative Cys3His zinc finger protein
                   [Arabidopsis thaliana]
                   119036
Seq. No.
                   2094 3.R1010
Contig ID
5'-most EST
                   jC-aTXLIB327435P3e07a1
Method
                  BLASTX
                  q3643609
NCBI GI
                   509
BLAST score
                   2.0e-51
E value
                   171
Match length
% identity
                   67
NCBI Description
                   (AC005395) putative Cys3His zinc finger protein
                   [Arabidopsis thaliana]
                  119037
Seq. No.
Contig ID
                   2096_1.R1010
                  g936<del>6</del>23
5'-most EST
Method
                  BLASTX
                  g2149127
NCBI GI
                   2284
BLAST score
                   0.0e + 00
E value
Match length
                   474
% identity
                   93
NCBI Description
                  (U81293) UDP-glucose:indole-3-acetate
                  beta-D-glucosyltransferase [Arabidopsis thaliana]
Seq. No.
                   119038
Contig ID
                   2098 1.R1010
5'-most EST
                   jC-aTXLIB327435P2c03a1
                  BLASTX
Method
                   q1764100
NCBI GI
BLAST score
                   1954
E value
                   0.0e + 00
                   373
Match length
% identity
                   100
                  (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  119039
                   2099 1.R1010
Contig ID
5'-most EST
                  LIB3176-114-P2-K1-G1
                  BLASTX
Method
                  q3080424
NCBI GI
BLAST score
                  1757
                  0.0e + 00
E value
Match length
```

```
% identity
                  95
                  (AL022604) NAD+ dependent isocitrate dehydrogenase subunit
NCBI Description
                  1 [Arabidopsis thaliana]
                  119040
Seq. No.
Contig ID
                  2100 1.R1010
                  PLN g_{1766047}
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2264380
BLAST score
                  1797
E value
                  0.0e + 00
Match length
                  367
% identity
                  97
                  (AC002354) NAD+ dependent isocitrate dehydrogenase subunit
NCBI Description
                  2 [Arabidopsis thaliana]
                  119041
Seq. No.
Contig ID
                  2101 1.R1010
5'-most EST
                  jC-atXP11C98M17T7074d1
                  BLASTX
Method
NCBI GI
                  g2289961
BLAST score
                  921
E value
                  2.0e-99
Match length
                  202
% identity
                  91
                  (U82434) AtRAB8 [Arabidopsis thaliana]
NCBI Description
                  119042
Seq. No.
Contig ID
                  2102 1.R1010
5'-most EST
                  jC-atXLIB327406P4c01b2
Method
                  BLASTX
NCBI GI
                  g4099092
BLAST score
                  2166
E value
                  0.0e + 00
Match length
                  454
                  93
% identity
NCBI Description (U83179) unknown [Arabidopsis thaliana]
                  119043
Seq. No.
Contig ID
                  2103 1.R1010
5'-most EST
                  jC-atXLIB327414P2a09b1
Method
                  BLASTX
NCBI GI
                  q2245378
BLAST score
                  3122
E value
                  0.0e+00
Match length
                  665
                  90
% identity
NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]
Seq. No.
                  119044
Contig ID
                  2104 1.R1010
5'-most EST
                  PLN g_{2435405}
Method
                  BLASTX
                  g2435406
NCBI GI
BLAST score
                  1277
E value
                  1.0e-141
Match length
                  245
```

```
% identity
                   95
NCBI Description
                  (U83490) thaumatin-like protein [Arabidopsis thaliana]
                   119045
Seq. No.
Contig ID
                  2106 1.R1010
5'-most EST
                  PLN g1885382
                  BLASTX
Method
NCBI GI
                  q1885383
                  4891
BLAST score
E value
                  0.0e + 00
Match length
                  961
% identity
                  96
                  (U84568) phospholipase D [Arabidopsis thaliana]
NCBI Description
                  119046
Seq. No.
                  2107 1.R1010
Contig ID
5'-most EST
                  LIB23-070-Q1-E1-D9
                  BLASTN
Method
                  g2160716
NCBI GI
BLAST score
                  1331
E value
                  0.0e + 00
Match length
                  1355
% identity
                  99
NCBI Description Arabidopsis thaliana GUT15 mRNA, complete cds
                  119047
Seq. No.
Contig ID
                  2107 2.R1010
5'-most EST
                  jC-atXP96C248A14T7b1
Method
                  BLASTN
                  g2160716
NCBI GI
                  1055
BLAST score
E value
                  0.0e + 00
Match length
                  1087
% identity
                  99
NCBI Description Arabidopsis thaliana GUT15 mRNA, complete cds
                  119048
Seq. No.
                  2107_3.R1010
Contig ID
5'-most EST
                  q937387
Method
                  BLASTN
NCBI GI
                  q2160716
BLAST score
                  324
                  0.0e + 00
E value
Match length
                  898
                  95
% identity
NCBI Description Arabidopsis thaliana GUT15 mRNA, complete cds
Seq. No.
                  119049
                  2108_1.R1010
Contig ID
5'-most EST
                  jC-atXP12C99M21T7d2
Method
                  BLASTX
                  q1850546
NCBI GI
BLAST score
                  1138
                  1.0e-125
E value
Match length
                  249
% identity
                  93
                  (U88045) syntaxin related protein AtVam3p [Arabidopsis
NCBI Description
```

Match length

% identity

189

89

Seq. No. 119050 2108 2.R1010 Contig ID 5'-most EST jC-aTXLIB327435P4b10b1 Method BLASTX NCBI GI g2149380 €. BLAST score 1153 E value 1.0e-126 Match length 255 % identity 91 (U85036) syntaxin homolog [Arabidopsis thaliana] NCBI Description 119051 Seq. No. Contig ID 2108 6.R1010 5'-most EST q2758348 Method BLASTX q1850546 NCBI GI 285 BLAST score " 2.0e-25 E value 80 Match length % identity NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana] 119052 Seq. No. 2111_1.R1010 Contig ID 5'-most EST PLN_g1842110 BLASTX Method g1842111 NCBI GI BLAST score 1068 1.0e-117 E value Match length 203 100 % identity NCBI Description (U87586) decoy [Arabidopsis thaliana] >gi 1931612 (U93308) decoy [Arabidopsis thaliana] 119053 Seq. No. Contig ID 2111 2.R1010 jC-atXLIB327426P2e09b1 5'-most EST Method BLASTN NCBI GI q1842110 BLAST score 361 E value 0.0e + 00Match length 393 93 % identity Arabidopsis thaliana decoy mRNA, complete cds NCBI Description 119054 Seq. No. Contig ID 2112 1.R1010 5'-most EST jC-atXP3C82D11T7d1 BLASTX Method NCBI GI q1872521 BLAST score 887 E value 2.0e-95

thalianal

```
(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
NCBI Description
                  >qi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis
                  thaliana]
                  119055
Seq. No.
                  2112 3.R1010
Contig ID
5'-most EST
                  jC-atXP100CE1C6T7b1
                  BLASTX
Method
NCBI GI
                  q1872521
BLAST score
                  508
E value
                  3.0e-51
Match length
                  111
                  68
% identity
                  (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
NCBI Description
                  >qi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis
                  thaliana]
Seq. No.
                  119056
                  2112 7.R1010
Contig ID
                  jC-atX25068Q1E1B04b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q1872520
BLAST score
                  190
                  1.0e-102
E value
Match length
                  342
                  100
% identity
                  Arabidopsis thaliana zinc-finger protein Lsd1 (LSD1) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  119057
                  2114 1.R1010
Contig ID
5'-most EST
                  PLN g1843627
Method
                  BLASTX
                  q1843628
NCBI GI
BLAST score
                  1168
E value
                  1.0e-128
                  229
Match length
% identity
                  100
NCBI Description
                  (U88061) SNF5 homolog BSH [Arabidopsis thaliana]
                  119058
Seq. No.
                  2115 1.R1010
Contig ID
                  PLN g1848290
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3914007
BLAST score
                  4508
                  0.0e + 00
E value
Match length
                  941
                  95
% identity
NCBI Description
                  MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >qi 1848291
                  (U88087) LON protease homolog [Arabidopsis thaliana]
                  119059
Seq. No.
                  2115 2.R1010
Contig ID
5'-most EST
                  g2749365
Method
                  BLASTX
NCBI GI
                  q2191174
```

NCBI GI

```
BLAST score
                   182
E value
                   3.0e-13
Match length
                   64
% identity
                   62
NCBI Description
                   (AF007270) similar to the peptidase family S16 [Arabidopsis
                  thaliana]
Seq. No.
                   119060
Contig ID
                   2116 1.R1010
                   PLN g1850600
5'-most EST
Method
                  BLASTX
                   g1850601
NCBI GI
BLAST score
                  1313
E value
                   1.0e-145
Match length
                   269
% identity
                   95
NCBI Description
                  (U88402) Rac-like protein [Arabidopsis thaliana]
                   119061
Seq. No.
                   2117 1.R1010
Contig ID
5'-most EST
                   q945758
Method
                   BLASTX
NCBI GI
                   q3168840
BLAST score
                   383
E value
                   1.0e-36
Match length
                   121
                   67
% identity
NCBI Description
                  (U88711) copper homeostasis factor [Arabidopsis thaliana]
                   119062
Seq. No.
Contig ID
                   2117 2.R1010
5'-most EST
                  LIB3177-010-P1-K2-F7
Method
                  BLASTX
NCBI GI
                   q3168840
BLAST score
                   370
E value
                   3.0e-35
Match length
                   121
% identity
                   65
NCBI Description
                  (U88711) copper homeostasis factor [Arabidopsis thaliana]
                   119063
Seq. No.
Contig ID
                   2118 1.R1010
5'-most EST
                   PLN g1872543
Method
                  BLASTX
NCBI GI
                   g1872544
BLAST score
                   812
E value
                   8.0e-87
Match length
                   195
% identity
NCBI Description
                   (U89014) early light-induced protein; ELIP [Arabidopsis
                  thalianal
Seq. No.
                   119064
                  2120 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327422P4g03b1
Method
                  BLASTX
```

q2209332

```
BLAST score
                  2032
                  0.0e + 00
E value
Match length
                  462
% identity
                  88
                  (U89272) chloroplast membrane protein ALBINO3 [Arabidopsis
NCBI Description
                  thaliana] >gi_3927828 (AC005727) chloroplast membrane
                  protein ALBINO3 [Arabidopsis thaliana]
                  119065
Seq. No.
Contig ID
                  2121_1.R1010
                  PLN_g2245389
5'-most EST
Method
                  BLASTX
                  g2245390
NCBI GI
BLAST score
                  2890
                  0.0e + 00
E value
                  608
Match length
                  90
% identity
                  (U89296) auxin response transcription factor 3; ARF3
NCBI Description
                  [Arabidopsis thaliana]
                  119066
Seq. No.
                  2122_1.R1010
Contig ID
5'-most EST
                  PLN_g2245393
Method
                  BLASTX
NCBI GI
                  g2245394
BLAST score
                  2183
                  0.0e + 00
E value
Match length
                  450
% identity
                  92
                  (U89771) ARF1-binding protein [Arabidopsis thaliana]
NCBI Description
                  119067
Seq. No.
                  2122_2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327426P1f09b1
Method
                  BLASTN
                  g2245393
NCBI GI
BLAST score
                  321
                  1.0e-180
E value
Match length
                  377
% identity
                  96
                  Arabidopsis thaliana ARF1-binding protein mRNA, complete
NCBI Description
                  119068
Seq. No.
Contig ID
                  2124_1.R1010
5'-most EST
                  PLN_g1890129
Method
                  BLASTX
NCBI GI
                  g3122914
BLAST score
                  5388
E value
                  0.0e + 00
Match length
                  1107
                  93
% identity.
                  VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)
NCBI Description
                  >gi 1890130 (U89986) valyl tRNA synthetase [Arabidopsis
                  thaliana]
```

119069

Seq. No.

BLAST score

```
Contig ID
                  2125 1.R1010
5'-most EST
                  PLN g2052507
Method
                  BLASTX
NCBI GI
                  g2052508
BLAST score
                  5322
E value
                  0.0e+00
Match length
                  1064
% identity
                  (U95759) lysine-ketoglutarate reductase/saccharopine
NCBI Description
                  dehydrogenase bifunctional enzyme [Arabidopsis thaliana]
Seq. No.
                  119070
                  2125 2.R1010
Contig ID
5'-most EST
                  iC-atXLIB327420P1d09b1
                  BLASTX
Method
NCBI GI
                  g2076884
BLAST score
                  5395
                  0.0e + 00
E value
                  1064
Match length
% identity
                  99
                  (U90522) lysine-ketoglutarate reductase/saccharopine
NCBI Description
                  dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  119071
                  2127_1.R1010
Contig ID
                  jC-atXP85C241C7T7b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1905876
                  2724
BLAST score
                  0.0e + 00
E value
                  537
Match length
% identity
                  99
NCBI Description
                  (U90879) biotin carboxylase subunit [Arabidopsis thaliana]
                  >gi_1916300 (U91414) heteromeric acetyl-CoA carboxylase
                  biotin carboxylase subunit [Arabidopsis thaliana]
                  >gi_3047099 (AF058826) Arabidopsis thaliana biotin
                  carboxylase subunit (GB:U90879) [Arabidopsis thaliana]
Seq. No. .
                  119072
                  2128 1.R1010
Contiq ID
                  PLN g_{2570339}
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3913732
BLAST score
                  1726
                  0.0e + 00
E value
Match length
                  331
                  100
% identity
NCBI Description
                  HYDROXYACYLGLUTATHIONE HYDROLASE MITOCHONDRIAL ISOZYME
                  PRECURSOR (GLYOXALASE II) (GLX II) >gi_2570340 (U90928)
                  glyoxalase II mitochondrial isozyme [Arabidopsis thaliana]
                  119073
Seq. No.
                  2130 1.R1010
Contig ID
5'-most EST
                  LIB24-094-Q1-E1-G1
Method
                  BLASTX
NCBI GI
                  q2149640
```

```
0.0e + 00
E value
Match length
                   934
% identity
                   96
NCBI Description
                   (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.
                   119074
                   2131_1.R1010
Contig ID
                   PLN_g2231697
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2262169
BLAST score
                   824
E value
                   2.0e-88
                   161
Match length
                   100
% identity
                   (AC002329) clathrin adaptor protein small chain subunit
NCBI Description
                  (AP19 protein) [Arabidopsis thaliana]
                   119075
Seq. No.
                   2132_1.R1010
Contig ID
5'-most EST
                   PLN_g2316015
                   BLASTX
Method
NCBI GI
                   g2316016
BLAST score
                   7213
                   0.0e + 00
E value
                   1507
Match length
% identity
                   94
                   (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
NCBI Description
                   119076
Seq. No.
                   2133 1.R1010
Contig ID
5'-most EST
                   jC-a\(\bar{1}\)X22085Q1E2C08b1
Method
                   BLASTX
NCBI GI
                   g1943751
BLAST score
                   5414
E value
                   0.0e + 00
Match length
                   1061
% identity
                   (U93845) Arabidopsis thaliana ER-type calcium pump
NCBI Description
                   protein, complete sequence >gi_2078292 (U96455) ER-type
                   Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]
                   119077
Seq. No.
Contig ID
                   2133 2.R1010
                   jC-atXLIB327413P1d10b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1742951
BLAST score
                   507
E value
                   3.0e-51
Match length
                   101
% identity
                   98
                   (Y09817) Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
                   119078
Seq. No.
                   2135 1.R1010
Contig ID
5'-most EST
                   PLN g2290527
Method
                   BLASTX
NCBI GI
                   g2290528
```

```
BLAST score
                   1834
E value
                   0.0e+00 .
Match length
                   346
% identity
                   100
                   (U94746) ATAN11 [Arabidopsis thaliana]
NCBI Description
                   119079
Seq. No.
                   2139_1.R1010
Contig ID
· 5'-most EST
                   jC-atXP96C250B6T7b1
Method
                   BLASTX
NCBI GI
                   g1934730
BLAST score
                   1042
                   1.0e-114
E value
Match length
                   204
% identity
                   100
                   (U95036) germin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   119080
Contig ID
                   2139 2.R1010
                   LIB3175-082-P1-K1-E8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1934730
BLAST score
                   646
E value
                   1.0e-67
Match length
                   135
% identity
                   94
NCBI Description
                   (U95036) germin-like protein [Arabidopsis thaliana]
Seq. No.
                   119081
                   2144 1.R1010
Contig ID
                   LIB2\overline{2}-045-Q1-E1-D11
5'-most EST
Method
                   BLASTX
                   g2352084
NCBI GI
                   3464
BLAST score
E value
                   0.0e + 00
Match length
                   810
% identity
                   85
                   (U96613) serine/threonine kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   119082
                   2144 2.R1010
Contig ID
5'-most EST
                   LIB24-037-Q1-E1-B10
Method
                   BLASTN
NCBI GI
                   g2352083
BLAST score
                   83
                   8.0e-39
E value
Match length
                   145
% identity
                   100
                   Arabidopsis thaliana serine/threonine kinase (SIK1) mRNA,
NCBI Description
                   complete cds
                   119083
Seq. No.
Contig ID
                   2145_1.R1010
5'-most EST
                   LIB35-036-Q1-E2-F11
Method
                   BLASTX
NCBI GI
                   g2104957
BLAST score
                   605
```

```
E value
                  9.0e-63
Match length
                  112
                  100
% identity
NCBI Description (U96924) immunophilin [Arabidopsis thaliana]
Seq. No.
                  119084
                  2147 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P1c09b1
Method
                  BLASTX
                  g2738248
NCBI GI
BLAST score
                  3773
E value
                  0.0e + 00
                  765
Match length
                  96
% identity
                  (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                  119085
Seq. No.
Contig ID
                  2147 2.R1010
                  g1268365
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2842490
BLAST score
                  315
E value
                  1.0e-28
Match length
                  101
% identity
                  60
                  (AL021749) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                  119086
Seq. No.
                  2147 3.R1010
Contig ID
                  jC-a\overline{1}XLIB327436P2c01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2738248
BLAST score
                   488
                   4.0e-51
E value
Match length
                  126
% identity
                  (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                  119087
Seq. No.
                   2147 4.R1010
Contig ID
                  LIB3177-041-P1-K2-C7
5'-most EST
Method
                  BLASTX
                   q2738248
NCBI GI
                   588
BLAST score
                   9.0e-61
E value
Match length
                  162
% identity
                   75
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                   119088
Seq. No.
                   2147 5.R1010
Contig ID
                   jC-atXLIB327410P2g03b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2738248
```

NCBI GI

```
BLAST score
                   130
E value
                   1.0e-89
Match length
                   241
                   85
% identity
NCBI Description
                   (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
                   119089
Seq. No.
                  2147_7.R1010
LIB25-039-Q1-E1-H12
Contig ID
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2738248
BLAST score
                   60
E value
                   1.0e-46
Match length
                   111
                   93
% identity
NCBI Description
                   (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
                   119090
Seq. No.
Contig ID
                   2147_10.R1010
                  jC-atXLIB327423P2h07b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q2842490
BLAST score
                   791
E value
                   2.0e-84
Match length
                   250
% identity
                   64
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]
                   119091
Seq. No.
                  2147 11.R1010
Contig ID
5'-most EST
                  LIB24-114-Q1-E1-F11
                  BLASTX
Method
NCBI GI
                   q2842490
BLAST score
                   562
E value
                   9.0e-58
Match length
                  173
% identity
                   68
NCBI Description (ALO21749) heat-shock protein [Arabidopsis thaliana]
                   119092
Seq. No.
Contig ID
                   2147 12.R1010
5'-most EST
                   jC-a1X24053Q1E1C08b1
Method
                  BLASTX
NCBI GI
                   q4567271
BLAST score
                   272
E value
                   6.0e-24
Match length
                   99
% identity
                   61
NCBI Description (AC006841) putative kinesin protein [Arabidopsis thaliana]
                  119093
Seq. No.
Contig ID
                  2147 20.R1010
5'-most EST
                  jC-atXP102CE5E9T7095d1
Method
                  BLASTX
```

g2738248

```
BLAST score
                  475
                  6.0e-48
E value
                  103
Match length
                  88
% identity
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                  [Arabidopsis thaliana]
                  119094
Seq. No.
                  2148_1.R1010
Contig ID
5'-most EST
                  g2704867
Method
                  BLASTX
NCBI GI
                  g2109293
BLAST score
                  1784
E value
                  0.0e + 00
Match length
                  347
                  97
% identity
                  (U97568) serine/threonine protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  119095
Seq. No.
                  2149 1.R1010
Contig ID
                  PLN_{g}^{2738253}
5'-most EST
                  BLASTX
Method
                  g2388571
NCBI GI
BLAST score
                  1672 -
                  0.0e + 00
E value
Match length
                  326
% identity
                  100
                   (AC000098) Strong similarity to Arabidopsis peroxidase
NCBI Description
                  ATPEROX7A (gb X98321). [Arabidopsis thaliana] >gi 2738254
                   (U97684) peroxidase precursor [Arabidopsis thaliana]
                  119096
Seq. No.
                  2165 1.R1010
Contig ID
5'-most EST
                  LIB23-020-Q1-E1-C8
Method
                  BLASTX
                  g584882
NCBI GI
BLAST score
                  4056
E value
                  0.0e + 00
                  759
Match length
% identity
                  98
                  CYCLOARTENOL SYNTHASE (2,3-EPOXYSQUALENE--CYCLOARTENOL
NCBI Description
                  CYCLASE) >qi 452446 (U02555) cycloartenol synthase;
                   (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]
Seq. No.
                  119097
Contig ID
                  2169 1.R1010
5'-most EST
                  LIB3175-017-P1-K1-A3
                  119098
Seq. No.
Contig ID
                  2170 1.R1010
5'-most EST
                  LIB146-001-Q1-E1-A12
Seq. No.
                  119099
Contig ID
                  2171 1.R1010
5'-most EST
                  LIB146-020-Q1-E1-E9
Method
                  BLASTX
```

```
NCBI GI
                  g112681
BLAST score
                  1088
                  0.0e + 00
E value
Match length
                  468
% identity
                  89
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  119100
Seq. No.
                  2171 2.R1010
Contig ID
                  LIB3168-032-P1-K1-C9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4204299
BLAST score
                  2155
E value
                  0.0e + 00
Match length
                  455
                  91
% identity
NCBI Description
                  (AC003027) 1cl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  119101
                  2171_3.R1010 ···
Contig ID
                                                                            ; ...
5'-most EST
                  LIB3168-023-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q167134
BLAST score
                  722
E value
                  2.0e-76
Match length
                  150
% identity
NCBI Description
                  (M16860) cruciferin precursor [Brassica napus]
Seq. No.
                  119102
                  2171 4.R1010
Contig ID
5'-most EST
                  LIB3168-057-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q1345840
BLAST score
                  213
E value
                  1.0e-48
Match length
                  147
% identity
                  78
                  CRUCIFERIN BNC1 PRECURSOR (11S GLOBULIN) (12S STORAGE
NCBI Description
                  PROTEIN) >gi_762919_emb_CAA41984_ (X59294) cruciferin
                  storage protein [Brassica napus]
Seq. No.
                  119103
                  2171_7.R1010
Contig ID
                  LIB3177-044-P1-K2-F7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1345841
BLAST score
                  218
E value
                  9.0e-19
Match length
                  98
% identity
                  37
NCBI Description CRUCIFERIN BNC2 PRECURSOR (11S GLOBULIN) (12S STORAGE
```

% identity

```
PROTEIN) >gi_762920_emb_CAA41985_ (X59295) cruciferin
                  storage protein [Brassica napus]
                  119104
Seq. No.
                  2171 8.R1010
Contig ID
5'-most EST
                  LIB3234-074-P1-K1-A4
                  BLASTX
Method
NCBI GI
                  q112682
BLAST score
                  237
E value
                  7.0e-20
Match length
                  73
% identity
                  74
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  119105
Seq. No.
                  2171 9.R1010
Contig ID
                  LIB3168-014-P1-K1-D2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g112681
                  530
BLAST score
                  2.0e-54
E value
Match length
                  101
                  100
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  119106
Seq. No.
Contig ID
                  2171_11.R1010
5'-most EST
                  LIB3168-031-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  a112682
BLAST score
                  274
                  4.0e-28
E value
                  121
Match length
% identity
                  64
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  119107
Seq. No.
Contig ID
                  2171 14.R1010
5'-most EST
                  LIB3168-069-P1-K1-A7
                  BLASTX
Method
NCBI GI
                  g112681
BLAST score
                  189
E value
                  2.0e-37
Match length
                  135
```

Seq. No.

Contig ID

119112

2177 1.R1010

```
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                 119108
Seq. No.
                  2173 1.R1010
Contig ID
                  jC-atXLIB327417P1g02b1
5'-most EST
                  BLASTX
Method
                  g4539422
NCBI GI
                  835
BLAST score
                  1.0e-107
E value
Match length
                  2.68
                  71
% identity
                  (AL049171) putative protein [Arabidopsis thaliana]
NCBI Description
                  119109
Seq. No.
                  2174 1.R1010
Contig ID
                  LIB3168-036-P1-K1-B5
5'-most EST
                  BLASTX
Method
                  g1076442
NCBI GI
BLAST score
                  1047
                  1.0e-114<sub>3</sub>
E value
Match length
                  203
% identity
                  92
                  beta-glucosidase (EC 3.2.1.21) - rape
NCBI Description
                  >gi 757740 emb CAA57913 (X82577) beta-glucosidase
                  [Brassica napus]
                  119110
Seq. No.
                  2175 1.R1010
Contig ID
5'-most EST
                  LIB146-001-Q1-E1-A8
                  BLASTX
Method
                  g3885334
NCBI GI
BLAST score
                  54
                  4.0e-13
E value
Match length
                  54
                  74
% identity
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                  119111
Seq. No.
                  2176 1.R1010
Contig ID
                  jC-atXLIB327430P1a10b1
5'-most EST
Method
                  BLASTX
                ~ g4581108
NCBI GI
BLAST score
                  534
                  1.0e-54
E value
                  105
Match length
% identity
                  100
                  (AC005825) putative chloroplast outer membrane protein
NCBI Description
                  86, also very similar to GTP-inding protein from pea
                  (GB:L36857) [Arabidopsis thaliana]
```

```
5'-most EST
                  g2748581
                   119113
Seq. No.
                   2179 1.R1010
Contig ID
5'-most EST
                  LIB146-020-Q1-E1-H5
Method
                  BLASTX
NCBI GI
                   q3785975
BLAST score
                   181
                   4.0e-13
E value
Match length
                   133
% identity
                   16
NCBI Description
                  (AC005560) hypothetical protein [Arabidopsis thaliana]
                   119114
Seq. No.
                   2186 1.R1010
Contig ID
                  jC-atXLIB327411P3d05b1
5'-most EST
Method
                  BLASTX
                  q2194142
NCBI GI
                   995
BLAST score
                  1.0e-108
E value
Match length
                  199
% identity
                   99
NCBI Description
                  (AC002062) ESTs gb N38288, gb T43486, gb AA395242 come from
                  this gene. [Arabidopsis thaliana]
                  119115
Seq. No.
                   2187 1.R1010
Contig ID
5'-most EST
                  LIB146-001-Q1-E1-C10
                  119116
Seq. No.
                   2190 1.R1010
Contig ID
5'-most EST
                  LIB3234-057-P1-K1-F8
Method
                  BLASTX
                  g82051
NCBI GI
BLAST score
                   426
E value
                   8.0e-42
                  183
Match length
% identity
                   49
NCBI Description
                  lipid body-associated membrane protein - carrot
                  >gi_259453_bbs_117620 (S47635) lipid body membrane
                  protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,
                   180 aa] [Daucus carota]
Seq. No.
                  119117
                  2191 1.R1010
Contig ID
5'-most EST
                   jC-a\overline{t}XP79C230M17T7b1
Method
                  BLASTX
NCBI GI
                  g2529665
                   644
BLAST score
E value
                  3.0e-67
Match length
                  127
% identity
                  (AC002535) putative ribosomal protein L7A [Arabidopsis
NCBI Description
                  thaliana]
                  119118
Seq. No.
                  2191_2.R1010
Contig ID
```

```
5'-most EST
                  jC-atXLIB327430P1a12b1
Method
                  BLASTX
                  q2529665
NCBI GI
BLAST score
                  1135
                  1.0e-124
E value
Match length
                  247
% identity
                  90
                  (AC002535) putative ribosomal protein L7A [Arabidopsis
NCBI Description
                  thaliana]
                  119119
Seq. No.
                  2191_3.R1010
Contig ID
5'-most EST
                  LIB3168-091-P1-K1-B2
Method
                  BLASTX
                  g112739
NCBI GI
BLAST score
                  622
E value
                  1.0e-64
Match length
                  158
                  78
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  119120
Contig ID
                  2191 4.R1010
5'-most EST
                  LIB3168-096-P1-K1-H8
                  BLASTX
Method
NCBI GI
                  g112741
                  603
BLAST score
E value
                  5.0e-73
                  156
Match length
                  94
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  119121
Seq. No.
                  2191 5.R1010
Contig ID
                  LIB3168-011-P1-K1-A2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2529665
BLAST score
                  1140
E value
                  1.0e-125
Match length
                  257
                  88 -
% identity
                  (AC002535) putative ribosomal protein L7A [Arabidopsis
NCBI Description
                  thaliana]
```

119122

Seq. No.

```
2191 7.R1010
Contig ID
5'-most EST
                   LIB3168-029-P1-K1-D3
Method
                   BLASTX
                   q4678299
NCBI GI
BLAST score
                   916
                   4.0e-99
E value
Match length
                   176
% identity
                   99
NCBI Description
                   (AL049655) cysteine proteinase precursor-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   119123
                   2191 8.R1010
Contig ID
                   LIB3168-062-P1-K1-E9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q112737
BLAST score
                   48
E value
                   4.0e-77
Match length
                   162
% identity
                   88
NCBI Description
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                   PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                   1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                   (224745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                   precursor [Arabidopsis thaliana]
Seq. No.
                   119124
                   2191 9.R1010
Contig ID
5'-most EST
                   LIB3176-101-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g2529665
BLAST score
                   463
E value
                   3.0e-46
Match length
                   144
% identity
                   67
NCBI Description
                   (AC002535) putative ribosomal protein L7A [Arabidopsis
                   thaliana]
                   119125
Seq. No.
                   2191 11.R1010
Contig ID
5'-most EST
                   LIB3168-090-P1-K1-E3
Method
                   BLASTX
                   q112741
NCBI GI
                   397
BLAST score
E value
                   1.0e-38
Match length
                   103
% identity
                   51
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                   Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi 4490712 emb CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
```

E value

2.0e-93

```
Seq. No.
                   119126
                   2191 13.R1010
Contig ID
5'-most EST
                   LIB3168-045-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g3006140
BLAST score
                   134
E value
                   8.0e-24
Match length
                   121
% identity
                   57
NCBI Description
                   (AL022299) ribosomal protein [Schizosaccharomyces pombe]
                   >gi 3123705 emb CAA04548 (AJ001133) ribosomal protein L7
                   [Schizosaccharomyces pombe]
                   119127
Seq. No.
                   2191 15.R1010 `
Contig ID
5'-most EST
                  LIB22-001-Q1-E1-C2
Method
                   BLASTX
NCBI GI
                   g2529665
BLAST score
                   294
                   2.0e-26
E value
                   81
Match length
% identity
                   75
NCBI Description
                   (AC002535) putative ribosomal protein L7A [Arabidopsis
                  thaliana]
                   119128
Seq. No.
Contig ID
                   2196 1.R1010
5'-most EST
                   jC-atXP87CG10A5T7b1
                   BLASTX
Method
NCBI GI
                   q3123188
BLAST score
                   2650
                   0.0e + 00
E value
Match length
                   492
                   99
% identity
NCBI Description
                  CATALASE 3 > gi 2347178 (U43147) catalase 3 [Arabidopsis
                   thaliana] >gi 2511726 (AF021937) catalase 3 [Arabidopsis
                   thalianal
Seq. No.
                   119129
                   2196 2.R1010
Contig ID
                   jC-atXP86CG9E10T7b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3096931
BLAST score
                   583
E value
                   4.0e-60
Match length
                   113
                   100
% identity
NCBI Description
                   (AL023094) putative ribosomal protein S16 [Arabidopsis
                   thaliana]
                   119130
Seq. No.
                   2196 3.R1010
Contig ID
5'-most EST
                   ARABL1-041-Q1-B1-A9
Method
                  BLASTX
NCBI GI
                   q2117612
BLAST score
                   191
```

NCBI GI

g633890

```
289
 Match length
 % identity
                    85
. NCBI Description
                    catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
 Seq. No.
                    119131
                    2196 5.R1010
 Contig ID
 5'-most EST
                    q152\overline{0}893
                    BLASTX
 Method
 NCBI GI
                    g3123188
 BLAST score
                    210
 E value
                    3.0e-26
 Match length
                    77
                    83
 % identity
                    CATALASE 3 >gi 2347178 (U43147) catalase 3 [Arabidopsis
 NCBI Description
                    thaliana] >gi 2511726 (AF021937) catalase 3 [Arabidopsis
                    thaliana]
                    119132
 Seq. No.
 Contig ID
                    2196_8.R1010
 5'-most EST
                    g1158810
 Method
                    BLASTX
 NCBI GI
                    q2117612
 BLAST score
                    910
                    2.0e-98
 E value ...
 Match length
                    215
 % identity
                    83
 NCBI Description
                    catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
                    119133
 Seq. No.
                    2196 10.R1010
 Contig ID
                    LIB23-020-Q1-E1-F6
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    q3123188
 BLAST score
                    547
 E value
                    5.0e-56
 Match length
                    118
                    92
 % identity
 NCBI Description
                    CATALASE 3 >gi 2347178 (U43147) catalase 3 [Arabidopsis
                    thaliana] >gi \overline{2}511726 (AF021937) catalase 3 [Arabidopsis
                    thalianal
 Seq. No.
                    119134
 Contig ID
                    2196_17.R1010
 5'-most EST
                    LIB3234-041-P1-K1-F11
 Method
                    BLASTX
 NCBI GI
                    g2117612
 BLAST score
                    356
 E value
                    3.0e-47
 Match length
                    95
 % identity
                    95
 NCBI Description
                    catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
 Seq. No.
                    119135
 Contig ID
                    2200 1.R1010
 5'-most EST
                    LIB146-017-Q1-E1-F2
 Method
                    BLASTX
```

NCBI GI

```
BLAST score
                   524
E value
                   3.0e-53
Match length
                   168
% identity
                   63
                   (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                   vulgare]
                   119136
Seq. No.
                   2201_1.R1010
Contig ID
5'-most EST
                   LIB25-079-Q1-E1-E7
Method
                   BLASTN
NCBI GI
                   q992705
                   89
BLAST score
                   2.0e-42
E value
                   89
Match length
                   100
% identity
NCBI Description
                   Arabidopsis ubiquitin conjugating enzyme E2 (UBC13) gene,
                   complete cds
                   119137
Seq. No.
                   2202_1.R1010
Contig ID
5'-most EST
                   g2413804
Method
                   BLASTX
                   q730456
NCBI GI
BLAST score \cdot_{\varsigma}.
                   536.
E value
                   2.0e-54
Match length
                   140
% identity
                   69
NCBI Description 40S RIBOSOMAL PROTEIN S19
                   119138
Seq. No.
                   2202 2.R1010
Contig ID
                   jC-a\overline{t}XLIB327423P3d09b1
5'-most EST
Method
                   BLASTX
NCBI GI.
                   g730456
BLAST score
                   469
                   6.0e-47
E value
Match length
                   114
% identity
                   73
NCBI Description 40S RIBOSOMAL PROTEIN S19
                   119139
Seq. No.
Contig ID
                   2206 1.R1010
5'-most EST
                   LIB146-003-Q1-E1-A1
                   BLASTX
Method
NCBI GI
                   q4678285
BLAST score
                   1162
E value
                   1.0e-127
Match length
                   378
% identity
                   56
NCBI Description (AL049660) putative protein [Arabidopsis thaliana]
                   119140
Seq. No.
Contig ID
                   2207 1.R1010
5'-most EST
                   jC-atXLIB327415P2g10b2
Method
                   BLASTN
```

g4585952

```
BLAST score
                   395
                  0.0e + 00
E value
                   443
Match length
                   97
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F26F24,
NCBI Description
                  complete sequence
                   119141
Seq. No.
Contig ID
                   2212_1.R1010
5'-most EST
                  LIB3175-015-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q4128133
                   537
BLAST score
                  1.0e-54
E value
                  198
Match length
                   53
% identity
NCBI Description (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
                  119142
Seq. No.
                   2218_1.R1010
Contig ID
                   jC-atXP5C89D24T7028a1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g2281632
BLAST score
                   479
E value
                  0.0e + 00
Match length
                   551
                   97
% identity
NCBI Description
                  Arabidopsis thaliana AP2 domain containing protein RAP2.4
                  mRNA, partial cds
                   119143
Seq. No.
                   2218 2.R1010
Contig ID
                   jC-a\overline{t}XP117C141P18T7a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2281632
BLAST score
                   457
                   0.0e + 00
E value
Match length
                   546
                   96
% identity
                  Arabidopsis thaliana AP2 domain containing protein RAP2.4
NCBI Description
                  mRNA, partial cds
                   119144
Seq. No.
Contig ID
                   2218 3.R1010
                   g115\overline{8}786
5'-most EST
                   119145
Seq. No.
Contig ID
                   2218 5.R1010
                   jC-atXLIB327419P2f12b2
5'-most EST
Method
                   BLASTX
                   g2281633
NCBI GI
                   686
BLAST score
                   5.0e-72
E value
                   170
Match length
% identity
                   78
                   (AF003097) AP2 domain containing protein RAP2.4
NCBI Description
```

[Arabidopsis thaliana]

14.

Match length

```
119146
Seq. No.
                   2218 9.R1010
Contig ID
5'-most EST
                   g2763824
                   BLASTX
Method
NCBI GI
                   g2281633
BLAST score
                   264
                  1.0e-22
E value
                   54
Match length
                   91
% identity
                   (AF003097) AP2 domain containing protein RAP2.4
NCBI Description
                   [Arabidopsis thaliana]
                   119147
Seq. No.
                   2220 1.R1010
Contig ID
5'-most EST
                  LIB3168-072-P1-K1-C12
Method
                  BLASTX
                  g4204298
NCBI GI
BLAST score
                   1940
E value
                   0.0e + 00
                   440
Match length
                   86
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   119148
Seq. No.
                   2220 2.R1010
Contig ID
5'-most EST
                   g4210244
Method
                   BLASTN
NCBI GI
                   g4199934
BLAST score
                   365
                   0.0e + 00
E value
                   527
Match length
                   99
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   119149
Seq. No.
                   2220 3.R1010
Contig ID
                   LIB3168-086-P1-K1-E11
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4204298
BLAST score
                   340
E value
                   9.0e-32
Match length
                   109
% identity
                   64
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   119150
Seq. No.
Contig ID
                   2220_5.R1010
                   LIB3168-009-P1-K1-H7
5'-most EST
                   BLASTN
Method
                   g4199934
NCBI GI
BLAST score
                   157
                   7.0e-83
E value
```

Match length

```
% identity
                   68
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                   119151
Seq. No.
                   2222_1.R1010
Contig ID
                  jC-atXLIB327420P3b08b1
5'-most EST
                  BLASTX
Method
                   g2828296
NCBI GI
BLAST score
                   1005
                  1.0e-109
E value
Match length
                  190
% identity
                  100
                  (AL021687) RNase L inhibitor [Arabidopsis thaliana]
NCBI Description
                  119152
Seq. No.
                   2223_1.R1010
Contig ID
                   jC-a XLIB327434P3b07b1
5'-most EST
                  BLASTX
Method
                  g3860247
NCBI GI
BLAST score
                   2040
                   0.0e + 00
E value
Match length
                   389
% identity
                   99
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   119153
Seq. No.
                   2223 3.R1010
Contig ID
                   q3450283
5'-most EST
Method
                   BLASTX
                   g3860247
NCBI GI
                   374
BLAST score
E value
                  1.0e-35
                   73
Match length
                   96
% identity
NCBI Description
                  (AC005824) unknown protein [Arabidopsis thaliana]
                   119154
Seq. No.
Contig ID
                   2223 4.R1010
5'-most EST
                   jC-atXLIB327425P3e12b1
                   BLASTN
Method
                  q3860243
NCBI GI
BLAST score
                   183
E value
                   3.0e-98
                   401
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC F15K20 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   119155
Contig ID
                   2223 6.R1010
5'-most EST
                   jC-atXLIB327410P3d12b1
                   BLASTX
Method
NCBI GI
                  g4510430
BLAST score
                   667
                   4.0e-70
E value
```

```
93
% identity
                   (AC006929) unknown protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  119156
                  2223 8.R1010
Contig ID
5'-most EST
                  g2596651
Method
                  BLASTX
NCBI GI
                  q3860247
BLAST score
                  509
E value
                  1.0e-58
Match length
                  146
                  83
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                  119157
Seq. No.
Contig ID
                  2224 1.R1010
5'-most EST
                  jC-atXP98CH8D10T7b1
                  BLASTN
Method
NCBI GI
                  q3169654
BLAST score
                  58
E value
                  2.0e-23
Match length
                  58
                  100
% identity
                  Cloning vector pSFI polylinker, complete polylinker
NCBI Description
                  sequence
Seq. No.
                  119158
Contig ID
                  2230 1.R1010
5'-most EST
                  LIB3168-043-P1-K1-A2
                  BLASTN
Method
NCBI GI
                  q2494110
BLAST score
                  517
E value
                  0.0e + 00
Match length
                  741
% identity
                  99
                  Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                  119159
Seq. No.
                  2231 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327417P1g11b1
Seq. No.
                  119160
Contig ID
                  2231_2.R1010
5'-most EST
                  LIB24-021-Q1-E1-E10
Seq. No.
                  119161
Contig ID
                  2233 1.R1010
                  jC-atXLIB327412P3f08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4538939
BLAST score
                  224
E value
                  3.0e-18
Match length
                  46
% identity
                  93
NCBI Description
                  (AL049483) Col-0 casein kinase I-like protein [Arabidopsis
```

BLAST score

247

thaliana] 119162 Seq. No. 2234 1.R1010 Contig ID jC-atXP85CG7H2T7b1 5'-most EST Method BLASTX g1200205 NCBI GI BLAST score ~331 3.0e-30 E value Match length 139 47 % identity (X95753) DAG [Antirrhinum majus] NCBI Description 119163 Seq. No. 2235_1.R1010 Contig ID LIB35-024-Q1-E1-A6 5'-most EST Method BLASTX g132659 NCBI GI 788 BLAST score 5.0e-84 E value Match length 174 83 % identity NCBI Description 50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13) >gi_81483_pir__A32033 ribosomal protein L13 precursor, chloroplast - spinach >gi_170133 (J04461) ribosomal protein L13 [Spinacia oleracea] 119164 Seq. No. 2238 1.R1010 Contig ID jC-atXP71CF1C5T7095d1 5'-most EST Method BLASTN g4220640 NCBI GI BLAST score 226 1.0e-124 E value Match length 663 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MPE11, complete sequence [Arabidopsis thaliana] 119165 Seq. No. 2238 2.R1010 Contig ID 5'-most EST LIB146-001-Q1-E1-H12 BLASTN Method NCBI GI q4220640 BLAST score 188 E value 1.0e-101 462 Match length % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MPE11, complete sequence [Arabidopsis thaliana] Seq. No. 119166 2242 1.R1010 Contig ID 5'-most EST LIB146-001-Q1-E1-H8 Method BLASTX NCBI GI g82228

```
E value
                    5.0e-21
Match length
                    78
                    69
% identity
NCBI Description hypothetical protein 77 - common topacco cnioropiast spin sqi 225199 prf 1211235AD ORF 77 [Nicotiana tabacum]
                    119167
Seq. No.
                    2243_1.R1010
Contig ID
                    LIB146-001-Q1-E1-H9
5'-most EST
                    BLASTX
Method
                    g3269286
NCBI GI
BLAST score
                    463
E value
                    7.0e-58
                    141
Match length
                    91
% identity
                    (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    119168
                    2246 1.R1010
Contig ID
5'-most EST
                    LIB146-002-Q1-E1-A12
                    BLASTX
Method
                    g4006871
NCBI GI
BLAST score
                    786
E value
                    6.0e-84
Match length
                    184
% identity
                    84
                    (Z99707) patatin-like protein [Arabidopsis thaliana]
NCBI Description
                    119169
Seq. No.
                    2249 1.R1010
Contig ID
5'-most EST
                    g2413893
                    BLASTN
Method
                    g4538990
NCBI GI
BLAST score
                    506
                    0.0e + 00
E value
                    1093
Match length
% identity
                    98
                    Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
NCBI Description
                    (ESSA project)
                    119170
Seq. No.
                    2249 2.R1010
Contig ID
5'-most EST
                    LIB146-024-Q1-E1-G6
Method
                    BLASTX
NCBI GI
                    g4539005
BLAST score
                    735
                    4.0e-78
E value
Match length
                    148
% identity
                    99
NCBI Description
                   (AL049481) putative oxidoreductase [Arabidopsis thaliana]
                    119171
Seq. No.
Contig ID
                    2251_1.R1010
                    jC-aIXLIB327434P3g01b1
5'-most EST
Method
                    BLASTN
                    g2760167
NCBI GI
                    352
BLAST score
```

```
E value
                  0.0e + 00
Match length
                  537
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCO15, complete sequence [Arabidopsis thaliana]
                  119172
Seq. No.
                  2254 1.R1010
Contig ID
5'-most EST
                  LIB23-011-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  g2244760
BLAST score
                  675
E value
                  3.0e-71
Match length
                  142
% identity
                  92
NCBI Description
                  (Z97335) selenium-binding protein [Arabidopsis thaliana]
                  119173
Seq. No.
Contig ID
                  2261 1.R1010
5'-most EST
                  LIB146-002-Q1-E1-B5
Method
                  BLASTX
NCBI GI
                  q529353
BLAST score
                  459
                  2.0e-45
E value
                  141
Match length
% identity
                  55
NCBI Description
                  (U12757) diphenol oxidase [Acer pseudoplatanus]
                  119174
Seq. No.
                  2266 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327415P4g01b1
Method
                  BLASTN
NCBI GI
                  q3869068
BLAST score
                  256
E value
                  1.0e-142
Match length
                  353
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDC16, complete sequence [Arabidopsis thaliana]
Seq. No.
                  119175
Contig ID
                  2268 1.R1010
5'-most EST
                  jC-atXLIB327430P1a06b1
Method
                  BLASTX
NCBI GI
                  q4417280
BLAST score
                  1125
E value
                  1.0e-123
Match length
                  240
                  95
% identity
                  (AC007019) putative ATP synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119176
                  2268 2.R1010
Contig ID
5'-most EST
                  LIB3176-057-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g4417280
```

519

BLAST score

Match length

```
E value
                    1.0e-52
 Match length
                    121
                    88
% identity
 NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana]
                    119177
 Seq. No.
                    2270 1.R1010
 Contig ID
                   LIB25-101-Q1-E1-F12
 5'-most EST
                    119178
 Seq. No.
                    2277_1.R1010
 Contig ID
 5'-most EST
                   LIB146-002-Q1-E1-D4
                    119179
 Seq. No.
                   2279 1.R1010
 Contig ID
 5'-most EST
                   LIB3168-051-P1-K1-G6
                   BLASTN
 Method
                    g3449331
 NCBI GI
 BLAST score
                    639
                    0.0e+00
 E value
                    683
 Match length
                    56
 % identity
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNC17, complete sequence [Arabidopsis thaliana]
                    119180
 Seq. No.
                    2282 1.R1010
 Contig ID
 5'-most EST
                    LIB146-011-Q1-E1-C1
 Method
                    BLASTN
                    g3582315
 NCBI GI
                    359
 BLAST score
                    0.0e + 00
 E value
                    387
 Match length
                    98
 % identity
                   Arabidopsis thaliana chromosome II BAC T27A16 genomic
 NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
                    119181
 Seq. No.
                    2288 1.R1010
 Contig ID
 5'-most EST
                    LIB146-002-Q1-E1-E3
 Method
                    BLASTN
 NCBI GI
                    q4220627
 BLAST score
                    428
 E value
                    0.0e + 00
 Match length
                    854
 % identity
                    98
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 NCBI Description
                    K20J1, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    119182
 Contig ID
                    2294 1.R1010
  5'-most EST
                    jC-atXP115C248G7T7091d1
                    BLASTX
 Method
                    g4538963
 NCBI GI
 BLAST score
                    701
 E value
                    7.0e-74
```

Contig ID

```
% identity
                  72
NCBI Description
                   (AL049488) chlorophyll a/b-binding protein-like
                   [Arabidopsis thaliana] >qi 4741958 gb AAD28776.1 AF134129 1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                  119183
                  2294 2.R1010.
Contig ID
5'-most EST
                  jC-atXLIB327413P4q10b1
Method
                  BLASTX
NCBI GI
                  q4538963
BLAST score
                  820
E value
                  8.0e-88
Match length
                  201
% identity
NCBI Description
                  (AL049488) chlorophyll a/b-binding protein-like
                  [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129 1
                  (AF134129) Lhcb5 protein [Arabidopsis thaliana]
                  119184
Seq. No.
                  2294_3.R1010
Contig ID
                  LIB3177-096-P1-K1-E5
5'-most EST
Method
                  BLASTX
NCBI GI
                  q100200
BLAST score
                  68
                  2.0e-45
E value
Match length
                  142
                  58
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                  119185
                  2294 4.R1010
Contig ID
5'-most EST
                  q2748031
Method
                  BLASTX
                  q4538963
NCBI GI
BLAST score
                  549
                  4.0e-56
E value
Match length
                  154
% identity
                  61
NCBI Description
                  (AL049488) chlorophyll a/b-binding protein-like
                  [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
                  (AF134129) Lhcb5 protein [Arabidopsis thaliana]
                  119186
Seq. No.
Contig ID
                  2294_5.R1010
                  jC-aTXLIB327428P1d11b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4538963
BLAST score
                  603
E value
                  2.0e-62
Match length
                  178
% identity
                  (AL049488) chlorophyll a/b-binding protein-like
NCBI Description
                  [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129 1
                  (AF134129) Lhcb5 protein [Arabidopsis thaliana]
                  119187
Seq. No.
```

2294_7.R1010

Match length

```
ARABL1-036-Q1-E1-H3
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4741957
BLAST score
                  18
E value
                  3.5e + 00
Match length
                  233
% identity
                  86
                  Arabidopsis thaliana Lhcb5 protein (Lhcb5) mRNA, complete
NCBI Description
Seq. No.
                  119188
                  2294 8.R1010
Contig ID
5'-most EST
                  jC-atXLIB327414P4b12a2
Method
                  BLASTX
NCBI GI
                  q4538963
BLAST score
                  56
E value
                  9.0e-21
Match length
                  142
% identity
                  55
NCBI Description
                   (AL049488) chlorophyll a/b-binding protein-like
                   [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
                  119189
Seq. No.
                  2294 10.R1010
Contig ID
5'-most EST
                  LIB3177-064-P1-K1-B4
                                   23.
Method
                  BLASTX
NCBI GI
                  q4538963
BLAST score
                  88
E value
                  8.0e-26
Match length
                  68
                  83
% identity
NCBI Description
                  (AL049488) chlorophyll a/b-binding protein-like
                   [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129 1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                  119190
Contig ID
                  2298 1.R1010
5'-most EST
                  iC-atXLIB327415P4q11b1
Method
                  BLASTX
NCBI GI
                  g3831440
BLAST score
                  499
E value
                  6.0e-56
Match length
                  144
                  78
% identity
NCBI Description
                  (AC005819) putative cytochrome P450 [Arabidopsis thaliana]
                  >gi 4415946 gb AAD20176 (AC006418) putative cytochrome
                  P450 [Arabidopsis thaliana]
Seq. No.
                  119191
Contig ID
                  2301 1.R1010
5'-most EST
                  iC-atXLIB327427P3q12b2
Method
                  BLASTN
NCBI GI
                  q4756963
BLAST score
                  346
E value
                  0.0e + 00
```

Method

BLASTX

```
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
                   119192
Seq. No.
                   2301 2.R1010
Contig ID
                  jC-atXLIB327411P3f11b1
5'-most EST
                  BLASTN
Method
                  g2760167
NCBI GI
BLAST score
                   424
                   0.0e + 00
E value
Match length
                   448
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCO15, complete sequence [Arabidopsis thaliana]
                   119193
Seq. No.
Contig ID
                  2301 3.R1010
5'-most EST
                  LIB22-080-Q1-E1-E1
                  BLASTN
Method
NCBI GI
                   g2760167
BLAST score
                   303
E value
                   1.0e-170
Match length
                   341
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCO15, complete sequence [Arabidopsis thaliana]
                  119194
Seq. No.
Contig ID
                  2303 1.R1010
5'-most EST
                   jC-atXmonuni26Callbl
                  BLASTX
Method
NCBI GI
                  g4063751
BLAST score
                   307
                   2.0e-33
E value
Match length
                  227
% identity
                   41
NCBI Description
                  (AC005851) putative white protein [Arabidopsis thaliana]
                  >gi 4510409 gb AAD21495.1 (AC006929) putative white
                  protein [Arabidopsis thaliana]
                  119195
Seq. No.
Contig ID
                  2308 1.R1010
5'-most EST
                  jC-atXLIB327415P2h09a2
Method
                  BLASTN
NCBI GI
                  g2570223
                   278
BLAST score
E value
                  1.0e-155
Match length
                  302
% identity
                  97
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,
                  complete sequence [Arabidopsis thaliana]
                  119196
Seq. No.
Contig ID
                  2311_1.R1010
                  jC-a\overline{1}XLIB327435P4g11b1
5'-most EST
```

BLAST score

988

```
NCBI GI
                  g728880
BLAST score
                  184
E value
                  3.0e-13
Match length
                  52
                  63
% identity
                  N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG
NCBI Description
                  >gi 517485 emb CAA54691 (X77588) ARD1 N-acetyl transferase
                  homologue [Homo sapiens] >gi 1302661 (U52112) ARD1 N-acetyl
                  transferase related protein [Homo sapiens]
                  119197
Seq. No.
                  2311 2.R1010
Contig ID
                  g2393561
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2924734
BLAST score
                  444
                  0.0e + 00
E value
                  513
Match length
                  96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXE10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  119198
Contig ID
                  2311 3.R1010
5'-most EST
                  jC-atXLIB327415P2h05b2
Method
                  BLASTX
NCBI GI
                  g728880
BLAST score
                  531
                  5.0e-54
E value
                  158
Match length
% identity
                  65
                  N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG
NCBI Description
                  >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase
                  homologue [Homo sapiens] >gi 1302661 (U52112) ARD1 N-acetyl
                  transferase related protein [Homo sapiens]
                  119199
Seq. No.
Contig ID
                  2316 1.R1010
                  LIB3175-027-P1-K1-D12
5'-most EST
                  119200
Seq. No.
Contig ID
                  2318 1.R1010
                  LIB3234-004-P1-K1-A11
5'-most EST
Method
                  BLASTX
                  g4539005
NCBI GI
BLAST score
                  321
E value
                  1.0e-29
                  159
Match length
% identity
                  42
                  (AL049481) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119201
Contig ID
                  2322 1.R1010
                  LIB22-009-Q1-E1-E5
5'-most EST
Method
                  BLASTX
                  q2961378
NCBI GI
```

**. *.

Method

BLASTX

```
E value
                  1.0e-107
Match length
                  229
% identity
                  46
                  (AL022141) putative protein [Arabidopsis thaliana]
NCBI Description
                  119202
Seq. No.
                                                                            ٠. . . .
Contig ID
                  2327 1.R1010
                  LIB3168-023-P1-K1-H11
5'-most EST
                  BLASTX
Method
                  g4204277
NCBI GI
BLAST score
                  695
E value
                  1.0e-73
Match length
                  128
                  100
% identity
NCBI Description
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
                  119203
Seq. No.
Contig ID
                  2330 1.R1010
5'-most EST
                  LIB3234-077-P1-K1-H1
                  BLASTX
Method
NCBI GI
                  g4337195
BLAST score
                  169
E value
                  6.0e-12
Match length
                  46
                  76
% identity
                  (AC006403) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  119204
Seq. No.
Contig ID .
                  2345 2.R1010
                  LIB22-037-Q1-E1-F10
5'-most EST
                  BLASTN
Method
NCBI GI
                  g4586019
BLAST score
                  188
E value
                  1.0e-101
Match length
                  393
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T3P4 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  119205
Contig ID
                  2347 1.R1010
5'-most EST
                  jC-atXP86CG4G2T7b1
Method
                  BLASTX
NCBI GI
                  g231683
BLAST score
                  100
E value
                  8.0e-43
Match length
                  128
                  74
% identity
NCBI Description
                  CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597
                  calnexin-like protein - Arabidopsis thaliana
                  >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog
                  [Arabidopsis thaliana]
                  119206
Seq. No.
Contig ID
                  2347 3.R1010
5'-most EST
                  jC-atXLIB327421P4c08b1
```

```
NCBI GI
                      q231683
  BLAST score
                      1103
                      1.0e-179
· E value
                      405
  Match length
  % identity
                      80
                      CALNEXIN HOMOLOG PRECURSOR >gi 421825 pir JN0597
  NCBI Description
                     calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog
                      [Arabidopsis thaliana]
  Seq. No.
                      119207
                      2347 4.R1010
  Contig ID
                      jC-atXP86CG4H4T7d2
  5'-most EST
  Method
                      BLASTX
  NCBI GI
                      q231683
  BLAST score
                      1097
  E value
                      1.0e-120
  Match length
                      219
  % identity
                      93
                      CALNEXIN HOMOLOG PRECURSOR >qi 421825 pir JN0597
  NCBI Description
                      calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog
                      [Arabidopsis thaliana]
                     .119208
  Seq. No.
                      2347 5.R1010
  Contig ID
  5'-most EST
                      jC-alX2508201E1E11b1
  Method
                      BLASTN
  NCBI GI
                      g2760165
  BLAST score
                      93
  E value
                      1.0e-44
  Match length
                      97
  % identity
                      99
                      Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
  NCBI Description
                      MAC9, complete sequence [Arabidopsis thaliana]
  Seq. No.
                      119209
  Contig ID
                      2351 1.R1010
  5'-most EST
                      LIB3234-039-P1-K1-C3
  Method
                      BLASTX
  NCBI GI
                      g4581108
  BLAST score
                      227
  E value
                      2.0e-18
  Match length
                      108
                      48
  % identity
  NCBI Description
                      (AC005825) putative chloroplast outer membrane protein
                      86, also very similar to GTP-inding protein from pea
                      (GB:L36857) [Arabidopsis thaliana]
  Seq. No.
                      119210
  Contig ID
                      2352 1.R1010
  5'-most EST
                      LIB146-015-Q1-E1-D8
  Method
                      BLASTX
  NCBI GI
                      g112737
  BLAST score
                      330
  E value
                      2.0e-30
  Match length
                      158
```

```
% identity
                   49
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                   1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                   119211
Seq. No.
Contig ID
                   2352 3.R1010
5'-most EST
                   g2596136
Method
                   BLASTN
                   q4159703
NCBI GI
                   276
BLAST score
                   1.0e-154
E value
Match length
                   276
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K5F14, complete sequence
                  119212
Seq. No.
Contig ID
                   2355_1.R1010
5'-most EST
                  LIB146-003-Q1-E1-E2
Method
                  BLASTX
NCBI GI
                   q4006887
BLAST score
                   489
E value
                   3.0e-49
Match length
                   94
                   99
% identity
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   119213
Seq. No.
Contig ID
                   2356 1.R1010
                   jC-atXLIB327416P4d06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   a2961346
                   994
BLAST score
E value
                   1.0e-164
                   295
Match length
                   97
% identity
                   (AL022140) pectinesterase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   119214
Seq. No.
                   2360 1.R1010
Contig ID
                  jC-a\overline{t}XLIB327414P2a11b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q2582640
BLAST score
                   42
                   8.0e-14
E value
                   74
Match length
                   91
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
```

119215

Seq. No.

% identity

```
Contig ID
                  2363 1.R1010
5'-most EST
                  jC-alXLIB327435P2f10a1
Method
                  BLASTN
                  g4519192
NCBI GI
BLAST score
                  249
                  1.0e-137
E value
Match length
                  459
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MBK21, complete sequence
                  119216
Seq. No.
                  2369 1.R1010
Contig ID
                  LIB3168-069-P1-K1-E10
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2258103
BLAST score
                  527
E value
                  0.0e + 00
Match length
                  705
                  93
% identity
NCBI Description
                  Arabidopsis thaliana chloroplast genes for trnC and rpoB,
                  partial cds
                  119217
Seq. No.
                  2374 1.R1010
Contig ID
5'-most EST
                  LIB3234-016-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  q3046852
BLAST score
                  244
E value
                  1.0e-135
Match length
                  450
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQJ16, complete sequence [Arabidopsis thaliana]
Seq. No.
                  119218
                  2375 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327423P3b10b1
Method
                  BLASTX
NCBI GI
                  q3024871
BLAST score
                  177
E value
                  1.0e-12
Match length
                  105
% identity
                  41
                  HYPOTHETICAL 77.3 KD PROTEIN SLL0005
NCBI Description
                  >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis]
             sp.]
                  119219
Seq. No.
Contig ID
                  2376 1.R1010
5'-most EST
                  LIB3234-058-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  g12279
BLAST score
                  81
                                                                  ,74- ·
E value
                  4.0e-37
Match length
                  135
```

```
NCBI Description Spinach chloroplast genes for the D2 and 44 kd reaction
                  centre, chlorophyll a-binding protein and for tRNA-Ser
                  (UGA)
                  119220
Seq. No.
                  2376 2.R1010
Contig ID
5'-most EST
                  g2580893
                  119221
Seq. No.
                  2376 4.R1010
Contig ID
                  LIB3234-065-P1-K1-D11
5'-most EST
                  BLASTN
Method
                  q343514
NCBI GI
                  67
BLAST score
E value
                  8.0e-29
                  91
Match length
                  93
% identity
NCBI Description Tobacco Thr-tRNA gene
                  119222
Seq. No.
                  2381 1.R1010
Contig ID
5'-most EST
                  jC-atXP89C245E24T7080d1
                  119223
Seq. No.
                  2381 2.R1010
Contig ID
5'-most EST
                  LIB3175-006-P1-K1-C2
                  119224
Seq. No.
                  2382 1.R1010
Contig ID
5'-most EST
                  LIB3234-060-P1-K1-A2
                  BLASTN
Method
NCBI GI
                  q3241927
BLAST score
                  362
                  0.0e + 00
E value
Match length
                  453
% identity
                  64
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTE17, complete sequence [Arabidopsis thaliana]
                  119225
Seq. No.
Contig ID
                  2387 1.R1010
5'-most EST
                  jC-atXLIB327413P1e09b1
                  BLASTN
Method
NCBI GI
                  g3869062
                  50
BLAST score
                  6.0e-19
E value
                  150
Match length
% identity
                  92
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K11I1, complete sequence [Arabidopsis thaliana]
                  119226
Seq. No.
                  2388 1.R1010
Contig ID
5'-most EST
                  LIB146-004-Q1-E1-A2
                  BLASTN
Method
                  g3228389
NCBI GI
BLAST score
                  426
```

E value

6.0e-81

```
E value
                  0.0e + 00
                  426
Match length
                  100
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F17L21,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  119227
Seq. No.
                  2391_1.R1010
Contig ID
                  LIB3168-037-P1-K1-F8
5'-most EST
Method
                  BLASTX
NCBI GI
                  q118927
BLAST score
                  200
                  3.0e-15
E value
Match length
                  201
                  31
% identity
                  DESSICATION-RELATED PROTEIN CLONE PCC3-06
NCBI Description
                  >gi 320603 pir C45509 desiccation-related protein (clone
                  PCC3-06) - Craterostigma plantagineum >gi 167475 (M62989)
                  dessication-related protein [Craterostigma plantagineum]
                  >gi_227779_prf__1710351C abscisic acid responsive protein C
                  [Craterostigma plantagineum]
Seq. No.
                  119228
Contig ID
                  2394_1.R1010
5'-most EST
                  LIB3175-027-P1-K1-B1
                  119229
Seq. No.
                  2395 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327418P4b01b1
Method
                  BLASTN
NCBI GI
                  g2924651
BLAST score
                  395
E value
                  0.0e + 00
Match length
                  474
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  119230
                  2397 1.R1010
Contig ID
                  LIB3176-123-P2-K1-G12
5'-most EST
                  BLASTN
Method
NCBI GI
                  q972937
BLAST score
                  274
                  1.0e-152
E value
Match length
                  487
% identity
                  100
NCBI Description
                  Arabidopsis thaliana putative chlorophyll synthetase (G4)
                  gene, complete cds
                  119231
Seq. No.
                  2398_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327427P3c04b2
                  BLASTX
Method
NCBI GI
                  g3928095
BLAST score
                  763
```

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```
Match length
                   230
% identity
                   67
                   (AC005770) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   119232
Seq. No.
                   2398 2.R1010
Contig ID
5'-most EST
                   LIB25-014-Q1-E1-B2
                   BLASTN
Method
NCBI GI
                   g166870
BLAST score
                   146
                   4.0e-76
E value
Match length
                   690
% identity
                   94
                   Arabidopsis thaliana 5S ribosomal RNA gene, complete cds
NCBI Description
Seq. No.
                   119233
                   2407 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327420P3d04b1
Method
                   BLASTX
                   g2394418
NCBI GI
BLAST score
                   167
                   2.0e-11
E value
Match length
                   105
% identity
                   17
                   (AF024491) contains similarity to ankyrin repeats and
NCBI Description
                   protein kinase motifs [Caenorhabditis elegans]
                   119234
Seq. No.
                   2407 2.R1010
Contig ID
5'-most EST
                   LIB146-011-Q1-E1-F11
                   119235
Seq. No.
                   2411 1.R1010
Contig ID
5'-most EST
                   g275<del>9</del>364
Method
                   BLASTX
                   g1532169
NCBI GI
BLAST score
                   868
E value .
                   1.0e-93
                   177
Match length
% identity
                   95
                   (U63815) similar to a E. coli hypothetical protein F402
NCBI Description
                   encoded by GenBank Accession Number S47768 [Arabidopsis
                   thaliana]
                   119236
Seq. No.
                   2413_1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327439P3f01b2
Method
                   BLASTX
NCBI GI
                   g1172873
BLAST score
                   1371
E value
                   1.0e-152
                   332
Match length
% identity
                   78
                   CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719
NCBI Description
                   drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                   precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
```

(D13043) thiol protease [Arabidopsis thaliana]

5'-most EST

```
Seq. No.
                  119237
                  2413 2.R1010
Contig ID
5'-most EST
                  q315299
Method
                  BLASTX
                  g1172873
NCBI GI
                  744
BLAST score
                  5.0e-81
E value
Match length
                  204
% identity
                  71
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                  (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                  119238
Contig ID
                  2421 1.R1010
                  LIB146-004-Q1-E1-D9
5'-most EST
Method
                  BLASTX
                  g2979562
NCBI GI
BLAST score
                  647
E value
                  6.0e-68
Match length
                  132
% identity
                  53
NCBI Description
                  (AC003680) unknown protein [Arabidopsis thaliana]
                  >gi 3386623 (AC004665) unknown protein [Arabidopsis
                  thalianal
                  119239
Seq. No.
                  2428 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327423P4b01b1
Method
                  BLASTX
NCBI GI
                  q2944446
                  453
BLAST score
E value
                  5.0e-45
Match length
                  143
% identity
                  57
NCBI Description
                  (AF050756) cysteine endopeptidase precursor [Ricinus
                  communis]
                  119240
Seq. No.
Contig ID
                  2431 1.R1010
                  LIB3234-083-Q1-K1-C1
5'-most EST
Method
                  BLASTX
                  g2129773
NCBI GI
                  924
BLAST score
                  1.0e-135
E value
Match length
                  254
% identity
NCBI Description
                  xyloglucan endotransglycosylase-related protein XTR3 -
                  Arabidopsis thaliana (fragment) >gi 1244752 (U43485)
                  xyloglucan endotransglycosylase-related protein
                  [Arabidopsis thaliana]
Seq. No.
                  119241
Contig ID
                  2434 1.R1010
```

LIB146-019-Q1-E1-E4

```
Method
                  BLASTX
NCBI GI
                  q1402878
BLAST score
                   475
                  1.0e-47
E value
Match length
                  141
% identity
                   62
                  (X98130) unknown [Arabidopsis thaliana]
NCBI Description
                  119242
Seq. No.
Contig ID
                  2437 1.R1010
5'-most EST
                  LIB23-005-Q1-E1-C8
Method
                  BLASTX
                  g2529229
NCBI GI
                  803
BLAST score
                  1.0e-90
E value
                  200
Match length
% identity
                  86
                  (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
                  119243
Seq. No.
                  2438_1.R1010
Contig ID
5'-most EST
                  LIB3176-088-P1-K1-E3
Method:
                  BLASTN
                  q2980757
NCBI GI
BLAST score
                  580
E value
                  0.0e + 00
                  1009
Match length
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18
NCBI Description
                   (ESSAII project)
                  119244
Seq. No.
Contig ID
                  2440 1.R1010
5'-most EST
                  jC-atXLIB327428P1a02b2
Method
                  BLASTX
NCBI GI
                  q3157937
                  1493
BLAST score
                  1.0e-166
E value
Match length
                  299
% identity
                  96
                   (AC002131) Identical to aspartic proteinase cDNA gb U51036
NCBI Description
                  from A. thaliana. ESTs gb N96313, gb T21893, gb R30158,
                  gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269,
                  gb T44552, gb T22542, gb T76533, gb T44350, gb Z34591,
                  gb_AA728734, gb
                  119245
Seq. No.
Contig ID
                  2440 2.R1010
                  g2748630
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3157937
BLAST score
                  1247
                  1.0e-138
E value
Match length
                  254
% identity
                  (AC002131) Identical to aspartic proteinase cDNA gb U51036
NCBI Description
                  from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158,
```

Contig ID

```
gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591,
                   gb_AA728734, gb
Seq. No.
                   119246
                   2440_3.R1010
Contig ID
                   LIB3175-003-P1-K1-C10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3157937
BLAST score
                   573
E value
                   5.0e-59
Match length
                   156
                   75
% identity
                   (ACO02131) Identical to aspartic proteinase cDNA gb U51036
NCBI Description
                   from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158,
                   gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591,
                   gb_AA728734, gb
                   119247
Seq. No.
                   2440 5.R1010
Contig ID
5'-most EST
                   ARABL1-033-Q1-E1-E7
Method
                   BLASTN
                   q2584827
NCBI GI
                   103
BLAST score
                   6.0e-51
E value
                   224
Match length
% identity
                   Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   119248
Seq. No.
Contig ID
                   2443_1.R1010
                   LIB146-004-Q1-E1-G10
5'-most EST
Method
                   BLASTN
NCBI GI
                   q2760164
                   453
BLAST score
                   0.0e + 00
E value
Match length
                   533
% identity
                   96
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18P6, complete sequence [Arabidopsis thaliana]
                   119249
Seq. No.
                   2450 1.R1010
Contig ID
                   LIB3234-012-P1-K1-E8
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4582411
BLAST score
                   584
E value
                   0.0e + 00
Match length
                   730
% identity
                   Arabidopsis thaliana chromosome 1 BAC T23K8 sequence,
NCBI Description
                   complete sequence
                   119250
Seq. No.
```

gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269,

2451 1.R1010

```
5'-most EST
                   LIB35-030-Q1-E1-E1
                   BLASTX
Method
                   g4585997
NCBI GI
BLAST score
                   274
                   4.0e-24
E value
                   103
Match length
% identity
                   60
                   (AC005287) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   119251
                   2453 1.R1010
Contig ID
                   jC-atXmonuni25Da08b1
5'-most EST
                   BLASTX
Method
                   q1653702
NCBI GI
                   279
BLAST score
                   2.0e-24
E value
Match length
                   75
% identity
                   73
                   (D90915) dihydrolipoamide acetyltransferase component (E2)
NCBI Description
                   of pyruvate dehydrogenase complex [Synechocystis sp.]
Seq. No.
                   119252
                   2457 1.R1010
Contig ID
                   LIB3234-016-P1-K1-H6
5'-most EST
Method
                   BLASTX
NCBI GI
                   q881615
BLAST score
                   799
E value
                   1.0e-85
Match length
                   154
% identity
                   99
NCBI Description
                   (U29142) fatty acid elongase 1 [Arabidopsis thaliana]
                   >gi 3096921 emb CAA18831.1 (AL023094) fatty acid elongase
                   1 [Arabidopsis thaliana]
Seq. No.
                   119253
                   2463 1.R1010
Contiq ID
5'-most EST
                   LIB23-023-Q1-E1-A1
Method
                   BLASTX
NCBI GI
                   q4432863
BLAST score
                   795
E value
                   4.0e-85
Match length
                   160
% identity
                   99
NCBI Description
                   (AC006300) putative phosphate/phosphoenolpyruvate
                   translocator protein [Arabidopsis thaliana]
Seq. No.
                   119254
                   2464 1.R1010
Contig ID
5'-most EST
                   LIB3168-030-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   q4115356
BLAST score
                   574
                   2.0e-59
E value
Match length
                   112
% identity
                   98
                   (AC005957) putative thionin variant protein [Arabidopsis
NCBI Description
                   thalianal
```

Match length

```
119255
Seq. No.
                  2470 1.R1010
Contig ID
                  jC-atXLIB327419P3c10b2
5'-most EST
                  BLASTN
Method
NCBI GI
                  q2244991
                  199
BLAST score
                  1.0e-108
E value
                  442
Match length
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                  119256
Seq. No.
                  2479_1.R1010
Contig ID
                  g2048097
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4662609
BLAST score
                  237
                  1.0e-130
E value
Match length
                  386
                  97
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F10A5,
                  complete sequence
                  119257
Seq. No.
                  2485 1.R1010
Contig ID
                  jC-atXLIB327408P2f10b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3250695
BLAST score
                  1043
                  1.0e-114
E value
Match length
                  238
% identity
                  89
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
                  119258
                  2487 1.R1010
Contig ID
5'-most EST
                  jC-alXLIB327435P4d04b1
Method
                  BLASTX
                  q3860277
NCBI GI
BLAST score
                  967
                  1.0e-105
E value
Match length
                  218
% identity
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  119259
Contig ID
                  2487_2.R1010
                  jC-atXP96C248A20T7b1
5'-most EST
Method
                  BLASTX
                  q3860277
NCBI GI
BLAST score
                  849
                  3.0e-91
E value
```

```
91
% identity
                  (ACO05824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi 4314394 gb AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  119260
                  2487 3.R1010
Contig ID
                  g315785
5'-most EST
Method
                  BLASTN
                  g16472
NCBI GI
                   427
BLAST score
                  0.0e + 00
E value
Match length
                   446
                  99
% identity
                  A.thaliana rRNA repeat unit, most frequent IGR type
NCBI Description
                  119261
Seq. No.
                  2487 4.R1010
Contig ID
                  jC-atXLIB327416P2f01b1
5'-most EST
                  BLASTX
Method
                  g2088662
NCBI GI
                   720
BLAST score
                   5.0e-76
E value
                  164
Match length
% identity
                   87
                  (AF002109) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119262
                  2487 5.R1010
Contig ID
                   jC-atXLIB327438P3e04a2
5'-most EST
Method
                   BLASTX
                   q2088662
NCBI GI
                   689
BLAST score
                  2.0e-72
E value
                   196
Match length
% identity
                  73
                   (AF002109) unknown protein [Arabidopsis thaliana]
NCBI Description
                  119263
Seq. No.
Contig ID
                  2487 6.R1010
5'-most EST
                   jC-atXmonuni25Ae12b1
Method
                   BLASTX
                   q3860277
NCBI GI
                   896
BLAST score
                   1.0e-96
E value
                   216
Match length
% identity
                   82
                   (ACO05824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  119264
Contig ID
                  2487 8.R1010
                   jC-alXLIB327434P1d01b1
5'-most EST
                   BLASTX
Method
                   q3860277
NCBI GI
                   564
BLAST score
```

Seq. No.

```
5.0e-58
E value
                  133
Match length
                  86
% identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi 4314394 gb AAD15604 (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
                  119265
Seq. No.
                  2487 10.R1010
Contig ID
                  q241\overline{3}961
5'-most EST
Method
                  BLASTX
                  q3860277
NCBI GI
BLAST score
                  167
                  7.0e-55
E value
Match length
                  136
% identity
                  79
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  119266
                  2487 11.R1010
Contig ID
                  LIB3234-046-P1-K1-C5
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1709970
BLAST score
                  391
E value
                  1.0e-37
Match length
                  124
% identity
                  68
NCBI Description
                  60S RIBOSOMAL PROTEIN L10A
                  119267
Seq. No.
                  2487 12.R1010
Contig ID
5'-most EST
                  LIB3176-020-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q3860277
BLAST score
                  59
E value
                  1.0e-36
Match length
                  109
% identity
                  74
NCBI Description
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
                  thaliana] >gi_4314394_gb_AAD15604 (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  119268
Contig ID
                  2490 1.R1010
5'-most EST
                  jC-atXP55C18601T7d2
Method
                  BLASTN
NCBI GI
                  q3985954
BLAST score
                  413
E value
                  0.0e + 00
Match length
                  459
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRG21, complete sequence [Arabidopsis thaliana]
```

```
2493 1.R1010
Contig ID
5'-most EST
                  jC-atXP79C239E4T7b1
Method
                  BLASTX
NCBI GI
                  g1871184
BLAST score
                  661
                  3.0e-69
E value
Match length
                  160
% identity
                  83
                  (U90439) unknown protein [Arabidopsis thaliana]
NCBI Description
                  119270
Seq. No.
                  2501_1.R1010
Contig ID
5'-most EST
                  LIB146-005-Q1-E1-F10
Method
                  BLASTX
                  g2191129
NCBI GI
BLAST score
                  771
                  4.0e-82
E value
                  188
Match length
                  82
% identity
                  (AF007269) similar to SPF1 DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  119271
Seq. No.
                  2503 1.R1010
Contig ID
                                                jC-atXP91C246J8T7b1
5'-most EST
Method
                  BLASTX
                  g4587525
NCBI GI
                  297
BLAST score
                  1.0e-41
E value
Match length
                  193
% identity
                  46
                  (AC007060) Contains the PF 00650 CRAL/TRIO
NCBI Description
                  phosphatidyl-inositol-transfer protein domain. ESTs
                  gb T76582, gb N06574 and gb Z25700 come from this gene.
                  [Arabidopsis thaliana]
                  119272
Seq. No.
Contig ID
                  2508 1.R1010
                  jC-atXLIB327422P4c12b1
5'-most EST
Method
                  BLASTX
                  g2541876
NCBI GI
                  342
BLAST score
                  1.0e-53
E value
                  441
Match length
                  32
% identity
                  (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                  [Nicotiana tabacum]
                  119273
Seq. No.
                  2508 3.R1010
Contig ID
5'-most EST
                  LIB3168-073-P1-K1-G3
Method
                  BLASTN
                  g4757414
NCBI GI
BLAST score
                  459
                  0.0e + 00
E value
Match length
                  467
```

100

% identity

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYF24, complete sequence
                                                      5
                  119274
Seq. No.
                  2514 1.R1010
Contig ID
5'-most EST
                  jC-atX25107Q1E1C04b1
                  BLASTN
Method
                  q4519193
NCBI GI
BLAST score
                  171
                  4.0e-91
E value
                  559
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDC11, complete sequence
                  119275
Seq. No.
                  2516 1.R1010
Contig ID
                  LIB146-005-Q1-E1-G3
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2832625
BLAST score
                  226
                  1.0e-18
E value
Match length
                  66
% identity
                  62
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                  119276
Seq. No.
                  2517 1.R1010
Contig ID
                  jC-atXP82CG1E11T7d3
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3287693
BLAST score
                  754
E value
                  5.0e-80
Match length
                  176
                  80
% identity
                  (AC003979) Similar to LIM17 gene product gb 1653769 from
NCBI Description
                  the genome of Synechocystis sp. gb D90916. [Arabidopsis
                  thaliana]
                  119277
Seq. No.
                  2518 1.R1010
Contig ID
5'-most EST
                  jC-atXP86CG9F2T7b1
Method
                  BLASTX
NCBI GI
                  g2245131
BLAST score
                  669
                  6.0e-70
E value
Match length
                  223
% identity
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  119278
Seq. No.
                  2518 3.R1010
Contig ID
5'-most EST
                  jC-atX35042Q1E1G07b1
                  119279
Seq. No.
                  2522 1.R1010
Contig ID
                  LIB146-005-Q1-E1-G9
5'-most EST
```

```
BLASTN
Method
NCBI GI
                   g3510339
BLAST score
                   263
                   1.0e-146
E value
Match length ...
                   403
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K3K7, complete sequence [Arabidopsis thaliana]
                   119280
Seq. No.
                   2523 1.R1010
Contig ID
                   LIB146-005-Q1-E1-H1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1848214
BLAST score
                   590
                   7.0e-61
E value
Match length
                   147
                   75
% identity
                   (Y11210) uracil phosphoribosyltransferase [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   119281
                   2529 1.R1010
Contig ID
                   jC-aIXLIB327435P2b07a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4103987
BLAST score
                   659
                   4.0e-69
E value
Match length
                   159
                   79
% identity
                   (AF030516) 5,10-methylenetetrahydrofolate
NCBI Description
                   dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase
                   [Pisum sativum]
                   119282
Seq. No.
                   2531 1.R1010
Contig ID
                   LIB35-028-Q1-E1-E12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2460200
BLAST score
                   267
                   5.0e-23
E value
Match length
                   201
% identity
                   37
                   (AF020833) eukaryotic translation initiation factor 3
NCBI Description
                   subunit [Homo sapiens]
Seq. No.
                   119283
                   2534 1.R1010 ·
Contig ID
5'-most EST
                   LIB146-017-Q1-E1-D2
Method
                   BLASTX
NCBI GI
                   q3335169
BLAST score
                   968
E value
                   1.0e-105
Match length
                   180
                   100
% identity
                   (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
```

>gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

```
119284
Seq. No.
Contig ID
                  2538 1.R1010
5'-most EST
                  LIB3176-035-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q3319341
BLAST score
                  853
E value
                  2.0e-91
Match length
                  255
% identity
                  68
                   (AF077407) similar to Medicago sativa nucleic acid binding
NCBI Description
                  protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]
                  119285
Seq. No.
                  2538 3.R1010
Contig ID
5'-most EST
                  q4714017
                  BLASTX
Method
NCBI GI
                  q3319341
BLAST score
                   306
                  9.0e-28
E value
Match length
                  52
% identity
                  100
                  (AF077407) similar to Medicago sativa nucleic acid binding
NCBI Description
                  protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]
Seq. No.
                  119286
                  2540 1.R1010
Contig ID
5'-most EST
                  LIB3168-082-P1-K1-D7
                  BLASTN
Method
NCBI GI
                  g2264314
BLAST score
                   419
E value
                  0.0e + 00
Match length
                  427
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                  119287
Contig ID
                  2542 1.R1010
5'-most EST
                  LIB23-046-Q1-E1-E3
Method
                  BLASTX
NCBI GI
                  g2160166
BLAST score
                   327
E value
                  1.0e-29
Match length
                  436
% identity
                  39
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119288
Contig ID
                  2543 1.R1010
5'-most EST
                  jC-atXP73C223J17T7b1
Method
                  BLASTN
NCBI GI
                  g2656024
BLAST score
                  61
                  2.0e-25
E value
Match length
                  243
```

```
87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K15E6
Seq. No.
                   119289
                   2543 2.R1010
Contig ID
                   jC-atXLIB327431P2c03a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2656024
BLAST score
                   61
E value
                   2.0e-25
Match length
                   193
                   87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K15E6
                   119290
Seq. No.
                   2543 3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327411P3b09b1
Method
                   BLASTX
NCBI GI
                   q4586058
BLAST score
                   761
E value
                   2.0e-80
Match length
                   424
                   40
% identity
                   (AC007020) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   119291
Contig ID
                   2545 1.R1010
5'-most EST
                   LIB146-006-Q1-E1-B7
Method
                   BLASTX
NCBI GI
                   q2642158
BLAST score
                   313
E value
                   8.0e-29
Match length
                   119
% identity
                   48
                   (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   119292
Contig ID
                   2559 1.R1010
5'-most EST
                   LIB146-006-Q1-E1-D1
Method
                   BLASTN
NCBI GI
                   g4691223
BLAST score
                   390
E value
                   0.0e + 00
Match length
                   414
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
NCBI Description
                   (ESSA project)
Seq. No.
                   119293
Contig ID
                   2561 1.R1010
5'-most EST
                   LIB146-018-Q1-E1-E11
Method
                   BLASTX
NCBI GI
                   g2583108
BLAST score
                   449
                   1.0e-44
E value
```

Match length

```
132
Match length
% identity
                   68
                   (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
                  119294
Seq. No.
                  2566 1.R1010
Contig ID
                  LIB3234-046-P1-K1-C7
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2244906
                   610
BLAST score
E value
                  3.0e-63
                  171
Match length
% identity
                  71
                   (Z97339) indole-3-acetate beta-glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                  119295
Seq. No.
                  2575 1.R1010
Contig ID
                  LIB3175-025-P1-K1-E11
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3550519
BLAST score
                   390
                  1.0e-37
E value
                  120
Match length
% identity
                   62
                  (AJ007630) oxygenase [Nicotiana tabacum]
NCBI Description
                   119296
Seq. No.
                   2575 2.R1010
Contig ID
                  LIB3176-114-P2-K1-C6
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3550519
BLAST score
                   602
E value
                   1.0e-62
Match length
                   157
                   70
% identity
                  (AJ007630) oxygenase [Nicotiana tabacum]
NCBI Description
                   119297
Seq. No.
                   2586 1.R1010
Contig ID
                  LIB3168-077-P1-K1-F12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4539005
BLAST score
                   382
                   1.0e-36
E value
Match length
                   186
% identity
                   44
                  (AL049481) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
                   119298
Seq. No.
                   2588 1.R1010
Contiq ID
                   g2758279
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3860243
BLAST score
                   311
                   1.0e-175
E value
```

```
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC F15K20 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   119299
                   2590 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327438P2b05a1
                   BLASTN
Method
NCBI GI
                   q4734011
BLAST score
                   195
E value
                   1.0e-105
Match length
                   331
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC F24C20 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   119300
                   2596 1.R1010
Contig ID
                   jC-a\overline{t}XP96C248B2T7b1
5'-most EST
                   BLASTX
Method
                   q3135751
NCBI GI
BLAST score
                   869
E value
                   2.0e-93
                   173
Match length
% identity
                   98
                   (AJ006095) 26S protease regulatory subunit 6 [Cicer
NCBI Description
                   arietinum]
                   119301
Seq. No.
                   2596 2.R1010
Contig ID
                   jC-alXLIB327436P4e06b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1709798
BLAST score
                   1845
                   0.0e + 00
E value
Match length
                   401
% identity
                   92
                  26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >qi 1155334
NCBI Description
                   (U43398) POTATP1 [Solanum tuberosum]
                   119302
Seq. No.
                   2596 4.R1010
Contig ID
                   jC-atXLIB327415P4c06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1709798
BLAST score
                   614
                   8.0e-64
E value
Match length
                   129
% identity
                   92
NCBI Description
                  26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >qi 1155334
                   (U43398) POTATP1 [Solanum tuberosum]
                   119303
Seq. No.
                   2602 1.R1010
Contig ID
5'-most EST
                  LIB3175-063-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q439434
```

```
BLAST score
                   205
E value
                   7.0e-16
Match length
                   158
% identity
                   36
NCBI Description
                   (L25941) integral nuclear envelope inner membrane protein
                   [Homo sapiens]
                   119304
Seq. No.
Contig ID
                   2605 1.R1010
5'-most EST
                   jC-alXLIB327436P2e07b1
Method
                   BLASTN
NCBI GI
                  q2582640
BLAST score
                   55
E value
                   2.0e-21
Match length
                   70
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                   119305
Seq. No.
Contig ID
                   2607 1.R1010
5'-most EST
                   LIB146-007-Q1-E1-A12
Seq. No.
                   119306
                   2612 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327406P4a02b2
                   BLASTX
Method
NCBI GI
                   g2407800
BLAST score
                   509
E value
                   3.0e-51
Match length
                   134
                   78
% identity
NCBI Description
                  (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
Seq. No.
                   119307
Contig ID
                   2621 1.R1010
5'-most EST
                  LIB3234-097-P1-K1-G5
Method
                   BLASTN
NCBI GI
                   q4512656
BLAST score
                   392
E value
                   0.0e + 00
Match length
                   966
                   94
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence; complete sequence
Seq. No.
                   119308
Contig ID
                   2621_2.R1010
5'-most EST
                  LIB24-061-Q1-E1-D10
Method
                  BLASTN
NCBI GI
                   q4512656
BLAST score
                   543
E value
                   0.0e + 00
Match length
                   948
% identity
                   96
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
```

```
Seq. No.
                  119309
Contig ID
                  2625 1.R1010
                  LIB23-055-Q1-E1-H8
5'-most EST
Method
                  BLASTX
                  g3056587
NCBI GI
BLAST score
                  1099
E value
                  1.0e-120
Match length
                  226
% identity
                  93
NCBI Description (AC004255) T1F9.8 [Arabidopsis thaliana]
Seq. No.
                  119310
                  2628 1.R1010
Contig ID
                  LIB3177-036-P1-K2-C1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2232354
BLAST score
                  217
E value
                  3.0e-17
Match length
                  96
                  44
% identity
NCBI Description
                  (AF006081) UDPG glucosyltransferase [Solanum berthaultii]
                  119311
Seq. No.
                  2631_1.R1010
Contig ID
                  LIB3175-052-P1-K1-H9
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2160147
BLAST score
                  514
                  3.0e-52
E value
Match length
                  135
% identity
                  77
                  (AC000375) EST gb ATTS3706 comes from this gene.
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  119312
                  2646 1.R1010
Contig ID
                  LIB3177-044-P1-K2-E5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g112742
BLAST score
                  640
                  5.0e-67
E value
Match length
                  159
                  79
% identity
                  NAPIN PRECURSOR (1.7S SEED STORAGE PROTEIN)
NCBI Description
                  >gi_81687_pir__S10018 napin (clone BngNAP1) - rape
                  >gi_1084352_pir__S52027 napin - rape
                  >gi 17833 emb CAA35580 (X17542) napin (AA 1-180) [Brassica
                  napus] >gi 468022 (U04945) napin [Brassica napus]
                  119313
Seq. No.
                  2647 1.R1010
Contig ID
5'-most EST
                  LIB3175-028-P1-K1-E11
                  119314
Seq. No.
                  2648 1.R1010
Contig ID
                  LIB146-007-Q1-E1-E4
5'-most EST
```

```
Method
                    BLASTN
 NCBI GI
                    q3985955
 BLAST score
                    126
                    1.0e-64
 E value
                    225
 Match length
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MTH16, complete sequence [Arabidopsis thaliana]
                    119315
 Seq. No.
 Contig ID
                    2655 1.R1010
 5'-most EST
                    jC-atXLIB327425P3f06b1
 Method
                    BLASTX
                    a2262167
 NCBI GI
                    1061
 BLAST score
                    1.0e-116
 E value
 Match length
                    227
 % identity
                    90
                    (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
 NCBI Description
                    thaliana]
                    119316
 Seq. No.
 Contig ID
                    2655_2.R1010
 5'-most EST
                    jC-atXLIB327401P3b07b2
 Method
                   BLASTX
                    g2262167
 NCBI GI
                    824
 BLAST score
                    1.0e-137
 E value
 Match length
                    252
 % identity
                    98
                    (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
 NCBI Description
                    thaliana]
                   119317
 Seq. No.
 Contig ID
                   2655 3.R1010
 5'-most EST
                    jC-atXLIB327432P3c05b1
 Method
                   BLASTX
 NCBI GI
                   q2262167
 BLAST score
                    690
 E value
                    1.0e-72
 Match length
                    149
                    91
 % identity
                    (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
 NCBI Description
                    thaliana]
                    119318
 Seq. No.
 Contig ID
                    2655 4.R1010
 5'-most EST
                    jC-alXLIB327436P4a05b1
                   BLASTX
 Method
 NCBI GI
                   q2262167
 BLAST score
                    703
 E value
                    4.0e-74
 Match length
                    164
                   85
% identity
 NCBI Description
                    (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
```

thaliana]

```
Seq. No.
                  119319
                  2655 5.R1010
Contig ID
5'-most EST
                  g498519
Method
                  BLASTX
NCBI GI
                  g3915865
BLAST score
                  524
E value
                  3.0e-53
Match length
                  124
% identity
                  84
NCBI Description 40S RIBOSOMAL PROTEIN S4
Seq. No.
                  119320
                  2655 6.R1010
Contig ID
                  q105\overline{3}263
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2262167
BLAST score
                  163
                  4.0e-19
E value
Match length
                  64
                  86
% identity
                  (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
                  thaliana]
                  119321
Seq. No.
Contig ID
                  2658 1.R1010
5'-most EST
                  LIB146-007-Q1-E1-F8
                  BLASTX
Method
NCBI GI
                  q464775
BLAST score
                  503
E value
                  6.0e-51
Match length
                  130
                  74
% identity
                  SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__S39492
NCBI Description
                  superoxide dismutase - Para rubber tree >gi 348137 (L11707)
                  superoxide dismutase (manganese) [Hevea brasiliensis]
                  119322
Seq. No.
Contig ID
                  2659 1.R1010
5'-most EST
                  LIB24-045-Q1-E1-C11
Method
                  BLASTX
                  g2961388
NCBI GI
BLAST score
                  258
E value
                  2.0e-22
Match length
                  128
% identity
                  48
NCBI Description
                  (AL022141) putative protein [Arabidopsis thaliana]
Seq. No.
                  119323
                  2663_1.R1010
Contig ID
                  LIB3175-042-P1-K1-C11
5'-most EST
                  BLASTX
Method
                  q4586263
NCBI GI
                  797
BLAST score
E value
                  3.0e-85
                  152
Match length
                  99
% identity
NCBI Description (ALO49640) putative protein [Arabidopsis thaliana]
```

Method

BLASTX

```
119324
Seq. No.
Contig ID
                   2666 1.R1010.
 5'-most EST
                   jC-atXP112C129M1T7d2
                   BLASTX
Method
NCBI GI
                   g4704766
BLAST score
                   756
                   3.0e-80
E value
Match length
                   195
% identity
                   44
NCBI Description
                   (AF131223) protein disulfide isomerase homolog; PDI
                   [Datisca glomerata]
                   119325
Seq. No.
                   2666 2.R1010
Contig ID
                   jC-atXLIB327422P3g08b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4704766
                   1420
BLAST score
                   0.0e+00
E value
Match length
                   475
                   48
% identity
NCBI Description
                   (AF131223) protein disulfide isomerase homolog; PDI
                   [Datisca glomerata]
                   119326
Seq. No.
Contig ID
                   2667 1.R1010
5'-most EST
                   LIB146-007-Q1-E1-G9
                   119327
Seq. No.
Contig ID
                   2675 1.R1010
                   LIB146-020-Q1-E1-C4
5'-most EST
Method
                   BLASTN
                   g4581161
NCBI GI
BLAST score
                   343
E value
                   0.0e + 00
Match length
                   455
% identity
                   18
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T20G20 genomic
                   sequence, complete sequence
                   119328
Seq. No.
Contig ID
                   2676 1.R1010
5'-most EST
                   LIB146-007-Q1-E1-H7
Method
                   BLASTN
                   g3757512
NCBI GI
BLAST score
                   214
E value
                   1.0e-117
Match length
                   317
% identity
                   98
                   Arabidopsis thaliana chromosome II BAC F12A24 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   119329
Seq. No.
Contig ID
                   2682 1.R1010
5'-most EST
                   jC-atXLIB327412P2f11b1
```

```
NCBI GI
                  q2829899
BLAST score
                  462
E value
                  1.0e-45
Match length
                  289
% identity
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                  gp_AJ001449_2465015 and major#latex protein,
                  gp X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                  119330
Contig ID
                  2682 2.R1010
5'-most EST
                  LIB3177-053-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q2829899
BLAST score
                  490
                  4.0e-49
E value
Match length
                  156
% identity
                  60
NCBI Description
                  (AC002311) similar to ripening-induced protein,
                  gp_AJ001449_2465015 and major#latex protein,
                  gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                  119331
                  2682_3.R1010
Contig ID
5'-most EST
                  g2413944
Method
                  BLASTX
NCBI GI
                  q2829899
BLAST score
                  183
E value
                  3.0e-13
Match length
                  83
% identity
                  46
NCBI Description
                  (AC002311) similar to ripening-induced protein,
                  gp_AJ001449_2465015 and major#latex protein,
                  gp_X91961_1107495 [Arabidopsis thaliana]
                  119332
Seq. No.
                  2682_5.R1010
Contig ID
                  g3450280
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2829899
BLAST score
                  206
                  5.0e-16
E value
Match length
                  74
% identity
                  54
NCBI Description
                  (AC002311) similar to ripening-induced protein,
                  gp_AJ001449_2465015 and major#latex protein,
                  gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                  119333
Contig ID
                  2682_6.R1010
                  jC-atXLIB327437P2b02a2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2829899
BLAST score
                  479
E value
                  1.0e-47
Match length
                  283
% identity
```

.

Method

BLASTX

```
NCBI Description
                  (AC002311) similar to ripening-induced protein,
                   gp AJ001449 2465015 and major#latex protein,
                   gp X91961 1107495 [Arabidopsis thaliana]
          42 45 ...
Seq. No.
                   119334
Contig ID
                   2682 7.R1010
5'-most EST
                   jC-atX35020Q1E1E05b1
                   BLASTX
Method
                   q2829899
NCBI GI
BLAST score
                   357
                   2.0e-33
E value
                   119
Match length
                   59
% identity
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp AJ001449 2465015 and major#latex protein,
                   gp X91961_1107495 [Arabidopsis thaliana]
                   119335
Seq. No.
                   2682 14.R1010
Contig ID
5'-most EST
                   jC-atXLIB327421P1b08b1
Method
                   BLASTX
NCBI GI
                   g2829899
BLAST score
                   240
                   5.0e-20
E value
Match length
                   101
% identity
                   50
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp AJ001449 2465015 and major#latex protein,
                   gp X91961 1107495 [Arabidopsis thaliana]
Seq. No.
                   119336
Contig ID
                   2687 1.R1010
                   LIB24-127-Q1-E1-C10
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2564051
BLAST score
                   175
                   2.0e-93
E value
Match length
                   605
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MWD9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   119337
                   2695 1.R1010
Contig ID
                   LIB24-082-Q1-E1-C5
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2252851
BLAST score
                   182
E value
                   2.0e-13
Match length
                   129
% identity
                   36
                   (AF013294) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   119338
                   2696 1.R1010
Contig ID
5'-most EST
                   LIB3168-045-P1-K1-E1
```

NCBI GI

E value

BLAST score

g2688830

1.0e-81

```
q118926
NCBI GI
BLAST score
                  594
E value
                  3.0e-66
Match length
                  272
% identity
                  50
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                  >gi 320600 pir E45509 desiccation-related protein (clone
                  PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
                  dessication-related protein [Craterostigma plantagineum]
                  >gi_227781_prf__1710351E abscisic acid responsive protein E
                  [Craterostigma plantagineum]
                  119339
Seq. No.
                  2698 1.R1010
Contig ID
5'-most EST
                  LIB146-008-Q1-E1-C12
Seq. No.
                  119340
                  2702 1.R1010
Contig ID
5'-most EST
                  g315605
Method
                  BLASTX
NCBI GI
                  g3688177
BLAST score
                  628
E value
                  9.0e-66
Match length
                  130
% identity
                  97
NCBI Description
                 (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                  119341
                  2705 1.R1010
Contig ID
                  jC-atXP68C217A5T7d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3738297
BLAST score
                  57
E value
                  3.0e-13
Match length
                  62
% identity
                  74
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                  119342
                  2711 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327411P1b09b1
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  60
E value
                  1.0e-24
Match length
                  72
                  97
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  119343
Seq. No.
                  2712 1.R1010
Contig ID
5'-most EST
                  LIB146-008-Q1-E1-D4
Method '
                  BLASTX
```

```
Match length
                   235
% identity
                   69
NCBI Description
                   (AF000952) putative sugar transporter [Prunus armeniaca]
                   119344
Seq. No.
                   2714 1.R1010
Contig ID
5'-most EST
                   9493\overline{3}61
Method
                   BLASTN
                   g4580512
NCBI GI
BLAST score
                   233
                   1.0e-128
E value
Match length
                   372
% identity
                   99
                  Arabidopsis thaliana scarecrow-like 1 (SCL1) mRNA, partial
NCBI Description
                   119345
Seq. No.
                   2719 1.R1010
Contig ID
                  LIB146-008-Q1-E1-E11
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4512651
BLAST score
                   296
                   9.0e-27
E value
Match length
                   129
% identity
                   46
                   (AC007048) putative tyrosine transaminase [Arabidopsis
NCBI Description
                   thaliana]
                   119346
Seq. No.
                   2720 1.R1010
Contig ID
5'-most EST
                   g2756845
Method
                   BLASTX
                   g2459446
NCBI GI
BLAST score
                   669
                   3.0e-70
E value
                   146
Match length
                   89
% identity
                   (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
                   119347
Seq. No.
                   2725 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327408P2h09b1
Seq. No.
                   119348
Contig ID
                   2726_1.R1010
5'-most EST
                  LIB146-008-Q1-E1-F1
Method
                   BLASTN
NCBI GI
                   g3510342
BLAST score
                   36
E value
                   9.0e-11
Match length
                  76
                  93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MGN6, complete sequence [Arabidopsis thaliana]
```

119349

Seq. No.

```
2730 1.R1010
Contig ID
                  LIB22-069-Q1-E1-F12
5'-most EST
Method
                  BLASTX
                  g2739385
NCBI GI
BLAST score
                  636
                  2.0e-66
E value
Match length
                  126
% identity
                  99
NCBI Description
                  (AC002505) putative beta-1,3-glucanase [Arabidopsis
                  thaliana]
Seq. No.
                  119350
                  2731 1.R1010
Contig ID
                  LIB24-048-Q1-E2-C2
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3426033
BLAST score
                  133
E value
                  2.0e-68
Match length
                  521
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F12C20 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  119351
Seq. No.
                  2732 1.R1010
Contig ID
5'-most EST
                  LIB146-008-Q1-E1-F8
Method
                  BLASTX
NCBI GI
                  g3327196
BLAST score
                  268
E value
                  2.0e-23
Match length
                  77
% identity
                  69
NCBI Description
                  (AB014591) KIAA0691 protein [Homo sapiens]
Seq. No.
                  119352
                  2735 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327426P2c04b1
Method
                  BLASTX
NCBI GI
                  q2924784
BLAST score
                  98
                  4.0e-03
E value
Match length
                  186
% identity
                  25
NCBI Description
                  (AC002334) similar to jasmonate inducible protein
                  [Arabidopsis thaliana]
Seq. No.
                  119353
                  2742 1.R1010
Contig ID
5'-most EST
                  LIB24-030-Q1-E1-G9
Method
                  BLASTX
NCBI GI
                  q4584255
BLAST score
                  225
                  3.0e-18
E value
Match length
                  72
% identity
                  60
NCBI Description (Y18471) SINA1p [Vitis vinifera]
```

NCBI GI

```
Seq. No.
                   119354
                   2746 1.R1010
 Contig ID
                   jC-atXLIB327425P3f10b1
 5'-most EST
Method
                   BLASTX
NCBI GI
                   g1175426
BLAST score
                   388
                   3.0e-48
E value
                   262
Match length
 % identity
                   42
                   PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06
NCBI Description
                   >gi 984214 emb CAA90819 (Z54140) probable ATP-dependent
                   RNA helicase [Schizosaccharomyces pombe]
                   119355
Seq. No.
                   2750 1.R1010
Contig ID
5'-most EST
                   LIB146-019-Q1-E1-D6
                   119356
Seq. No.
Contig ID
                   2753 1.R1010
5'-most EST
                   LIB146-009-Q1-E1-A1
Method
                   BLASTX
NCBI GI
                   q3297824
BLAST score
                   193
                   1.0e-14
,E value
Match length
                   80
% identity
                   51
NCBI Description
                   (AL031032) bZIP transcription factor-like protein
                   [Arabidopsis thaliana]
                   119357
Seq. No.
                   2754 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327409P1d05a1
Method
                   BLASTN
NCBI GI
                   q2290120
BLAST score
                   49
                   4.0e-18
E value
Match length
                   65
% identity
                   94
                   HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                   gene, partial cds
Seq. No.
                   119358
                   2754 2.R1010
Contig ID
 5'-most EST
                   jC-atXLIB327409P1d05b1
Method
                   BLASTX
NCBI GI
                   g4539459
BLAST score
                   961
E value
                   1.0e-104
Match length
                   313
 % identity
                   (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
                   119359
Seq. No.
                   2757 1.R1010
Contig ID
                   jC-atXLIB327416P4g07b1
 5'-most EST
                   BLASTX
Method
```

q2815493

```
BLAST score
                   1140
E value
                   1.0e-125
Match length
                   322
% identity
                   63
NCBI Description
                   SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
                   (CP-MI) >gi_1731988_emb_CAA70816_ (Y09603) serine
                   carboxypeptidase I, CP-MI [Hordeum vulgare]
Seq. No.
                   119360
                   2765 1.R1010
Contig ID
5'-most EST
                   g2758833
Method
                   BLASTN
NCBI GI
                   q2160132
BLAST score
                   567
E value
                   0.0e + 00
Match length
                   625
% identity
                   75
                   Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                   119361
Seq. No.
Contig ID
                   2767 1.R1010
5'-most EST
                   LIB146-009-Q1-E1-B11
Method
                   BLASTX
                   a3892050
NCBI GI · .
BLAST score
                   341
                   6.0e-32
E value
Match length
                   130
% identity
                   58
                   (AC002330) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   119362
Seq. No.
Contig ID
                   2774 1.R1010
                   jC-atXP37C157G15T7d2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4587541
BLAST score
                   612
                   2.0e-63
E value
Match length
                   124
% identity
                   (AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T44453, gb_T04815,
NCBI Description
                   gb T45993, gb R30138, gb AI099570 and gb T22281 come from
                   this gene. [Arabidopsis thaliana]
                   119363
Seq. No.
Contig ID
                   2774_2.R1010
5'-most EST
                   q276\overline{2}696
Method
                   BLASTX
NCBI GI
                   q4587542
BLAST score
                   1917
                   0.0e + 00
E value
Match length
                   380
% identity
                  -97
NCBI Description
                   (AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase
                   with GDSL-motif family. ESTs gb_T45815, gb_T45130 and
```

gb Z38046 come from this gene. [Arabidopsis thaliana]

```
119364
Seq. No.
                   2782 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327415P4a08b1
                  BLASTX
Method
                   g4680661
NCBI GI
BLAST score
                   147
                   5.0e-09
E value
                   100
Match length
                   25
% identity
                   (AF132945) CGI-11 protein [Homo sapiens]
NCBI Description
Seq. No.
                   119365
                   2782 2.R1010
Contig ID
                   jC-atXLIB327418P4a01b1
5'-most EST
Method
                   BLASTN
                   q2582640
NCBI GI
BLAST score
                   55
                   1.0e-21
E value
                   55
Match length
                   100
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   119366
Seq. No.
                   2782 4.R1010
Contig ID
5'-most EST
                   jC-atX24106Q1E1D10a1
                   119367
Seq. No.
                   2783 1.R1010
Contig ID
                  LIB3168-024-P1-K1-F7
5'-most EST
                   119368
Seq. No.
Contig ID
                   2783 2.R1010
5'-most EST
                   g276\overline{3}182
                   119369
Seq. No.
                   2784_1.R1010
Contig ID
                   LIB3<u>1</u>68-060-P1-K1-C5
5'-most EST
Method
                   BLASTX
                   g4263771
NCBI GI
BLAST score
                   326
E value
                   3.0e - 30
Match length
                   84
% identity
                   70
                   (AC006218) putative nonspecific lipid-transfer protein
NCBI Description
                   precursor [Arabidopsis thaliana]
                   >gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative
                   nonspecific lipid-transfer protein precursor [Arabidopsis
                   thaliana]
                   119370
Seq. No.
Contig ID
                   2786_1.R1010
                   jC-atXLIB327403P3d02b2
5'-most EST
Method
                   BLASTX
                   g1084415
NCBI GI
                   335
BLAST score
```

NCBI Description

```
E value
                  4.0e-31
Match length
                  111
                  60
% identity
NCBI Description
                  RNA-binding protein - Wood tobacco >gi 624925 dbj BAA05170
                  (D26182) RNA-binding glycine rich protein (RGP-2)
                  [Nicotiana sylvestris]
                  119371
Seq. No.
                  2789 1.R1010
Contig ID
5'-most EST
                  LIB25-029-Q1-E1-A8
Method
                  BLASTX
NCBI GI
                  q3548801
BLAST score
                  281
                  9.0e-25
E value
Match length
                  161
% identity
                  (AC005313) putative transmembrane protein [Arabidopsis
NCBI Description
                  thaliana] >gi 4335768 gb AAD17445 (AC006284) putative
                  integral membrane protein [Arabidopsis thaliana]
                  119372
Seq. No.
                  2790 1.R1010
Contig ID
                  jC-atXLIB327420P4d11b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2760168
BLAST score
                  203
                  1.0e-110
E value
Match length
                  326
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MEE6, complete sequence [Arabidopsis thaliana]
                  119373
Seq. No.
                  2794 1.R1010
Contig ID
5'-most EST
                  LIB22-013-Q1-E1-G2
Method
                  BLASTX
                  q266731
NCBI GI
                  304
BLAST score
E value
                  1.0e-58
                  171
Match length
% identity
                  PHENYLALANINE AMMONIA-LYASE 1 >gi_282927_pir__S25303
NCBI Description
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - garden pea
                  >gi_217980_dbj_BAA00885_ (D10001) phenylalanine
                  ammonia-lyase [Pisum sativum] >gi 217982 dbj_BAA00886_
                  (D10002) phenylalanine ammonia-lyase [Pisum sativum]
Seq. No.
                  119374
                  2797 1.R1010
Contig ID
5'-most EST
                  LIB146-009-Q1-E1-E2
                  BLASTN
Method
                  q2182287
NCBI GI
BLAST score
                  491
                  0.0e+00
E value
Match length
                  512
                  99
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T7N9,
```

Seq. No.

119379

Seq. No. 119375 Contig ID 2798 1.R1010 5'-most EST jC-atXLIB327419P4a03b1 Method BLASTX NCBI GI g549975 BLAST score 748 E value 4.0e-84 Match length 165 % identity 99 NCBI Description (U12858) nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707 [Arabidopsis thaliana] 119376 Seq. No. 2798 2.R1010 Contig ID 5'-most EST LIB146-009-Q1-E1-E4 BLASTN Method NCBI GI q1946354 BLAST score 50 E value 5.0e-19 Match length 110 % identity 86 Arabidopsis thaliana chromosome II BAC T06B20 genomic NCBI Description sequence, complete sequence Seq. No. 119377 2802 1.R1010 Contig ID 5'-most EST LIB146-010-Q1-E1-H5 BLASTX Method NCBI GI q112743 BLAST score 812 E value 5.0e-87 Match length 166 % identity 91 NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor -Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1 (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana] Seq. No. 119378 Contig ID 2803 1.R1010 5'-most EST LIB146-009-Q1-E1-F1 Method BLASTN NCBI GI q4006885 BLAST score 87 E value 7.0e-41Match length 137 91 % identity Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig NCBI Description fragment No

complete sequence [Arabidopsis thaliana]

```
Contig ID
                  2803 2.R1010
5'-most EST
                  LIB24-065-01-E1-G8
Method
                  BLASTX
NCBI GI
                  g4507703
BLAST score
                  194
E value
                  1.0e-14
                  141
Match length
                  37
% identity
                  tumor suppressing subtransferable candidate 1
NCBI Description
                  >gi_2655037_gb_AAC51911_ (AF019952) tumor suppressing STF
                  cDNA 1 [Homo sapiens]
                  119380
Seq. No.
                  2805 1.R1010
Contig ID
                  LIB23-026-01-E1-F11
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3860274
                  382
BLAST score
                  2.0e-42
E value
                  164
Match length
% identity
                  64
NCBI Description
                  (AC005824) unknown protein [Arabidopsis thaliana]
                  >gi 4314397 gb AAD15607 (AC006232) putative zinc finger
                  protein [Arabidopsis thaliana]
                  119381
Seq. No.
                  2812_1.R1010
Contig ID
5'-most EST
                  LIB25-110-Q1-E1-B6
                  BLASTX
Method
                  q4741940
NCBI GI
                  1237
BLAST score
                  1.0e-136
E value
Match length
                  226
                  100
% identity
NCBI Description
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
Seq. No.
                  119382
                  2812_3.R1010
Contig ID
5'-most EST
                  q933641
                  BLASTX
Method
NCBI GI
                  q4741940
BLAST score
                  225
E value
                  4.0e-31
Match length
                  87
                  90
% identity
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119383
Contig ID
                  2812 4.R1010
                  jC-atXLIB327431P4d03a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4741940
BLAST score
                  722
E value
                  2.0e-76
Match length
                  175
% identity
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
```

% identity

```
Seq. No.
                  119384
Contig ID
                  2813 1.R1010
5'-most EST
                  LIB146-009-Q1-E1-F9
Method
                  BLASTX
NCBI GI
                  g1731146
BLAST score
                  285
E value
                   1.0e-25
Match length
                   97
% identity
                  55
NCBI Description
                  HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III
                  >gi_3881615_emb_CAA87435_ (Z47358) similar to YJU2 protein
                   [Caenorhabditis elegans]
                  119385
Seq. No.
                  2815 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327413P4g08a1
                  BLASTN
Method
NCBI GI
                  q3449317°
BLAST score
                  281
E value
                  1.0e-156
Match length
                  475
% identity
                  95
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MKM21, complete sequence [Arabidopsis thaliana]
                  119386
Seq. No.
Contig ID
                  2815 2.R1010
                  jC-atXLIB327405P3b11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3915826
BLAST score
                  701
E value
                  9.0e-74
Match length
                  184
% identity
                  70
NCBI Description
                  60S RIBOSOMAL PROTEIN L5
                  119387
Seq. No.
Contig ID
                  2815 3.R1010
5'-most EST
                  iC-atXLIB327405P1e11b2
Method
                  BLASTX
NCBI GI
                  q3915826
BLAST score
                  879
E value
                  2.0e-94
Match length
                  293
                  62
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L5
                  119388
Seq. No.
Contig ID
                  2815 4.R1010
5'-most EST
                  jC-atXLIB327413P4g08b1
Method
                  BLASTX
NCBI GI
                  q3915826
BLAST score
                  650
E value
                  5.0e-68
Match length
                  164
```

```
NCBI Description 60S RIBOSOMAL PROTEIN L5
                   119389
Seq. No.
                   2815 5.R1010
Contig ID
                   jC-atXP109C219K7T7s1
5'-most EST
Method
                   BLASTX
                   q3915824
NCBI GI
                   355
BLAST score
                   2.0e-33
E value
Match length
                   76
% identity
                   91
NCBI Description
                  [Segment 2 of 2] 60S RIBOSOMAL PROTEIN L5
                   119390
Seq. No.
                   2815_6.R1010
Contig ID
                  LIB22-088-Q1-E1-E1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g542157
BLAST score
                   329
E value
                   1.0e-30
Match length
                   102
                   68
% identity
NCBI Description
                  ribosomal 5S RNA-binding protein - Rice
                   119391
Seq. No.
                   2829 1.R1010
Contig ID
5'-most EST
                  LIB25-074-Q1-E1-H8
Method
                   BLASTX
                   g3005931
NCBI GI
BLAST score
                   771
                   5.0e-82
E value
Match length
                   247
                   42
% identity
NCBI Description
                  (AJ005016) ABC transporter [Homo sapiens]
                   119392
Seq. No.
Contig ID
                   2830_1.R1010
5'-most EST
                  LIB3234-016-P1-K1-F6
Method
                  BLASTX
                   g1929056
NCBI GI
BLAST score
                   474
                   1.0e-47
E value
Match length
                   127
                  76
% identity
                  (Y12090) putative 3,4-dihydroxy-2-butanone kinase
NCBI Description
                   [Lycopersicon esculentum]
                  119393
Seq. No.
Contig ID
                   2834_1.R1010
5'-most EST
                  LIB24-088-Q1-E1-B1
Method
                  BLASTN
NCBI GI
                  q3292807
BLAST score
                   472
                  0.0e + 00
E value
Match length
                   646
% identity
                  100
```

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19

Method

BLASTX

(ESSAII project)

Seq. No. 119394 Contig ID 2838 1.R1010 5'-most EST LIB3175-065-P1-K1-C9 Method BLASTN NCBI GI q4006885 BLAST score 327 E value 0.0e + 00Match length 508 % identity 99 NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No Seq. No. 119395 Contig ID 2842 1.R1010 5'-most EST $LIB1\overline{4}6-010-Q1-E1-A4$ 119396 Seq. No. 2844 1.R1010 Contig ID 5'-most EST jC-atXLIB327424P1h03a1 Method BLASTN g2462264 NCBI GI BLAST score 36 E value 1.0e-10 Match length 44 95 % identity NCBI Description Cucumis sativus mRNA for patatin-like protein, partial 119397 Seq. No. Contig ID 2848_1.R1010 5'-most EST LIB146-018-Q1-E1-F6 Method BLASTX NCBI GI q3687228 BLAST score 841 E value 1.0e-90 Match length 169 % identity 98 NCBI Description (AC005169) putative malate dehydrogenase [Arabidopsis tha:liana] 119398 Seq. No. Contig ID 2852 1.R1010 $jC-a\overline{1}XLIB327435P3e06b1$ 5'-most EST BLASTN Method NCBI GI q4191771 BLAST score 327 E value 0.0e + 00Match length 736 % identity 96 Arabidopsis thaliana chromosome II BAC F3P11 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 119399 Seq. No. 2852 2.R1010 Contig ID 5'-most EST jC-atXLIB327419P4c02b1

```
NCBI GI
                  q4191778
BLAST score
                  1156
E value
                  1.0e-127
Match length
                  261
                  87
% identity
                  (AC005917) putative nucleosome assembly protein I
NCBI Description
                  [Arabidopsis thaliana]
                  119400
Seq. No.
                  2854 1.R1010
Contig ID
                  jC-atXLIB327420P3b06b1
5'-most EST
                  BLASTX
Method
                  q4539292
NCBI GI
BLAST score
                  457
                  2.0e-45
E value
                  98
Match length
                  89
% identity
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  119401
                  2854 2.R1010
Contig ID
                  jC-atXP101CE2D4T7055d1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4539292
BLAST score
                  223
                  6.0e-18
E value
Match length
                  104
                  40
% identity
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  119402
                  2857 1.R1010
Contig ID
                  LIB146-010-Q1-E1-B9
5'-most EST
                  BLASTN
Method
NCBI GI
                  q1296310
                  191
BLAST score
                  1.0e-103
E value
                  492
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome I cosmid g17311 DNA
NCBI Description
                  119403
Seq. No.
                  2858 1.R1010
Contig ID
                  LIB23-026-Q1-E1-C9
5'-most EST
                  119404
Seq. No.
                  2869 1.R1010
Contig ID
                  LIB24-099-Q1-E1-A11
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1076660
BLAST score
                  155
                  8.0e-22
E value
Match length
                  150
% identity
                  42
                  D13F(MYBST1) protein - potato >gi 786426_bbs_159122
NCBI Description
```

Method NCBI GI

E value

BLAST score

```
(S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]
```

```
119405
Seq. No.
Contig ID
                   2873 1.R1010
                  LIB1\overline{4}6-010-Q1-E1-D4
5'-most EST .
Method
                   BLASTN
                   g4587641
NCBI GI
BLAST score
                   291
E value
                   1.0e-162
Match length
                   382
                   100
% identity
                   Arabidopsis thaliana chromosome I BAC F20D21 genomic
NCBI Description
                   sequence, complete sequence
                   119406
Seq. No.
                   2875 1.R1010
Contig ID
5'-most EST
                   LIB146-010-Q1-E1-D6
Method
                   BLASTX
                   g2832620
NCBI GI
BLAST score
                   325
E value
                   3.0e-30
Match length
                   133
.% identity
                   48
NCBI Description
                  (AL021711) hypothetical protein [Arabidopsis thaliana]
                   119407
Seq. No.
Contig ID
                   2881 1.R1010
                   g2759873
5'-most EST
Method
                   BLASTX
                   g3413705
NCBI GI
BLAST score
                   650
                   5.0e-68
E value
Match length
                   156
% identity
                   87
                   (AC004747) putative glycine dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   119408
Seq. No.
                   2881 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327408P4b08b1
Method
                   BLASTX
NCBI GI
                   g3688182
BLAST score
                   1491
                   1.0e-166
E value
                   295
Match length
% identity
                   95
NCBI Description
                   (AL031804) P-Protein - like protein [Arabidopsis thaliana]
Seq. No.
                   119409
                   2882 1.R1010
Contig ID
5'-most EST
                   LIB146-010-Q1-E1-E5
```

BLASTX

701

g3201554

5.0e-74

5'-most EST

```
Match length
                   173
% identity
                   75
                   (AJ006501) beta-D-glucosidase [Tropaeolum majus]
NCBI Description
Seq. No.
                   119410
                   2883 1.R1010
Contig ID
                  jC-atXP22C114P3T7035a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1710780
BLAST score
                   694
E value
                   6.0e-73
Match length
                   170
% identity
                   78
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
NCBI Description
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                  anserina]
                  119411
Seq. No.
                   2883 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327411P1g12b1
                  BLASTX
Method
NCBI GI
                  q1710780
BLAST score
                   504
                   6.0e-51
E value
Match length
                   131
                   75
% identity
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
NCBI Description
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                  anserina]
Seq. No.
                   119412
                   2883_3.R1010
Contig ID
                  jC-atXLIB327432P3d08b1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q2582640
BLAST score
                   64
E value
                   2.0e-27
Match length
                  76
% identity
                   96
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
Seq. No.
                   119413
Contig ID
                   2886 1.R1010
5'-most EST
                  LIB146-010-Q1-E1-F1
Method
                  BLASTN
NCBI GI
                  q3789706
BLAST score
                   126
E value
                   2.0e-64
Match length
                   456
                  99
% identity
                  Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  119414
Seq. No.
                  2907 1.R1010
Contig ID
```

LIB146-010-Q1-E1-H6

```
Method
                   BLASTX
                   g4038491
NCBI GI
                   299
BLAST score
E value
                   7.0e-27
Match length
                   202
                   35
% identity
                   (AJ131705) poly(ADP-ribose) polymerase [Arabidopsis
NCBI Description
                   thaliana]
                   119415
Seq. No.
                   .2913 1.R1010
Contig ID
                   LIB3234-016-P1-K1-C3
5'-most EST
                   BLASTX
Method
                   q2583125
NCBI GI
BLAST score
                   581
E value
                   4.0e-60
Match length
                   128
% identity
                   86
                   (AC002387) putative transketolase precursor [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   119416
                   2915 1.R1010
Contig ID
                   jC-atXLIB327430P4d08b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3869066
BLAST score
                   370
                   0.0e + 00
E value
Match length .
                   664
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBM17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   119417
                   2920 1.R1010
Contig ID
                   LIB3\overline{2}34-092-P1-K1-F6
5'-most EST
Method
                   BLASTN
NCBI GI.
                   g2760173
BLAST score
                   450
                   0.0e + 00
E value
                   597
Match length
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYH19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   119418
                   2921 1.R1010
Contig ID
5'-most EST
                   jC-atXP20C113G21T7d2
Method
                   BLASTX
NCBI GI
                   g2078350
BLAST score
                   625
E value
                   4.0e-65
Match length
                   169
% identity
                   74
NCBI Description
                  (U95923) transaldolase [Solanum tuberosum]
```

119419

Seq. No.

NCBI GI

```
2922 1.R1010
Contig ID
                  LIB22-020-01-E1-C5
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4510360
BLAST score
                  581
E value
                  0.0e + 00
Match length
                  670
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
                  sequence, complete sequence
Seq. No.
                  119420
                  2922_2.R1010
Contig ID
                  LIB22-022-01-E1-C7
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4510360
BLAST score
                  236
                  1.0e-130
E value
                  351
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  119421
                  2924 1.R1010
Contig ID
                  jC-atXLIB327426P2f10b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3176668
BLAST score
                  794
                  1.0e-84
E value
                  166
Match length
                  93
% identity
NCBI Description
                  (AC004393) Similar to ribosomal protein L17 gb X62724 from
                  Hordeum vulgare. ESTs gb Z34728, gb F19974, gb T75677 and
                  gb Z33937 come from this gene. [Arabidopsis thaliana]
                  119422
Seq. No.
                  2934 1.R1010
Contig ID
                  jC-atXLIB327421P4c02b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2264311
BLAST score
                  463
E value
                  0.0e + 00
Match length
                  471
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MLN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  119423
                  2936 2.R1010
Contig ID
5'-most EST
                  LIB3168-075-P1-K1-D7
Seq. No.
                  119424
Contig ID
                  2938 1.R1010
5'-most EST
                  jC-atXLIB327418P1c05b1
Method
                  BLASTX
```

q4454472

Method

```
694
BLAST score
E value
                   4.0e-73
Match length
                  162
                  81
% identity
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
                  119425
Seq. No.
Contig ID
                  2947 1.R1010
5'-most EST
                  LIB146-027-Q1-K1-E4
                  BLASTX
Method
NCBI GI
                  q4432839
BLAST score
                  1288
                  1.0e-142
E value
Match length
                  392
                  69
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                  119426
Seq. No.
Contig ID
                  2949 1.R1010
5'-most EST
                  LIB3168-079-P1-K1-B5
                  BLASTX
Method
                  g1800307
NCBI GI
BLAST score
                  360
E value
                  6.0e-34
                ... 244
Match length
                  27
% identity
NCBI Description (U83883) p105 coactivator [Rattus norvegicus]
                  119427
Seq. No.
                  2950 1.R1010
Contig ID
                  LIB3175-037-P1-K1-A12
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4249382
BLAST score
                  622
                  8.0e-65
E value
Match length
                  161
                  73
% identity
                  (ACO05966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
                  119428
Seq. No.
Contig ID
                  2951 1.R1010
5'-most EST
                  LIB3234-049-P1-K1-F12
                  BLASTN
Method
NCBI GI
                  q2570223
BLAST score
                  311
                  1.0e-175
E value
                  392
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  119429
Seq. No.
Contig ID
                  2952 1.R1010
5'-most EST
```

13060

LIB3234-058-P1-K1-D1

BLASTX

Seq. No.

```
NCBI GI
                   q4510397
BLAST score
                   1400
                   1.0e-156
E value
Match length
                   293
% identity
                   91
                   (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
NCBI Description
                   119430
Seq. No.
                   2952 2.R1010
Contig ID
                  LIB3\overline{2}34-086-Q1-K1-E2
5'-most EST
Method
                   BLASTX
                   g4510397
NCBI GI
                   648
BLAST score
                   8.0e-68
E value
                   208
Match length
% identity
                   68
                   (ACO06587) putative preproMP27-MP32 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   119431
                   2956 1.R1010
Contig ID
5'-most EST
                  LIB3168-041-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g3157930
BLAST score
                   663
E value
                   1.0e-69
Match length
                   148
% identity
                   85
NCBI Description
                   (AC002131) Strong similarity to
                   amino-cyclopropane-carboxylic acid oxidase gb L27664 from
                   Brassica napus. ESTs gb Z48548 and gb Z48549 come from
                   this gene. [Arabidopsis thaliana]
                   119432
Seq. No.
                   2964 1.R1010
Contig ID
                  LIB23-056-Q1-E1-B12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3451071
BLAST score
                   635
                   2.0e-66
E value
                   125
Match length
                   100
% identity
                   (AL031326) beta adaptin - like protein [Arabidopsis
NCBI Description
                   thaliana]
                  119433
Seq. No.
                   2965 1.R1010
Contig ID
                   LIB146-018-Q1-E1-F11
5'-most EST
                  BLASTX
Method
                   q2706455
NCBI GI
BLAST score
                   425
                   1.0e-41
E value
                  156
Match length
                   47
% identity
                   (AL021046) probable involvement in transcription initiation
NCBI Description
                   [Schizosaccharomyces pombe]
```

```
2967 1.R1010
Contig ID
5'-most EST
                     g958046
Method
                     BLASTN
NCBI GI
                     g4589418
                     297
BLAST score
                     1.0e-166
E value
Match length
                     377
                     96
% identity
                    Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                     K21G20, complete sequence
                     119435
Seq. No.
                     2967 2.R1010
Contig ID
5'-most EST
                     g473289
                     BLASTN
Method
                     g4589418
NCBI GI
                     259
BLAST score
                     1.0e-144
E value
Match length
                     370
                     95
% identity
NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                    K21G20, complete sequence
                     119436
Seq. No.
                     2970 1.R1010
Contig ID
5'-most EST
                    LIB3177-042-P1-K2-A6
Method
                     BLASTX
NCBI GI
                     g114532
BLAST score
                     629
                     2.0e-65
E value
Match length
                     146
% identity
                     87
                    ATP SYNTHASE ALPHA CHAIN >gi_67824_pir_PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain -
NCBI Description
                     common tobacco chloroplast >gi 11769 emb CAA23471 (V00162)
                     alpha subunit of ATPase [Nicotiana tabacum]
                    >gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit
[Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha
                     [Nicotiana tabacum]
                     119437
Seq. No.
                    2970_3.R1010
Contig ID
                     q105\overline{3}463
5'-most EST
                    BLASTX
Method
NCBI GI
                     g114532
BLAST score
                     474
                     3.0e-47
E value
Match length
                    113
% identity
                    85
                    ATP SYNTHASE ALPHA CHAIN >gi 67824 pir PWNTA
NCBI Description
                    H+-transporting ATP synthase (EC 3.6.1.34) alpha chain -
                    common tobacco chloroplast >gi 11769 emb CAA23471 (V00162)
                    alpha subunit of ATPase [Nicotiana tabacum]
                    >gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit
[Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha
                     [Nicotiana tabacum]
```

```
119438
 Seq. No.
                   2971 1.R1010
 Contig ID
 5'-most EST
                   jC-atXLIB327408P1b12a1
 Method
                   BLASTX
 NCBI GI
                   g534982
 BLAST score
                   628
                   3.0e-87
 E value
                   223
 Match length
 % identity
                   69
                   (X75898) phosphoglucomutase [Spinacia oleracea]
 NCBI Description
                   119439
 Seq. No.
                   2971 3.R1010
 Contig ID
                   jC-atXP67C213O16T7032a1
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   g534982
                   194
 BLAST score
                   1.0e-14
 E value
                   55
 Match length
% identity
                   60
 NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]
                   119440
 Seq. No.
                   2973 1.R1010
 Contig ID
 5'-most EST
                   g3719110
 Method
                   BLASTN
 NCBI GI
                   g2462264
 BLAST score
                   50
                   2.0e-18
 E value
 Match length
                   54
                   98
 % identity
 NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
 Seq. No.
                   119441
                   2977 1.R1010
 Contig ID
                   LIB146-011-Q1-E1-H3
 5'-most EST
 Method
                   BLASTN
 NCBI GI
                   g4559319
 BLAST score
                   293
                    1.0e-164
 E value
                   300
 Match length
 % identity
                    69
                   Arabidopsis thaliana chromosome II BAC F14N22 genomic
 NCBI Description
                   sequence, complete sequence
 Seq. No.
                   119442
                   2978 1.R1010
 Contig ID
 5'-most EST
                   jC-atXLIB327432P3g09b1
                   119443
 Seq. No.
                   2985 1.R1010
 Contig ID
                   LIB146-012-Q1-E1-A6
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   g2160151
 BLAST score
                   1596
                   1.0e-178
 E value
```

354

Match length

5'-most EST

BLAST score

Method

NCBI GI

```
88
% identity
NCBI Description
                   (AC000375) Strong similarity to Brassica aspartic protease
                   (gb X77260). [Arabidopsis thaliana]
                   119444
Seq. No.
                   2987 1.R1010
Contig ID
                  LIB3234-081-Q1-K1-G4
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4581161
                   147
BLAST score
                  7.0e-77
E value
Match length
                   499
                   27
% identity
                  Arabidopsis thaliana chromosome II BAC T20G20 genomic
NCBI Description
                   sequence, complete sequence
                   119445
Seq. No.
                   2988 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327417P4a04b1
Method
                   BLASTN
NCBI GI
                  g3193282
BLAST score
                   190
E value
                   1.0e-102
Match length
                   488
% identity
                   76
NCBI Description Arabidopsis thaliana BAC T14P8
Seq. No.
                   119446
                  2992 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327420P1d04b1
Method
                   BLASTX
NCBI GI
                   g4102980
BLAST score
                   140
E value
                   5.0e-08
Match length
                   227
% identity
NCBI Description
                   (AF019082) virulent strain associated lipoprotein [Borrelia
                  burgdorferi}
Seq. No.
                   119447
                   2992 2.R1010
Contig ID
                   jC-atXP5C90E23T7d1
5'-most EST
Method
                  BLASTN
                  g3869065
NCBI GI
                   351
BLAST score
E value
                  0.0e + 00
Match length
                   440
% identity
                   95
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K24M7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  119448
                  2996 1.R1010
Contig ID
```

13064

LIB146-012-Q1-E1-C11

BLASTX g2244754

% identity

```
E value
                   2.0e-36
Match length
                   94
                   77
% identity
NCBI Description
                   (Z97335) heat shock transcription factor homolog
                   [Arabidopsis thaliana]
Seq. No.
                   119449
Contig ID
                   3034 1.R1010
5'-most EST
                   q276\overline{3}236
                   119450
Seq. No.
                   3038 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327417P2c12b1
Method
                   BLASTX
                   g4220446
NCBI GI
BLAST score
                   1200
                   1.0e-132
E value
Match length
                   256
% identity
                   93
                   (AC006216) Strong similarity to gi 2062155 T02004.2
NCBI Description
                  mitochondrial processing peptidase alpha subunit precusor
                   isolog from Arabidopsis thaliana BAC gb AC001645. ESTs
                   gb Z18504 and gb AA395715 come from this gene. [Arabidopsis
                   thaliana]
                   119451
Seq. No.
                   3041 1.R1010
Contig ID
                   LIB3234-056-P1-K1-A6
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4757401
BLAST score
                   137
                   6.0e-71
E value
Match length
                   421
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGH6, complete sequence
                   119452
Seq. No.
                   3043 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327417P1b03b1
Method
                   BLASTX
NCBI GI
                   q4567312
BLAST score
                   161
                   2.0e-10
E value
                   95
Match length
% identity
                   (AC005956) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   119453
Seq. No.
                   3056 1.R1010
Contig ID
5'-most EST
                  LIB146-013-Q1-E1-B12
Method
                   BLASTN
                   g4581084
NCBI GI
BLAST score
                   780
E value
                   0.0e + 00
                   792
Match length
```

% identity

```
NCBI Description Arabidopsis thaliana chromosome I BAC T30F21 genomic
                   sequence, complete sequence
Seq. No.
                   119454
                   3058 1.R1010
Contig ID
5'-most EST
                   LIB3176-064-P1-K1-H7
Method
                   BLASTN
                   g2894591
NCBI GI
BLAST score
                   412
E value
                   0.0e + 00
                   412
Match length
                   100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21
NCBI Description
                   (ESSAII project)
                   119455
Seq. No.
                   3059 1.R1010
Contig ID
5'-most EST
                   LIB3234-037-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g1619602
BLAST score
                   803
                   1.0e-85
E value
                   237
Match length
                   67
% identity
                  (Y08726) MtN3 [Medicago truncatula]
NCBI Description
Seq. No.
                   119456
                   3062 1.R1010
Contig ID
                  LIB1\overline{4}6-022-Q1-E1-F12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4056502
BLAST score
                   1031
E value
                   1.0e-112
Match length
                   207
                   100
% identity
NCBI Description
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
                  119457
Seq. No.
                   3062 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327419P3d07b2
Method
                  BLASTX
NCBI GI
                   g4056502
BLAST score
                   992
E value
                   1.0e-108
Match length
                   207
% identity
                   95
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
                  119458
Seq. No.
                  3067 1.R1010
Contig ID
                   q506\overline{5}99
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4454022
BLAST score
                   264
E value
                  1.0e-147
Match length
                  370
```

NCBI GI

```
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
                   (ESSAII project)
                   119459
Seq. No.
                   3068 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327412P3d02a1
                   BLASTX
Method
NCBI GI
                   q4335739
                   342
BLAST score
E value
                   1.0e-31
Match length
                   108
% identity
                   56
                  (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   119460
Seq. No.
                   3075 1.R1010
Contig ID
                   g1520865
5'-most EST
Method
                   BLASTX
                   q131360
NCBI GI
BLAST score
                   241
E value
                   6.0e-20
Match length
                   61
% identity
                   82
                   PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR
NCBI Description
                   >gi 81727 pir S02115 photosystem II protein psbK precursor
                   - white mustard chloroplast >gi_12209_emb_CAA31909_
(X13558) K preprotein (AA -24 to 37) [Sinapis alba]
                   119461
Seq. No.
                   3087 1.R1010
Contig ID
5'-most EST
                   jC-atXP70C220H9T7d1
Method
                   BLASTX
NCBI GI
                   q2244910
BLAST score
                   288
E value
                   2.0e-25
Match length
                   208
% identity
                   40
NCBI Description
                  (Z97339) unnamed protein product [Arabidopsis thaliana]
                   119462
Seq. No.
                   3089 1.R1010
Contig ID
5'-most EST
                   LIB3168-077-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q4325282
BLAST score
                   774
E value
                   2.0e-82
Match length
                   173
% identity
                   87
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                   >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
Seq. No.
                   119463
                   3091 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327413P1a04b1
                   BLASTX
Method
```

q4455342

```
820
BLAST score
E value
                    5.0e-88
Match length
                    160
% identity
                    100
                    (AL035522) O-methyltransferase-like protein [Arabidopsis
NCBI Description
                    thaliana]
                    119464
Seq. No.
                    3100 1.R1010
Contig ID
                    LIB3176-117-P2-K1-F12
5'-most EST
                    BLASTX
Method
                    q4490737
NCBI GI
BLAST score
                    1412
                    1.0e-157
E value
Match length
                    296
% identity
                    94
                    (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                    119465
Seq. No.
Contig ID
                    3101 1.R1010
5'-most EST
                    LIB22-039-Q1-E1-D3
                    119466
Seq. No.
                    3106 1.R1010
Contig ID
                    jC-atXLIB327429P1e06a2
5'-most EST
Method
                    BLASTN
NCBI GI
                    g2924257
BLAST score
                    78
                    2.0e-35
E value
                    78
Match length
% identity
                    100
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                    119467
                    3106 2.R1010
Contig ID
5'-most EST
                    LIB146-025-Q1-E1-F12
Method
                    BLASTX
NCBI .GI
                    q133960
BLAST score
                    888
                    2.0e-95
E value
Match length
                    200
% identity
                    89
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi 70876 pir R3NT4
NCBI Description
                    ribosomal protein S4 - common tobacco chloroplast >gi_11834_emb_CAA77354_ (Z00044) ribosomal protein S4 [Nicotiana tabacum] >gi_225202_prf__1211235AG ribosomal
                    protein S4 [Nicotiana tabacum]
                    119468
Seq. No.
                    3118 1.R1010
Contig ID
                    LIB146-014-Q1-E1-A8
5'-most EST
                    BLASTN
Method
NCBI GI
                    g3402745
BLAST score
                    273
                    1.0e-152
E value
Match length
                    559
                    94
% identity
```

NCBI GI

```
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
                  (ESSAII project)
                  119469
Seq. No.
                  3119 1.R1010
Contig ID
                  LIB3234-098-P1-K1-G2
5'-most EST
                  BLASTX
Method
                  g267055
NCBI GI
BLAST score
                  357
                  6.0e-34
E value
Match length
                  78
% identity
                  95
                  SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
NCBI Description
                  >qi 66572 pir YUMU sucrose synthase (EC 2.4.1.13) -
                  Arabidopsis thaliana >gi 16526 emb CAA43303 (X60987)
                  sucrose synthase [Arabidopsis thaliana]
                  119470
Seq. No.
                  3121_1.R1010
Contig ID
                  LIB25-088-Q1-E1-C9
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2459429
BLAST score
                  1061
                  1.0e-116
E value
                  202
Match length
                  100
% identity
                 (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                  119471
Seq. No.
                  3121 2.R1010
Contig ID
                  LIB3176-027-P1-K1-B3
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2459429
BLAST score
                  557
E value
                  2.0e-57
Match length
                  107
                  100
% identity
                 (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                  119472
Seq. No.
                  3130 1.R1010
Contig ID
5'-most EST
                  LIB3168-073-P1-K1-E11
                  BLASTX
Method
NCBI GI
                  q4063751
BLAST score
                  409
                  1.0e-39
E value
                  278
Match length
% identity
                  34
                  (AC005851) putative white protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4510409 gb AAD21495.1_ (AC006929) putative white
                  protein [Arabidopsis thaliana]
                  119473
Seq. No.
                  3131 1.R1010
Contig ID
5'-most EST
                  LIB146-014-Q1-E1-C12
Method
                  BLASTX
```

q4582470

```
BLAST score
                  460
                  4.0e-56
E value
Match length
                  131
% identity
                  40
NCBI Description (AC007071) unknown protein [Arabidopsis thaliana]
Seq. No.
                 119474
                  3137 1.R1010
Contig ID
                  jC-atXP101CE2D5T7063d1
5'-most EST
                  BLASTN
Method
                  g3413510
NCBI GI
                  43
BLAST score
                  1.0e-14
E value
Match length
                  43
                  100
% identity
                  Spinacia oleracea mRNA (nuclear-encoded) for chloroplast
NCBI Description
                  glucose-6-phosphate isomerase
                  119475
Seq. No.
Contig ID
                  3137 2.R1010
5'-most EST
                  g2757239
                  119476
Seq. No.
                  3138 1.R1010
Contig ID
                  LIB146-014-Q1-E1-D10
5'-most EST
                  BLASTN
Method
                  g3805755
NCBI GI
                  330
BLAST score
                  0.0e+00
E value
                  386
Match length
                  96
% identity
                  Arabidopsis thaliana chromosome II BAC T25N22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  119477
Seq. No.
                  3143 1.R1010
Contiq ID
                  jC-atXLIB327407P1h10b2
5'-most EST
Method
                  BLASTX
                  g729479
NCBI GI
                  543
BLAST score
                  2.0e-55
E value
Match length
                  151
                  70
% identity
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi 551131
NCBI Description
                  (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]
                  119478
Seq. No.
                  3145 1.R1010 ·
Contig ID
                  jC-atXLIB327410P1h05b1
5'-most EST
                  BLASTX
Method
                  q4006941
NCBI GI
BLAST score
                  234
                  4.0e-19
E value
Match length
                  60
                  75
% identity
                  (AJ131391) voltage-dependent anion-selective channel
NCBI Description
```

protein [Arabidopsis thaliana]

BLAST score

```
119479
Seq. No.
Contig ID
                   3145 2.R1010
5'-most EST ·
                   jC-atX23021Q2E1D03b1
Method
                   BLASTX
                   g1172555
NCBI GI
BLAST score
                   630
E value
                   1.0e-103
                   276
Match length
                   69
% identity
                   34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
NCBI Description
                   (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   (POM 34) >gi_629720_pir__S46936 34K porin - potato >gi_1076682_pir__A55364 porin (clone pPOM-34) - potato
                   mitochondrion >gi_516166_emb_CAA56599_ (X80386) 34 kDA
                   porin [Solanum tuberosum]
                   119480
Seq. No.
                   3145 3.R1010
Contig ID
                   q501876
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1724100
BLAST score
                   362
E value
                   3.0e-34
Match length
                   161
% identity
NCBI Description
                   (U79765) porin [Mesembryanthemum crystallinum]
                   119481
Seq. No.
                   3145 4.R1010
Contig ID
                   LIB35-028-Q1-E1-G3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1256259
BLAST score
                   445
E value
                   3.0e-44
Match length
                   116
% identity
                   75
NCBI Description
                   (U50900) voltage-dependent anion channel protein [Spinacia
                   oleracea]
                   119482
Seq. No.
                   3146 1.R1010
Contig ID
5'-most EST
                   LIB146-014-Q1-E1-E10
Method
                   BLASTX
NCBI GI
                   g3128189
BLAST score
                   646
E value
                   8.0e-68
Match length
                   125
% identity
                   99
                  (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   119483
                   3150 1.R1010
Contig ID
5'-most EST
                   LIB146-014-Q1-E1-E6
Method
                   BLASTN
                   q4558521
NCBI GI
```

Contig ID

5'-most EST

```
E value
                  1.0e-128
                  507
Match length
                  97
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T10024,
NCBI Description
                  complete sequence
                  119484
Seq. No.
                  3151_1.R1010
Contig ID
                  LIB24-039-Q1-E1-G11
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2244788
BLAST score
                  442
E value
                  0.0e + 00
Match length
                  531
                  93
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  119485
Seq. No.
Contig ID
                  3156 1.R1010
                  jC-atXLIB327438P4f10b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4193388
                  652
BLAST score
                  7.0e-68
E value
Match length
                  168
% identity
                  75
NCBI Description
                  (AF091455) translationally controlled tumor protein [Hevea
                  brasiliensis]
                  119486
Seq. No.
                  3156 2.R1010
Contig ID
5'-most EST
                  jC-atXP78C236A8T7b1
                  BLASTN
Method
                  q3510347
NCBI GI
BLAST score
                  90
                  1.0e-42
E value
Match length
                  582
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
                  119487
Seq. No.
                  3156_3.R1010
Contig ID
                  g272\overline{2}969
5'-most EST
                  BLASTN
Method
NCBI GI
                  q3510347
BLAST score
                  86
                  3.0e-40
E value
Match length
                  404
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  119488
```

3156 4.R1010

LIB3176-009-P1-K2-F1

NCBI Description

```
Method
                   BLASTX
NCBI GI
                   q3337356
BLAST score
                 - 919
E value
                   2.0e-99
Match length
                   185
% identity
                   99
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
Seq. No.
                   119489
Contig ID
                   3156 5.R1010
5'-most EST
                   jC-atXP123C117B22T7075a1
Method
                   BLASTN
NCBI GI
                   q4159706
BLAST score
                   231
E value
                   1.0e-126
Match length
                   271
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGL6, complete sequence
Seq. No.
                   119490
Contig ID
                   3156 6.R1010
5'-most EST
                   jC-atXLIB327410P3a01a1
                  BLASTX
Method
NCBI GI
                   q4193388
BLAST score
                   230
E value
                   9.0e-42
Match length
                   130
                   62
% identity
NCBI Description
                   (AF091455) translationally controlled tumor protein [Hevea
                  brasiliensis]
Seq. No.
                   119491
                   3156 7.R1010
Contig ID
5'-most EST
                   LIB3168-054-P1-K1-H3
Method
                   BLASTN
NCBI GI
                   q3510347
BLAST score
                   264
E value
                   1.0e-146
Match length
                   431
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   119492
Contig ID
                   3156 8.R1010
5'-most EST
                   jC-atXP57C190M5T7030a1
Method
                   BLASTX
NCBI GI
                   q4193388
BLAST score
                   471
E value
                   7.0e-51
Match length
                   154
% identity
                   71
                   (AF091455) translationally controlled tumor protein [Hevea
```

brasiliensis]

```
Seq. No.
                   119493
Contig ID
                   3156 9.R1010
5'-most EST
                   jC-atXP27C128017T7d2
                   BLASTX
Method
NCBI GI
                   q2979553
BLAST score
                   454
E value
                   4.0e-45
Match length
                   164
% identity
                   55
                   (AC003680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   119494
                   3156 11.R1010
Contig ID
5'-most EST
                   jC-atXLIB327410P3c01a1
Method
                  BLASTX
NCBI GI
                   g1922278
BLAST score
                   395
E value
                   7.0e-42
Match length
                   165
% identity
                   59
NCBI Description
                  (Z86091) TCTP protein [Fragaria x ananassa]
Seq. No.
                   119495
                  3156_12.R1010
Contig ID
5'-most EST
                  q152\overline{0}762
                  BLASTX
Method
NCBI GI
                  q4193388
BLAST score
                   271
E value
                   2.0e-23
Match length
                   72
% identity
                  78
NCBI Description
                   (AF091455) translationally controlled tumor protein [Hevea
                  brasiliensis]
Seq. No.
                   119496
                   3156 15.R1010
Contig ID
5'-most EST
                   jC-atXLIB327411P2b04b1
Method.
                  BLASTX
NCBI GI
                  q3337356
BLAST score
                   411
E value
                   4.0e-40
Match length
                  79
% identity
                  100
                  (ACO04481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
Seq. No.
                  119497
                   3156 16.R1010
Contig ID
5'-most EST
                  LIB24-034-Q1-E1-H10
Method
                  BLASTX
NCBI GI
                  q3337356
BLAST score
                  330
                  1.0e-30
E value
Match length
                  70
                  100-
% identity
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
```

```
119498
Seq. No.
                  3156 17.R1010
Contig ID
                  LIB3168-077-P1-K1-E2
5'-most EST
                  BLASTX
Method.
                  g3337356
NCBI GI
                  597
BLAST score
                  5.0e-62
E value
                  118
Match length
                  99
% identity
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
                  119499
Seq. No.
                  3156 18.R1010
Contig ID
                  g2758079
5'-most EST
                  119500
Seq. No.
                  3156 19.R1010
Contig ID
5'-most EST
                  LIB3175-025-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q3337356
BLAST score
                  160
                  1.0e-34
E value
                  84
Match length
                  94
% identity
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                  119501
Seq. No.
Contig ID
                  3157 1.R1010
                  g2763920
5'-most EST
                  BLASTX
Method
                  q549975
NCBI GI
                   304
BLAST score
                  1.0e-41
E value
Match length
                  141
% identity
                   66
                   (U12858) nucleosome assembly protein I-like protein;
NCBI Description
                   similar to mouse nap I, PIR Accession Number JS0707
                   [Arabidopsis thaliana]
                  119502
Seq. No.
                   3159 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327410P1c05b1
Method
                  BLASTX
                  g3287696
NCBI GI
BLAST score
                  858
                   4.0e-92
E value
Match length
                  238
                   69
% identity
                   (AC003979) Strong similarity to phosphoribosylanthranilate
NCBI Description
                  transferase gb D86180 from Pisum sativum. This ORF may be
                  part of a larger gene that lies in the overlapping region.
                   [Arabidopsis thaliana]
                  119503
Seq. No.
```

```
Contig ID
                  3159 2.R1010
5'-most EST
                  jC-atXLIB327410P1d06a1
Method
                  BLASTX
NCBI GI
                  q3287696
BLAST score
                  173
E value
                  4.0e-45
Match length
                  123
% identity
                  72
NCBI Description
                  (AC003979) Strong similarity to phosphoribosylanthranilate
                  transferase gb D86180 from Pisum sativum. This ORF may be
                  part of a larger gene that lies in the overlapping region.
                   [Arabidopsis thaliana]
                  119504
Seq. No.
                  3167 1.R1010
Contia ID
5'-most EST
                  q506958
Method
                  BLASTX
NCBI GI
                  q3201633
BLAST score
                  1373
E value
                  1.0e-152
Match length
                  315
% identity
NCBI Description
                  (AC004669) putative cell division protein [Arabidopsis
                  thalianal'
Seq. No.
                  119505
Contig ID
                  3169 1.R1010
5'-most EST
                  LIB146-014-Q1-E1-G9
                  119506
Seq. No.
                  3176 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327416P4d08a1
                  119507
Seq. No.
                  3176 2.R1010
Contig ID
                  jC-alXLIB327434P4f08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2493133
BLAST score
                  597
E value
                  2.0e-61
Match length
                  261
% identity
                  49
NCBI Description
                  VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT)
                  >gi_2183244 (AF002134) Vma8p [Candida albicans]
Seq. No.
                  119508
Contig ID
                  3181 1.R1010
5'-most EST
                  jC-alXLIB327434P4c03b1
Method
                  BLASTN
NCBI GI
                  q3510343
BLAST score
                  517
                  0.0e + 00
E value
Match length
                  551
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MJC20, complete sequence [Arabidopsis thaliana]

```
119509
Seq. No.
Contig ID
                   3181 2.R1010
5'-most EST
                   jC-atXP79CF4H11T7d2
Method
                  BLASTN
                   g3510343
NCBI GI
BLAST score
                   735
                   0.0e+00
E value
                  759
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
                   119510
Seq. No.
                   3185_1.R1010
Contig ID
                   jC-aTXP112C130C10T7d2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4753653
                   594
BLAST score
E value
                   4.0e-72
Match length
                  274
                  59
% identity
                  (AL049751) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119511
                  3186_1.R1010
Contig ID
5'-most EST
                  LIB3234-013-P1-K1-B8
Method
                  BLASTX
                  g3193310
NCBI GI
BLAST score
                   794
                   8.0e-85
E value
Match length
                  179
                  88
% identity
                   (AF069300) contains similarity to Nicotiana tabacum hin1
NCBI Description
                   (GB:Y07563) [Arabidopsis thaliana]
                   119512
Seq. No.
                   3198 1.R1010
Contig ID
5'-most EST
                  LIB3234-026-Q1-K1-C10
                   119513
Seq. No.
                   3200 1.R1010
Contig ID
5'-most EST
                  LIB146-015-Q1-E1-C10
                  BLASTX
Method
NCBI GI
                  q4758816
BLAST score
                   671
                   3.0e-74
E value
                   248
Match length
% identity
                   55
                  N-myristoyltransferase 2 >gi 3005065 (AF043325)
NCBI Description
                  N-myristoyltransferase 2 [Homo sapiens]
                   119514
Seq. No.
Contig ID
                   3201_1.R1010
5'-most EST
                  LIB3234-053-P1-K1-C3
                   119515
Seq. No.
Contig ID
                  3204 1.R1010
```

```
5'-most EST
                  jC-atXLIB327431P1g05a1
Method
                  BLASTX
                  q3128225
NCBI GI
                  166
BLAST score
                  5.0e-63
E value
Match length
                  240
                  58
% identity
                  (AC004077) unknown protein [Arabidopsis thaliana]
NCBI Description
                  119516
Seq. No.
Contig ID
                  3205 1.R1010
5'-most EST
                  LIB25-054-Q1-E1-H7
Method
                  BLASTX
                  a4107343
NCBI GI
                  208
BLAST score
                  3.0e-16
E value
Match length
                  136
% identity
                  36
NCBI Description
                  (AJ224922) ATP citrate lyase [Sordaria macrospora]
                  119517
Seq. No.
                  3205_2.R1010
Contig ID
                  jC-atXLIB327415P4f03b1
5'-most EST
Method
                  BLASTN
                  g4220633.
NCBI GI
BLAST score
                  41
                  1.0e-13
E value
Match length
                  296
% identity
                  88
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K7J8, complete sequence [Arabidopsis thaliana]
                  119518
Seq. No.
Contig ID
                  3207_1.R1010
                  jC-atXLIB327417P1e11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2129789
BLAST score
                  452
E value
                  7.0e-71
Match length
                  240
                  64
% identity
                  biotin carboxyl carrier protein precursor (clone BP4) -
NCBI Description
                  rape >gi_1070006_emb_CAA62264_ (X90730) Biotin carboxyl
                  carrier protein [Brassica napus] >gi 1589043 prf 2210244D
                  Ac-CoA carboxylase: ISOTYPE=bp4 [Brassica napus]
                  119519
Seq. No.
Contig ID
                  3207_2.R1010
                  LIB24-094-Q1-E1-A10
5'-most EST
Method
                  BLASTX
                  q2129789
NCBI GI
                  458
BLAST score
E value
                  1.0e-79
Match length
                  238
                                5.1
% identity
                  71
NCBI Description
                  biotin carboxyl carrier protein precursor (clone BP4) -
                  rape >gi 1070006 emb CAA62264 (X90730) Biotin carboxyl
```

Seq. No.

Method

Contig ID

5'-most EST

119524

BLASTX

3238 1.R1010

jC-aTXLIB327401P4b08b2

```
carrier protein [Brassica napus] >qi 1589043 prf 2210244D
                  Ac-CoA carboxylase:ISOTYPE=bp4 [Brassica napus]
                  119520
Seq. No.
Contig ID
                  3208 1.R1010
                  g936682
5'-most EST
                  BLASTN
Method
NCBI GI
                  g4220644
BLAST score
                  103
E value
                  2.0e-50
Match length
                  520
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MXL8, complete sequence [Arabidopsis thaliana]
                  119521
Seq. No.
                  3222 1.R1010
Contig ID
                  LIB3176-041-P1-K1-A10
5'-most EST
                  BLASTN
Method
                  q2351061
NCBI GI
BLAST score
                  135
E value
                  9.0e-70
Match length
                  367
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAF19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  119522
                  3231_1.R1010
Contig ID
                  LIB3175-077-P1-K1-G2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3334244
BLAST score
                  866
E value
                  3.0e-93
Match length
                  185
% identity
                  LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
NCBI Description
                  (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE
                  MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)
                  >gi 2113825 emb CAA73691 (Y13239) Glyoxalase I [Brassica
                  juncea]
Seq. No.
                  119523
                  3234 1.R1010
Contig ID
                  LIB3177-098-P1-K1-F9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2980770
BLAST score
                  863
E value
                  4.0e-93
Match length
                  164
% identity
                  98
                  (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
```

```
g4220474
NCBI GI
BLAST score
                   318
E value
                   6.0e-29
Match length
                   173
% identity
                   50
NCBI Description
                   (AC006069) putative myosin heavy chain [Arabidopsis
                   thaliana]
                   119525
Seq. No.
Contig ID
                   3238_2.R1010
5'-most EST
                   jC-atXLIB327402P2g07a1
Method
                  BLASTN
                  q2462264
NCBI GI
BLAST score
                   44
                   2.0e-15
E value
Match length
                   48
% identity
                  98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  119526
Seq. No.
                  3244 1.R1010
Contig ID
5'-most EST
                  LIB146-015-Q1-E1-G5
Method
                  BLASTX
NCBI GI
                  g2459446 -
BLAST score
                  878
E value
                  1.0e-94
Match length
                  170
                  100
% identity
NCBI Description
                   (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
                  thaliana]
                  119527
Seq. No.
Contig ID
                  3244_2.R1010
                  jC-a\overline{t}XP38C158M22T7s2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2459448
BLAST score
                   429
E value
                  2.0e-42
Match length
                  84
% identity
                  100
                  (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
                  119528
Seq. No.
                  3264_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P2e07b1
Method
                  BLASTX
NCBI GI
                  q3063449
                  477
BLAST score
E value
                  7.0e-48
Match length
                  118
% identity
                  75
                  (AC003981) F22013.11 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119529
                  3264 2.R1010
Contig ID
                  LIB23-027-Q1-E1-C6
5'-most EST
```

eu.

```
Method
                   BLASTX
NCBI GI
                   q3063449
BLAST score
                   487
                   4.0e-49
E value
Match length
                   122
% identity
                   74
                  (AC003981) F22013.11 [Arabidopsis thaliana]
NCBI Description
                   119530
Seq. No.
                   3265 1.R1010
Contig ID
5'-most EST
                   q2749659
                   119531
Seq. No.
Contig ID
                   3265 2.R1010
5'-most EST
                   q907125
                   BLASTX
Method
NCBI GI
                   q2760832
BLAST score
                   223
                   9.0e-48
E value
                   149
Match length
                   72
% identity
NCBI Description
                   (AC003105) similar to barley ids-4 gene product
                   [Arabidopsis thaliana]
                   119532
Seq. No.
                   3265 3.R1010
Contig ID
                  LIB3176-036-P1-K1-A12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3860272
BLAST score
                   478
                   4.0e-48
E value
Match length
                   92
% identity
                   99
                   (AC005824) putative suppressor protein [Arabidopsis
NCBI Description
                   thaliana] >gi 4314399 gb AAD15609 (AC006232) putative skd1
                  protein [Arabidopsis thaliana]
                   119533
Seq. No.
Contig ID
                   3266 1.R1·010
5'-most EST
                   iC-atXLIB327417P2c07b1
Method
                   BLASTN
NCBI GI
                   g2582640
BLAST score
                   57
E value
                   4.0e-23
Match length
                   77
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                   factor, RSp40
Seq. No.
                   119534
Contig ID
                   3267 1.R1010
5'-most EST
                   LIB3168-009-P1-K1-A1
Method
                   BLASTX
NCBI GI
                  g131289
BLAST score
                   2313
E value
                   0.0e + 00
Match length
                   473
```

E value

0.0e + 00

```
% identity
                    PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN)
NCBI Description
                    (CP43) >gi_72709_pir__F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast
                    >gi 225285 prf 1211235W photosystem II 44kD protein
                    [Nicotiana tabacum]
                    119535
Seq. No.
Contig ID
                    3273_1.R1010
LIB3234-079-P1-K1-E4
5'-most EST
Method
                    BLASTX
NCBI GI
                    q3915961
BLAST score
                    1209
E value
                    1.0e-133 -
Match length
                    276
% identity
                    HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
NCBI Description
                    >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana
tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical
                    protein [Nicotiana tabacum]
Seq. No.
                    119536
Contig ID
                    3286 1.R1010
5'-most EST
                    LIB22-078-Q1-E1-D5
                    BLASTX
Method
NCBI GI
                    q4775271
BLAST score
                    340.
E value
                    6.0e-32
Match length
                    81
                    75
% identity
NCBI Description
                    (AJ131214) SF2/ASF-like splicing modulator Srp30, variant 1
                    [Arabidopsis thaliana]
                    119537
Seq. No.
Contig ID
                    3287 1.R1010
5'-most EST
                    jC-atXLIB327411P1f02b1
Method
                    BLASTX
NCBI GI
                    q972921
BLAST score
                    352
E value
                    3.0e-33
Match length
                    84
                    85
% identity
NCBI Description
                    (U18411) IAA9 [Arabidopsis thaliana]
                    >gi_2832666_emb_CAA16692_ (AL021684) auxin-induced protein
                    IAA9 [Arabidopsis thaliana]
Seq. No.
                    119538
                    3297 1.R1010
Contig ID
5'-most EST
                    g16822
Seq. No.
                    119539
Contig ID
                    3300 1.R1010
5'-most EST
                    jC-atXP86CG8E6T7d2
Method
                    BLASTN
NCBI GI
                    g4159704
BLAST score
                    644
```

Match length

```
Match length
                   668
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MCB17, complete sequence
Seq. No.
                   119540
                  3300 2.R1010
Contig ID
5'-most EST
                  LIB146-016-Q1-E1-F7
Method
                   BLASTN
NCBI GI
                   q4159704
BLAST score
                   478
E value
                   0.0e + 00
Match length
                   548
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MCB17, complete sequence
Seq. No.
                   119541
Contig ID
                   3300_3.R1010
                  jC-atXLIB327408P1a06b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4159704
BLAST score
                   900
                   0.0e+00
E value .
                   910
Match length
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MCB17, complete sequence
                  119542
Seq. No.
Contig ID
                   3304 1.R1010
5'-most EST
                  LIB146-016-Q1-E1-G12
                   119543
Seq. No.
Contig ID
                   3311 1.R1010
5'-most EST
                  LIB3234-009-P1-K1-D4
                   119544
Seq. No.
Contig ID
                  3313 1.R1010
5'-most EST
                  q3449677
Method
                  BLASTN
NCBI GI
                   g3063438
BLAST score
                   151
E value
                   3.0e-79
Match length
                   307
                   99
% identity
                  Complete sequence of Arabidopsis F22013, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   119545
                   3313 2.R1010
Contig ID
5'-most EST
                  LIB3168-032-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g3063444.
BLAST score
                   629
E value
                  2.0e-65
```

```
% identity
NCBI Description (AC003981) F22013.5 [Arabidopsis thaliana]
Seq. No.
                  119546
                  3313_3.R1010
Contig ID
5'-most EST
                  g2414121
                  BLASTN
Method
                  q3063438
NCBI GI
                  285
BLAST score
E value
                  1.0e-159
Match length
                  426
% identity
                  Complete sequence of Arabidopsis F22013, complete sequence
NCBI Description
                  [Arabidopsis thaliana]
                  119547
Seq. No.
Contig ID
                  3313 4.R1010
                  jC-atXP83CG3C8T7013d1
5'-most EST
Method
                  BLASTX
                  g3063444
NCBI GI
                  296
BLAST score
E value
                  1.0e-26
Match length
                  78
% identity
                  78
NCBI Description (AC003981) F22013.5 [Arabidopsis thaliana]
                  119548
Seq. No.
Contig ID
                  3313 6.R1010
5'-most EST
                  q940462
Method
                  BLASTX
                  q3063444
NCBI GI
BLAST score
                  499
E value
                  2.0e-94
Match length
                  184
% identity
                  99
NCBI Description (AC003981) F22013.5 [Arabidopsis thaliana]
                  119549
                                                                 \gamma_1^{(i)}.
Seq. No.
Contig ID
                  3320_1.R1010
5'-most EST
                  LIB22-082-Q1-E2-C4
                  BLASTX
Method
NCBI GI
                  g4581109
BLAST score
                  367
E value
                  7.0e-35
                  155
Match length
% identity
                  46
                  (AC005825) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119550
Contig ID
                  3325_1.R1010
                  LIB24-131-Q1-E1-B1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2290120
BLAST score
                  41
E value
                  3.0e-13
Match length
                  65
% identity
```

```
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env)
                  gene, partial cds
                   119551
Seq. No.
                   3325 2.R1010
Contig ID
                   jC-a\(\bar{1}\)XLIB327434P4f03b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4582468
BLAST score
                   614
E value
                   1.0e-133
Match length
                   250
% identity
                   100
                   (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                  C-terminal domain [Arabidopsis thaliana]
                   119552
Seq. No.
                   3325_3.R1010
Contig ID
                   LIB24-092-Q1-E1-G10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2393724
BLAST score
                   144
E value
                   1.0e-08
Match length
                   70
% identity
                  (U80819) glutathione-S-transferase homolog [Mus musculus]
NCBI Description
Seq. No.
                   119553
                   3325 5.R1010
Contig ID
                   g757591
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4582468
BLAST score
                   482
E value
                   3.0e-48
Match length
                   111
% identity
                   90
                   (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                  C-terminal domain [Arabidopsis thaliana]
                   119554
Seq. No.
                   3325 6.R1010
Contig ID
5'-most EST
                   g2733543
Seq. No.
                   119555
                   3325 7.R1010
Contig ID
                   g276\overline{2}595
5'-most EST
Method
                  BLASTX
NCBI GI
                   q417170
BLAST score
                   183
E value
                   2.0e-13
Match length
                   111
% identity
                   38
                  HYDANTOIN UTILIZATION PROTEIN C (ORF4) >gi 151284 (M72717)
NCBI Description
                   DL-hydantoinase [Pseudomonas sp.] >gi 216833 dbj BAA01379_
                   (D10494) N-carbamyl-L-amino acid amidohydrolase
                   [Pseudomonas sp.]
```

119556

Seq. No.

```
Contig ID
                  3325 9.R1010
5'-most EST
                   LIB2\overline{4}-074-Q1-E1-H9
                  BLASTX
Method
NCBI GI
                   q4582468
BLAST score
                   525
E value
                   6.0e-54
Match length
                   125
                   94
% identity
                   (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                  C-terminal domain [Arabidopsis thaliana]
Seq. No.
                   119557
Contig ID
                   3325 15.R1010
5'-most EST
                  jC-atXP125C140B17T7d1
Method
                   BLASTN
                  g3449316
NCBI GI
BLAST score
                   71
E value
                   9.0e-32
Match length
                   112
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9D7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   119558
Contig ID
                   3327 1.R1010
                  jC-a\overline{t}XLIB327408P3e03b1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q2645198
                   296
BLAST score
E value
                   1.0e-165
Match length
                   687
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T26J12 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                   119559
Seq. No.
                  3341_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P2d07b2
Method
                   BLASTN
                   a2281081
NCBI GI
BLAST score
                   236
                   1.0e-130
E value
                   482
Match length
% identity
                   98
                  Arabidopsis thaliana chromosome II BAC F18019 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   119560
                   3341_2.R1010
Contig ID
                  jC-atXLIB327408P3d06b1
5'-most EST
Method
                  BLASTN
                  q2281081
NCBI GI
BLAST score
                  611
                  0.0e+00
E value
Match length
                  1305
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F18019 genomic
```

Match length

178

119561 Seq. No. 3341 3.R1010 Contig ID jC-atXLIB327439P1d08b2 5'-most EST BLASTN Method g2281081 NCBI GI BLAST score 454 0.0e + 00E value 469 Match length 76 % identity Arabidopsis thaliana chromosome II BAC F18019 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 119562 Seq. No. 3341 4.R1010 Contig ID jC-atXLIB327439P1f07b2 5'-most EST Method BLASTN g2281081 NCBI GI BLAST score 130 1.0e-66 E value 409 Match length 97 % identity NCBI Description *Arabidopsis thaliana chromosome II BAC F18019 genomic sequence, complete sequence [Arabidopsis thaliana] 119563 Seq. No. 3341 7.R1010 Contig ID 5'-most EST LIB24-046-Q1-E1-E1 BLASTN Method NCBI GI g2281081 BLAST score 287 1.0e-160 E value Match length 651 97 % identity Arabidopsis thaliana chromosome II BAC F18019 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 119564 Seq. No. Contig ID 3350_1.R1010 LIB25-041-Q1-E1-E11 5'-most EST Method BLASTX NCBI GI g2245048 BLAST score 214 E value 2.0e-57 Match length 277 29 % identity (Z97342) resistance gene homolog [Arabidopsis thaliana] NCBI Description Seq. No. 119565 3357 1.R1010 Contig ID jC-atXLIB327419P4f07b1 5'-most EST Method BLASTX q4586116 NCBI GI BLAST score 567 2.0e-59 E value

sequence, complete sequence [Arabidopsis thaliana]

BLAST score

```
73
% identity
                   (ALO49638) putative C-4 sterol methyl oxidase [Arabidopsis
NCBI Description
Seq. No.
                   119566
                   3357 2.R1010
Contig ID
                   jC-atXP46C172G14T7044a1
5'-most EST
Method
                   BLASTN
                   q3927822
NCBI GI
                   391
BLAST score
E value
                   0.0e + 00
                   528
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC F8N16 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   119567
Seq. No.
                   3357 3.R1010
Contig ID
                   jC-aIXLIB327435P2e10a1
5'-most EST
Method
                   BLASTN
                   g3927822
NCBI GI
BLAST score
                   395
                   0.0e+00
E value
Match length
                   477
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC F8N16 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   119568
Seq. No.
                   3357 4.R1010
Contig ID
                   g241\overline{4}030
5'-most EST
Method
                   BLASTN
                   q3927822
NCBI GI
BLAST score
                   367
                   0.0e + 00
E value
                   522
Match length
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC F8N16 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   119569
Seq. No.
                   3357 6.R1010
Contig ID
                   LIB3176-092-P1-K1-F10
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2827552
                   271
BLAST score
                   8.0e-24
E value
Match length
                   122
% identity
                   39
                  (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                   119570
Seq. No.
                   3357 9.R1010
Contig ID
                   g1216751
5'-most EST
                   BLASTN
Method
                   g3927822
NCBI GI
```

E value

```
1.0e-108
E value
Match length
                   354
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC F8N16 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   119571
Seq. No.
                   3359_1.R1010
Contig ID
5'-most EST
                  LIB146-017-Q1-E1-F10
                   119572
Seq. No.
Contig ID
                   3360_1.R1010
5'-most EST
                  jC-alXLIB327436P4d11b1
                   119573
Seq. No.
                   3364 1.R1010
Contig ID
                  jC-atXLIB327440P4c06b2
5'-most EST
Method
                  BLASTN
                  g3063690
NCBI GI
BLAST score
                   745
                   0.0e + 00
E value
Match length
                  764
                   100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
                   (ESSAII project)
                  119574
Seq. No.
                   3372 1.R1010
Contig ID
5'-most EST
                  LIB3168-024-P1-K1-B9
                  BLASTX
Method
NCBI GI
                   g2961390
BLAST score
                   734
                   5.0e-78
E value
Match length
                   134
                   100
% identity
                  (AL022141) beta-galactosidase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   119575
Seq. No.
Contig ID
                   3375 1.R1010
5'-most EST
                  jC-atXLIB327410P1f03b1
Method
                  BLASTX
                  g587566
NCBI GI
BLAST score
                  1730
E value
                   0.0e + 00
Match length
                   466
% identity
                   71
                   (X80237) mitochondrial processing peptidase [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   119576
                   3375_2.R1010
Contig ID
5'-most EST
                   jC-atXP86CG10C5T7d2
Method
                  BLASTX
NCBI GI
                  g477819
                   617
BLAST score
                  5.0e-64
```

```
Match length
                  151
% identity
                  77
                  mitochondrial processing peptidase (EC 3.4.99.41) beta
NCBI Description
                  chain precursor - potato >gi 410634 bbs 136741 cytochrome c
                  reductase-processing peptidase subunit II, MPP subunit II,
                  P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                  530 aa]
Seq. No.
                  119577
                  3375 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P1f03a1
Method
                  BLASTX
                  a477819
NCBI GI
BLAST score
                  102
E value
                  1.0e-03
Match length
                  91
% identity
                  24
                  mitochondrial processing peptidase (EC 3.4.99.41) beta
NCBI Description
                  chain precursor - potato >gi 410634 bbs 136741 cytochrome c
                  reductase-processing peptidase subunit II, MPP subunit II,
                  P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                  530 aa]
                  119578
Seq. No.
                  3375 4.R1010
Contig ID
5'-most EST
                  jC-atXLIB327426P4b04a1
                  BLASTN
Method
NCBI GI
                  q2462264
BLAST score
                  57
E value
                  4.0e-23
Match length
                  57
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  119579
Contig ID
                  3376 1.R1010
5'-most EST
                  jC-atXP14C104P23T7s1
Method
                  BLASTX
NCBI GI
                  q3786001
BLAST score
                  1107
E value
                  1.0e-121
Match length
                  211
                  99
% identity
NCBI Description
                  (AC005499) unknown protein [Arabidopsis thaliana]
                  119580
Seq. No.
Contig ID
                  3381_1.R1010
5'-most EST
                  LIB3176-029-P1-K1-D12
                  BLASTN
Method
NCBI GI
                  g2351068
BLAST score
                  316
E value
                  1.0e-177
Match length
                  549
                  97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MRH10, complete sequence [Arabidopsis thaliana]

Contig ID

```
119581
Seq. No.
                  3386 1.R1010
Contig ID
                  LIB3176-010-P1-K1-D9
5'-most EST
                  BLASTX
Method
                  g131770
NCBI GI
BLAST score
                   320
                   6.0e-33
E value
Match length
                  119
% identity
                   61
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
NCBI Description
                   (VEGETATIVE SPECIFIC PROTEIN V12) >gi 70880 pir R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi 7353 emb CAA29844 (X06636) rp1024 protein
                   [Dictyostelium discoideum]
                  119582
Seq. No.
                   3394 1.R1010
Contig ID
                  LIB25-060-Q1-E1-E11
5'-most EST
                  119583
Seq. No.
                  3399 1.R1010
Contig ID
                  q244\overline{5}970
5'-most EST
Method
                  BLASTN
                  q4454447
NCBI GI
BLAST score
                   207
                   1.0e-112
E value
Match length
                   543
                  95
% identity
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   119584
                   3399 2.R1010
Contig ID
                  ARABLI-09-Q1-B1-H2
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4454447
BLAST score
                   218
                  1.0e-119
E value
Match length
                   322
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                   119585
Seq. No.
                   3413 1.R1010
Contig ID
                  LIB3175-039-P1-K1-E2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4539312
BLAST score
                   353
                  2.0e-50
E value
Match length
                  115
% identity
                  81
                   (AL035679) putative ubiquitin-dependent proteolytic protein
NCBI Description
                   [Arabidopsis thaliana]
                  119586
Seq. No.
```

3418 1.R1010

```
jC-atXLIB327407P1c11b2
5'-most EST
Method
                    BLASTX
NCBI GI
                   q2129944
                    426
BLAST score
                    9.0e-42
E value
Match length
                    142
% identity
                   RNA-binding protein RZ-1 - wood tobacco
NCBI Description
                   >gi_1395193_dbj_BAA12064_ (D83696) RNA-binding protein RZ-1
                   [Nicotiana sylvestris] >gi_1435062_dbj_BAA06012 (D28861) RNA binding protein, RZ-1 [Nicotiana sylvestris]
                   119587
Seq. No.
                   3420 1.R1010
Contig ID
                   jC-atXLIB327422P3g10b2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4512667
                    692
BLAST score
                    9.0e-80
E value
                    153
Match length
                    96
% identity
NCBI Description
                   (AC006931) putative MAP kinase [Arabidopsis thaliana]
Seq. No.
                   119588
Contig ID
                    3424_1.R1010
                    jC-atXP46C174H11T7080d1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q2098816
                    231
BLAST score
                    1.0e-127
E value
                    648
Match length
                    97
% identity
NCBI Description
                   Arabidopsis thaliana BAC F19G10, complete sequence
                    119589
Seq. No.
                    3424 2.R1010
Contig ID
                    jC-atXLIB327431P4a05a1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q2462826
                    730
BLAST score
                    5.0e-81
E value
                   159
Match length
                    93
% identity
NCBI Description
                   (AF000657) unknown protein [Arabidopsis thaliana]
                   119590
Seq. No.
                    3425 1.R1010
Contig ID
5'-most EST
                   LIB146-018-Q1-E1-D8
                   BLASTN
Method
NCBI GI
                    q4220641
                    269
BLAST score
                    1.0e-150
E value
                    301
Match length
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MUL3, complete sequence [Arabidopsis thaliana]

```
. 119591
Seq. No.
Contig ID
                  3431_1.R1010
                  jC-atXL1025Q1B1G06a1
5'-most EST
                  BLASTX
Method
                  g3036801
NCBI GI
BLAST score
                   158
                   3.0e-10
E value
Match length
                  81
                   47
% identity
                  (AL022373) putative ascorbate peroxidase [Arabidopsis
NCBI Description
                  thaliana] >gi_3805863_emb_CAA21483_ (AL031986) putative
                  ascorbate peroxidase [Arabidopsis thaliana]
Seq. No.
                  119592
Contig ID
                   3436_1.R1010
                  LIB3168-087-P1-K1-H12
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2832620
BLAST score
                   483
E value
                   1.0e-48
Match length
                  125
                  71
% identity
                  (AL021711) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  119593
Seq. No.
Contig ID
                   3437 1.R1010
5'-most EST
                   jC-atXLIB327411P1c12b1
Method
                  BLASTX
                  g2369714
NCBI GI
BLAST score
                   2523
                  0.0e + 00
E value
Match length
                   561
% identity
                   86
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   119594
Seq. No.
Contig ID
                   3437 2.R1010
                  LIB25-107-Q1-E1-G12
5'-most EST
Method
                  BLASTX
                  q2369714
NCBI GI
BLAST score
                   1363
E value
                   1.0e-151
                   290
Match length
% identity
                   91
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   119595
Seq. No.
                   3437 3.R1010
Contig ID
5'-most EST
                  q2413932
Method
                  BLASTX
NCBI GI
                   q2369714
BLAST score
                   301
E value
                   5.0e-27
Match length
                   79
% identity
                  78
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
```

```
Seq. No.
                  119596
                  3437 5.R1010
Contig ID
                  LIB25-031-Q1-E1-F12
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2369714
BLAST score
                  1283
                  1.0e-142
E value
                  314
Match length
% identity
                  78
NCBI Description (297178) elongation factor 2 [Beta vulgaris]
                  119597
Seq. No.
                  3441 1.R1010
Contig ID
                  LIB25-041-Q1-E1-B8
5'-most EST
                  BLASTX
Method
NCBI GI
                  g345829
BLAST score
                  330
                  1.0e-30
E value
Match length
                  96
% identity
                  66
NCBI Description ubiquitin carrier protein E2 - human
                  119598
Seq. No.
                  3447 1.R1010
Contig ID
                  jC-atXP118C144N12T7062d2
5'-most EST
Method
                  BLASTN
NCBI GI
                  q1848276
BLAST score
                  41
                  2.0e-13
E value
Match length
                  41
% identity
                  100
NCBI Description Human telomerase-associated protein TP-1 mRNA, complete cds
Seq. No.
                  119599
                  3448 1.R1010
Contig ID
                  jC-atXLIB327432P2h04b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3043760
BLAST score
                  599
                  7.0e-62
E value
Match length
                  200
% identity
                  56
NCBI Description (AB012759) rPOP [Rattus norvegicus]
                  119600
Seq. No.
                  3458 1.R1010
Contig ID
                  LIB3234-015-P1-K1-C10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4586249
BLAST score
                  457
                  1.0e-45
E value
Match length
                  140
% identity
                  60
NCBI Description
                  (AL049640) putative pollen surface protein [Arabidopsis
                  thaliana]
```

119601

Seq. No.

Match length

118

```
Contig ID
                  3460 1.R1010
5'-most EST
                  LIB3176-062-P1-K1-C2
Method
                  BLASTX
                  q2702281
NCBI GI
                  554
BLAST score
E value
                  5.0e-57
                  134
Match length
% identity
                  44
                   (AC003033) putative protein disulfide isomerase precursor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  119602
                  3463_1.R1010
Contig ID
                  ARABLI-09-Q1-B1-F6
5'-most EST
Method
                  BLASTX
                  q4038055
NCBI GI
BLAST score
                  381
E value
                  2.0e-37
Match length
                  157
% identity
                  56
                  (AC005897) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  >gi_4557077_gb_AAD22516.1_AC007045_16 (AC007045) putative
                  cytochrome p450 [Arabidopsis thaliana]
Seq. No.
                  119603
Contig ID
                  3464 1.R1010
5'-most EST
                  q932037
                  BLASTX
Method
                  g116527
NCBI GI
BLAST score
                  548
E value
                  4.0e-56
Match length
                  120
% identity
                  85
                  PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196)
NCBI Description
                  >gi_1143166 (U32397) ClpP protease [Nicotiana tabacum]
                  >gi 2924270 emb_CAA77422 (Z00044) ATP-dependent protease
                  proteolytic subuni [Nicotiana tabacum]
                  119604
Seq. No.
Contig ID
                  3464 2.R1010
5'-most EST
                  jC-atXP100C268F7T7b1
Method
                  BLASTN
                  g531828
NCBI GI
BLAST score
                  46
E value
                  2.0e-16
Match length
                  58
                  95
% identity
                  Cloning vector pSport1, complete cds
NCBI Description
Seq. No.
                  119605
Contig ID
                  3464_3.R1010
                  LIB3168-089-P1-K1-E2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q116525
BLAST score
                  101
E value
                  3.0e-03
```

Contig ID

5'-most EST

```
69
% identity
                  PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 203)
NCBI Description
                  >gi_81339_pir__A05056 hypothetical protein 203 - liverwort
                  (Marchantia polymorpha) chloroplast
                  >gi_456519_emb_CAA28109_ (X04465) ORF203 [Marchantia
                  polymorpha]
                  119606
Seq. No.
                  3468 1.R1010
Contig ID
5'-most EST
                  LIB23-045-Q1-E1-A10
                  BLASTX
Method
NCBI GI
                  g4510406
BLAST score
                  619
                  3.0e-64
E value
                  170
Match length
% identity
                  (AC006587) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  119607
Seq. No.
                  3479_1.R1010
Contig ID
                  LIB146-019-Q1-E1-B11
5'-most EST
                  BLASTN
Method
                  g4757404
NCBI GI
BLAST score
                  122
                  4.0e-62
E value
Match length
                  301
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
NCBI Description
                  MLJ15, complete sequence
                  119608
Seq. No.
                  3483 1.R1010
Contig ID
                  jC-aTXLIB327436P1h03b1
5'-most EST
                  BLASTX
Method
                  g4773906
NCBI GI
                  560
BLAST score
                  2.0e-57
E value
Match length
                  117
% identity
                  91
                   (AF074021) putative symbiosis-related protein [Arabidopsis
NCBI Description
                  thaliana]
                  119609
Seq. No.
                   3483 2.R1010
Contig ID
                   jC-aTXLIB327434P3e01b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4773906
BLAST score
                   621
                   2.0e-64
E value
Match length
                  122
% identity
                   (AF074021) putative symbiosis-related protein [Arabidopsis
NCBI Description
                  thaliana]
                  119610
Seq. No.
```

747 c

3484 1.R1010

jC-atXLIB327418P4e05b1

Contig ID

```
Method
                   BLASTX
NCBI GI
                   q1561730
BLAST score
                   157
                   3.0e-10
E value
Match length
                   61
% identity
NCBI Description
                   (U65491) Dreg-3 protein [Drosophila melanogaster]
                   119611
Seq. No.
Contig ID
                   3486 1.R1010
5'-most EST
                   jC-alXLIB327434P1b05b1
Method
                   BLASTX
NCBI GI
                   q1438883
BLAST score
                   234
E value
                   2.0e-19
Match length
                   79
% identity
                   57
NCBI Description
                  (U43840) GmCK3p [Glycine max]
Seq. No.
                   119612
Contig ID
                   3495 1.R1010
5'-most EST
                  LIB25-022-Q1-E1-A1
Seq. No.
                   119613
                   3499 1.R1010
Contig ID
5'-most EST
                   LIB146-019-Q1-E1-D11
Seq. No.
                   119614
                   3500 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327431P4b06a1
Method
                   BLASTX
NCBI GI
                   g2911085
BLAST score
                   723
E value
                   2.0e-76
Match length
                   226
% identity
NCBI Description
                   (AL021960) photosystem II oxygen-evolving complex protein
                   3-like [Arabidopsis thaliana] >gi 3402748_emb_CAA20194.1
                   (AL031187) photosystem II oxygen-evolving complex protein 3

    like [Arabidopsis thaliana]

                   119615
Seq. No.
Contig ID
                   3500 2.R1010
                   jC-a\overline{t}XLIB327427P1c06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2911085
BLAST score
                   209
E value
                   2.0e-32
Match length
                   126
% identity
NCBI Description
                   (AL021960) photosystem II oxygen-evolving complex protein
                   3-like [Arabidopsis thaliana] >gi 3402748 emb CAA20194.1
                   (AL031187) photosystem II oxygen-evolving complex protein 3

    like [Arabidopsis thaliana]

Seq. No.
                   119616
```

3500 4.R1010

```
LIB3177-018-P1-K1-F1
5'-most EST
Method
                    BLASTX
                    q2911085 ·
NCBI GI
BLAST score
                    346
                    2.0e-32
E value
Match length
                    116
                    62
% identity /
                    (AL021960) photosystem II oxygen-evolving complex protein
NCBI Description
                    3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_
                    (AL031187) photosystem II oxygen-evolving complex protein 3
                    - like [Arabidopsis thaliana]
                    119617
Seq. No.
                    3500 6.R1010
Contig ID
                    jC-atXP8C92J23T7d1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q2911085
                    346
BLAST score
                    2.0e-32
E value
Match length
                    89
% identity
                    74
NCBI Description
                    (AL021960) photosystem II oxygen-evolving complex protein
                    3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_
                    (AL031187) photosystem II oxygen-evolving complex protein 3

    like [Arabidopsis thaliana]

                    119618
Seq. No.
Contig ID
                    3509 1.R1010
                    LIB3176-092-P1-K1-G3
5'-most EST
Method
                    BLASTX
                    q133320
NCBI GI
                    87
BLAST score
E value
                    1.0e-31
Match length
                    131
% identity
                    53
NCBI Description
                    DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (A135)
                    (RNA POLYMERASE I SUBUNIT 2) >gi_101446_pir__A39607
                    DNA-directed RNA polymerase (EC 2.7.7.6) I 135K chain -
                    yeast (Saccharomyces cerevisiae) >gi_172464 (M62804) RNA
                    polymerase I (second largest subunit) [Saccharomyces
                    cerevisiae] >gi_887587_emb_CAA90154_ (Z49919) Rpa2p [Saccharomyces cerevisiae] >gi_939744 (U31900) Rpa135p [Saccharomyces cerevisiae] >gi_1314085_emb_CAA95050_
                    (Z71255) Rpa2p [Saccharomyces cerevisiae]
                    119619
Seq. No.
Contig ID
                    3514 1.R1010
5'-most EST
                    LIB146-019-Q1-E1-E8
Method
                    BLASTX
                    q3033375
NCBI GI
BLAST score
                    191
E value
                    2.0e-14
Match length
                    135
% identity
NCBI Description
                    (AC004238) putative berberine bridge enzyme [Arabidopsis
```

thaliana]

```
119620
Seq. No.
Contig ID
                  3515_1.R1010
5'-most EST
                  LIB24-071-Q1-E1-H9
                  BLASTX
Method
                  g2832619
NCBI GI
BLAST score
                  559
                  1.0e-57
E value
Match length
                  118
                   62
% identity
NCBI Description
                   (AL021711) major intrinsic protein (MIP) - like [Arabidopsis
                  thaliana]
                  119621
Seq. No.
                  3522_1.R1010
Contig ID
                  LIB146-019-Q1-E1-F4
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4757798
BLAST score
                  220
                  9.0e-18
E value
                  128
Match length
                  33
% identity
                  apoptosis specific protein >gi_2995198_emb_CAA72327_
NCBI Description
                   (Y11588) apoptosis specific protein [Homo sapiens]
                  119622
Seq. No.
                  3524 1.R1010
Contig ID
5'-most EST
                  LIB146-019-Q1-E1-F6
                  119623
Seq. No.
Contig ID
                  3525 1.R1010
5'-most EST
                  jC-atXLIB327431P2g10a1
                  BLASTN
Method
NCBI GI
                  g836895
BLAST score
                  45
                  1.0e-15
E value
Match length
                  52
% identity
                  98
                  Saccharomyces cerevisiae CSP2 gene, complete cds
NCBI Description
Seq. No.
                  119624
Contig ID
                  3525 2.R1010
5'-most EST
                  jC-atXLIB327416P2e06b1
Method
                  BLASTN
NCBI GI
                  g540252
BLAST score
                  50
                  9.0e-19
E value
Match length
                  61
                  97
% identity
                  Cloning vector pSVSport1 beta-lactamase gene, complete cds
NCBI Description
Seq. No.
                  119625
                  3525_3.R1010
Contig ID
5'-most EST
                  jC-atXmonuni25Ab01b1
Method
                  BLASTX
NCBI GI
                  g2342723
                  198
BLAST score
```

1.0e-14

E value

5'-most EST

```
Match length
                   268
% identity
                   32
                   (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                   119626
Seq. No.
                   3527 1.R1010
Contig ID
                   LIB2\overline{3}-068-Q1-E1-B6
5'-most EST
                   BLASTX
Method
                   q4584525
NCBI GI
BLAST score
                   220
E value
                   2.0e-23
Match length
                   59
                   98
% identity
                   (AL049607) protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   119627
Seq. No.
                   3528 1.R1010
Contig ID
                   LIB146-019-Q1-E1-G1
5'-most EST
                   119628
Seq. No.
Contig ID
                   3532_1.R1010
5'-most EST
                   LIB22-052-Q1-E1-F9
Method
                   BLASTX
                   g4056488
NCBI GI
BLAST score
                   375
                   6.0e-36
E value
Match length
                   69
                   97
% identity
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
                   119629
Seq. No.
Contig ID
                   3532_2.R1010
                   g1217335
5'-most EST
Method
                   BLASTN
                   g4056476
NCBI GI
BLAST score
                   244
                  "1.0e-134
E value
                                                                              ....
Match length
                   402 ...
                   99
% identity
                   Arabidopsis thaliana chromosome II BAC F3G5 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   119630
                   3532_3.R1010
Contig ID
                   jC-atXLIB327404P1f02b1
5'-most EST
Method
                   BLASTX
                   q4056503
NCBI GI
BLAST score
                   190
E value
                   3.0e-14
Match length
                   36
% identity
                   100
NCBI Description
                   (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                   119631
Contig ID
                   3535 1.R1010
```

LIB24-067-Q1-E1-E3

```
Method
                  BLASTX
NCBI GI
                  g3128168
BLAST score
                  226
                  2.0e-18
E value
Match length
                  91
                  47
% identity
                  (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                  [Arabidopsis thaliana]
                  119632
Seq. No.
Contig ID
                  3546_1.R1010
5'-most EST
                  LIB3234-008-P1-K1-D4
Method
                  BLASTX
                  g3068713
NCBI GI
BLAST score
                  487
                  4.0e-49
E value
Match length
                  140
% identity
                  73
                  (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                  119633
Seq. No.
                  3546 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327419P2d05b2
Method
                  BLASTN
NCBI GI
                  q3068702
BLAST score
                  415
                  0.0e + 00
E value
Match length
                  467
% identity
                  98
NCBI Description
                  Arabidopsis thaliana putative transmembrane protein G1p
                  (AtG1), putative nuclear DNA-binding protein G2p (AtG2),
                  Eml protein (ATEM1), putative chlorophyll synthetase
                  (AtG4), putative transmembrane protein G5p (AtG5), put
                  119634
Seq. No.
                  3553_1.R1010
Contig ID
5'-most EST
                  LIB3234-088-Q1-K1-C1
                  BLASTX
Method
NCBI GI
                  g3169059
BLAST score
                  208
E value
                  2.0e-16
Match length
                  81
                  49
% identity
                  (AL023704) weak similarity to B.subtilis spore outgrowth f
NCBI Description
                  actor B [Schizosaccharomyces pombe]
                  119635
Seq. No.
                  3554 1.R1010
Contig ID
5'-most EST
                  LIB24-121-Q1-E1-G11
Method
                  BLASTN
NCBI GI
                  q4558656
BLAST score
                  382
                  0.0e + 00
E value
Match length
                  382
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T10F5 genomic
                  sequence, complete sequence
```

```
119636
. Seq. No.
                    3555_1.R1010
 Contig ID
                    jC-atXP108C158H9T7059d1
 5'-most EST
                    BLASTX
 Method
                    g1935914
 NCBI GI
 BLAST score
                    268
                    2.0e-76
 E value
                    148
 Match length
                    94
 % identity
                   (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]
 NCBI Description
                    119637
 Seq. No.
                    3555 4.R1010
 Contig ID
                    g933705
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g1935914
 BLAST score
                    883
 E value
                    2.0e-95
 Match length
                    195
 % identity
                    86
                   (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]
 NCBI Description
 Seq. No. ..
                    119638
                    3557 1.R1010
 Contig ID
 5'-most EST
                    LIB3177-021-P1-K2-H8
                    119639
 Seq. No.
                    3571 1.R1010
 Contig ID
 5'-most EST
                    LIB3168-072-P1-K1-G9
                    BLASTX
 Method
 NCBI GI
                    g82232
 BLAST score
                    1625
                    0.0e + 00
 E value
 Match length
                    410
 % identity
                    80
 NCBI Description rpoC protein homolog - common tobacco chloroplast
 Seq. No.
                    119640
                    3575 1.R1010
 Contig ID
                    g934706
 5'-most EST
                    BLASTN
 Method
 NCBI GI
                    q4589434
 BLAST score
                    467
 E value
                    0.0e + 00
 Match length
                    487
 % identity
                    99
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MNJ7, complete sequence
                    119641
 Seq. No.
                    3583 1.R1010
 Contig ID
 5'-most EST
                    LIB146-020-Q1-E1-D9
 Seq. No.
                    119642
 Contig ID
                    3587 1.R1010
                   LIB3168-052-P1-K1-D2
 5'-most EST
```

```
BLASTX
   Method
                       g3885334
   NCBI GI
                       729
   BLAST score
                       1.0e-77
· · · E value
   Match length.
                       138
                       100
   % identity
                       (AC005623) putative argonaute protein [Arabidopsis
   NCBI Description
                       thaliana]
                       119643
   Seq. No.
                       3599 1.R1010
   Contig ID
                       LIB146-020-Q1-E1-F6
   5'-most EST
                       BLASTX
   Method
                       g1174470
   NCBI GI
   BLAST score
                       378
   E value
                       2.0e-38
   Match length
                       131
   % identity
                       62
                       OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
   NCBI Description
                       (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A
                       integral membrane protein [Mus musculus]
                       119644
   Seq. No.
                       3603 1.R1010
   Contig ID
                       LIB22-043-Q1-E1-F9
   5'-most EST
   Method
                       BLASTX
                       g3036816
   NCBI GI
   BLAST score
                       216
                       3.0e-17
   E value
                       92
   Match length
   % identity
                       49
                       (AL022373) myosin-like protein [Arabidopsis thaliana]
   NCBI Description
                       119645
   Seq. No.
                       3606 1.R1010
   Contig ID
                       jC-atXLIB327426P2c09b1
   5'-most EST
   Method
                       BLASTN
                       g4220640
   NCBI GI
   BLAST score
                       643
                       0.0e + 00
   E value
                       822
   Match length
   % identity
                       99
                       Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
   NCBI Description
                       MPE11, complete sequence [Arabidopsis thaliana]
                       119646
   Seq. No.
                       3614 1.R1010
   Contig ID
   5'-most EST
                       jC-atXLIB327432P2a11b2
   Method
                       BLASTX
                       g2960364
   NCBI GI
   BLAST score
                       739
                       2.0e-78
   E value
   Match length
                       194
   % identity
                       73
                       (AJ224986) cinnamoyl CoA reductase [Populus balsamifera
   NCBI Description
```

subsp. trichocarpa]

40

```
119647
  Seq. No.
                    3619 1.R1010
  Contig ID
  5'-most EST
                    LIB146-020-Q1-E1-H4
                    BLASTN
  Method
  NCBI GI
                    q2351065
  BLAST score
                    368
  E value
                    0.0e + 00
  Match length
                    396
  % identity
                    98
  NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MHF15, complete sequence [Arabidopsis thaliana]
                    119648
  Seq. No.
  Contig ID
                    3622 1.R1010
  5'-most EST
                    LIB3168-006-P1-K1-B9
  Method
                    BLASTN
NCBI GI
                    g2182289
  BLAST score
                    59
                    2.0e-24
  E value
                    358
  Match length
  % identity
                    89
  NCBI Description
                    Arabidopsis thaliana chromosome I BAC F11P17 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
                    119649
  Seq. No.
                    3623 1.R1010
  Contig ID
  5'-most EST
                    LIB146-020-Q1-E1-H8
  Method
                    BLASTN
                    q3449326
  NCBI GI
  BLAST score
                    224
                    1.0e-123
  E value
 Match length
                    391
  % identity
                    100
  NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                    K19M22, complete sequence [Arabidopsis thaliana]
                    119650
  Seq. No.
  Contig ID
                    3626 1.R1010
  5'-most EST
                    LIB3177-070-P1-K1-F7
  Method
                    BLASTX
  NCBI GI
                    q3128168
  BLAST score
                    252
  E value
                    2.0e-21
 Match length
                    80
  % identity
                    55
                    (AC004521) putative carboxyl-terminal peptidase
 NCBI Description
                    [Arabidopsis thaliana]
  Seq. No.
                    119651
  Contig ID
                    3628 1.R1010
  5'-most EST
                    LIB23-008-Q1-E1-E4
  Method
                    BLASTX
  NCBI GI
                    g4218014
  BLAST score
                    727
  E value
                    3.0e-77
 Match length
                    142
```

Contig ID

```
% identity
                   99
                  (AC006135) putative spliceosomal protein (RNA binding
NCBI Description
                  protein) [Arabidopsis thaliana]
                   119652
Seq. No.
                   3639 1.R1010
Contig ID
                   g757637
5'-most EST
                   BLASTX
Method
                   g3377802
NCBI GI
BLAST score
                   479
E value
                   4.0e-48
Match length
                   96
% identity
                  100
                   (AF075597) Similar to sucrose synthase; T2H3.8 [Arabidopsis
NCBI Description
                   thaliana]
                   119653
Seq. No.
                   3644 1.R1010
Contig ID
                  LIB2\overline{5}-042-Q1-E1-G2
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4757662
BLAST score
                   927
E value
                   0.0e + 00
Match length
                  995 ----
% identity
                  98
                  Genomic sequence for Arabidopsis thaliana BAC F10B6 from
NCBI Description
                  chromosome I, complete sequence
Seq. No.
                  119654
                   3653 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327437P4h02b2
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                   66
E value
                   2.0e-28
Match length
                  74
                  97
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  119655
Seq. No.
                   3656 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327425P1f09b1
                   119656
Seq. No.
                   3658 1.R1010
Contig ID
                  LIB3168-009-P1-K1-G9
5'-most EST
Method
                  BLASTX
                  g3738335
NCBI GI
BLAST score
                   312
                  2.0e-28
E value
                  113
Match length
% identity
                   58
                  (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
                   119657
Seq. No.
```

3659_1.R1010

```
5'-most EST
                  jC-atXLIB327416P3d11b1
                  BLASTX
Method
                  g2677828
NCBI GI
BLAST score
                  813
                  9.0e-93
E value
                  262
Match length
                  69
% identity
                  (U93166) cysteine protease [Prunus armeniaca]
NCBI Description
                  119658
Seq. No.
                  3659 2.R1010
Contig ID
                  jC-atXLIB327412P1f08b1
5'-most EST
                  BLASTX
Method
                  g2677828
NCBI GI
BLAST score
                  1378
                  1.0e-153
E value
Match length
                  333
                  75
% identity
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
Seq. No.
                  119659
                  3659 3.R1010
Contig ID
                  jC-atXP50C179H20T7076d1
5'-most EST
Method ·
                  BLASTX
NCBI GI
                  g2677828
BLAST score
                  42
                  4.0e-13
E value
Match length
                  150
% identity
                  31
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
Seq. No.
                  119660
                  3659 4.R1010
Contig ID
                  LIB3175-080-P1-K1-F10
5'-most EST
                  BLASTX
Method
                  g2677828
NCBI GI
BLAST score
                  246
E value
                  6.0e-21
Match length
                  70
% identity
                  71
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
Seq. No.
                  119661
                  3664 1.R1010
Contig ID
                  g2048164
5'-most EST
Method
                  BLASTX
                  g4467128
NCBI GI
BLAST score
                  560
E value
                  1.0e-57
Match length
                  182
% identity
                  58
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                  119662
                  3672 1.R1010
Contig ID
5'-most EST
                  LIB3175-016-P1-K1-F1
```

BLASTX

Method

```
NCBI GI
                  g2225877
BLAST score
                  368
                  3.0e - 35
E value
Match length
                  99
                  70
% identity
                  (AB002406) TIP49 [Rattus norvegicus] >gi 4106528 (AF100694)
NCBI Description
                  Pontin52 [Mus musculus] >gi_4521276_dbj_BAA76313.1_
                   (AB001581) DNA helicase p50 [Rattus norvegicus]
                  119663
Seq. No.
Contig ID
                  3673_1.R1010
5'-most EST
                  LIB23-046-Q1-E1-C9
Method
                  BLASTX
                  q4733981
NCBI GI
                  339
BLAST score
                  6.0e-32
E value
Match length
                  72
% identity
                  85
                  (AC007268) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                  thaliana]
                  119664
Seq. No.
Contig ID
                  3677 1.R1010
5'-most EST
                  g1327702
Method
                  BLASTX
                  g1346831
NCBI GI
BLAST score
                  148
                  3.0e-09
E value
Match length
                  32.
                  91
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I)
NCBI Description
                  >gi 984310 (U26948) photosystem I component [Glycine max]
Seq. No.
                  119665
                  3699_1.R1010
Contig ID
5'-most EST
                  LIB3176-070-P1-K1-E8
                  119666
Seq. No.
Contig ID
                  3702_1.R1010
5'-most EST
                  jC-atXP18C108N4T7053a1
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                   60
E value
                  5.0e-25
Match length
                  60
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  119667
Seq. No.
Contig ID
                  3707 1.R1010
5'-most EST
                  LIB146-022-Q1-E1-A12
Method
                  BLASTX
NCBI GI
                  q4263711
                  304
BLAST score
                  2.0e-27
E value
Match length
                  87
% identity
                  68
```

Method

BLASTN

```
NCBI Description
                  (AC006223) putative CCR4-associated transcription factor
                   [Arabidopsis thaliana]
                  119668
Seq. No.
                  3708 1.R1010
Contig ID
                  LIB3176-063-P1-K1-B8
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3941289
BLAST score
                  314
E value
                  8.0e-29
Match length
                  118
% identity
                  54
NCBI Description (AF018093) similarity to SCAMP37 [Pisum sativum]
                  119669
Seq. No.
                  3710 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327422Pld11b1
                  BLASTX
Method
                  q4588779
NCBI GI
                  299
BLAST score
                  7.0e-27
E value
Match length
                  129
% identity
                  48
                  (AF117267) UDP glucose: flavonoid 3-0-glucosyl transferase
NCBI Description
                  [Malus domestica]
Seq. No.
                  119670
Contig ID
                  3712 1.R1010
                  LIB146-022-Q1-E1-A8
5'-most EST
                  BLASTX
Method
                  q4584528
NCBI GI
                  482
BLAST score
E value
                  2.0e-48
                  104
Match length
% identity
                  91
NCBI Description (AL049607) putative protein [Arabidopsis thaliana]
                  119671
Seq. No.
Contig ID
                  3721 1.R1010
5'-most EST
                  LIB146-022-01-E1-B9
                  119672
Seq. No.
Contig ID
                  3723 2.R1010
                  jC-aTXmonuni25Dg09b1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q16476
BLAST score
                  434
E value
                  0.0e + 00
Match length
                  462
% identity
                  17
NCBI Description
                  Arabidopsis thaliana DNA for rRNA intergenic
                  region; heterogeneous EcoRI fragment
                  119673
Seq. No.
Contig ID
                  3723 3.R1010
5'-most EST
                  jC-atXLIB327423P3f11b1
```

Method

BLASTX

```
g3150006
NCBI GI
BLAST score
                   166
                   3.0e-88
E value
                   768
Match length
% identity
NCBI Description
                  CIC5B11.1 check: 4870 from: 1 to: 167234, complete
                  sequence [Arabidopsis thaliana]
                   119674
Seq. No.
Contig ID
                   3723 4.R1010
5'-most EST
                   jC-atXmonuni25Db02b1
Method
                   BLASTN
                   g16474
NCBI GI
BLAST score
                   342
                   0.0e + 00
E value
                   968
Match length
% identity
                   31
                  Arabidopsis thaliana ribosomal DNA spacer (variant #3)
NCBI Description
                   119675
Seq. No.
                   3739_1.R1010
Contig ID
5'-most EST
                   jC-atxP69C217N16T7044d1
Method
                  BLASTX
                   q4467096
NCBI GI
                   285
BLAST score
                   3.0e-84
E value
Match length
                   314
% identity
                   59
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   119676
Seq. No.
                   3739_2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327413P4g12a1
                   BLASTN
Method
NCBI GI
                   q4314354
BLAST score
                   553
                   0.0e + 00
E value
Match length
                   583
% identity
                   71
                  Arabidopsis thaliana chromosome II BAC T9I22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   119677
Seq. No.
Contig ID
                   3739 3.R1010
5'-most EST
                  jC-atXLIB327411P3c07b1
                  BLASTX
Method
NCBI GI
                   q4314363
BLAST score
                   709
E value
                   5.0e-75
Match length
                   144
                   52
% identity
NCBI Description
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
                   119678
Seq. No.
Contig ID
                   3739 4.R1010
5'-most EST
                  jC-atXLIB327413P4g12b1
```

Contig ID

```
NCBI GI
                  q4314363
                  1523
BLAST score
                  1.0e-170
E value
                  340
Match length
                  69
% identity
NCBI Description
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
                  119679
Seq. No.
                  3739 6.R1010
Contig ID
5'-most EST
                  g2748898
Method
                  BLASTN
NCBI GI
                  q4314354
BLAST score
                  354
                  0.0e + 00
E value
                  446
Match length
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T9I22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  119680
Seq. No.
                  3740 1.R1010
Contig ID
5'-most EST
                  LIB146-022-Q1-E1-F10
Method
                  BLASTN
                  q3766106
NCBI GI
                  201
BLAST score
                  1.0e-109
E value
                  511
Match length
% identity
                  Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  119681
Seq. No.
Contig ID
                  3744_1.R1010
5'-most EST
                  g2762932
Method
                  BLASTN
NCBI GI
                  g2351073
BLAST score
                  299
E value
                  1.0e-167
Match length
                  467
% identity
                  92
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  119682
Contig ID
                  3749 1.R1010
5'-most EST
                  jC-atXLIB327423P2f11b1
                BLASTX
Method
NCBI GI
                  q3257003
BLAST score
                  232
E value
                  5.0e-19
Match length
                  121
% identity
                  (AP000002) 376aa long hypothetical dehydrogenase
NCBI Description
                  [Pyrococcus horikoshii]
Seq. No.
                  119683
```

3752 1.R1010

Match length

101

```
5'-most EST
                  LIB35-046-Q1-E1-B4
Method
                  BLASTX
                  g2661422
NCBI GI
                  787
BLAST score
E value
                  4.0e-84
Match length
                  161
% identity
                  94
                  (AJ001342) Putative S-phase-specific ribosomal protein
NCBI Description
                   [Arabidopsis thaliana] >gi 3096936 emb CAA18846.1
                   (AL023094) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana]
                  119684
Seq. No.
                  3753 1.R1010
Contig ID
                  LIB3234-037-P1-K1-C7
5'-most EST
Method
                  BLASTN
                  g4559375
NCBI GI
                  156
BLAST score
E value
                  2.0e-82
Match length
                  278
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC F11C10 genomic
NCBI Description
                  sequence, complete sequence
                  119685
Seq. No.
                  3770 1.R1010
Contia ID
5'-most EST
                  jC-atXLIB327421P4a06b1
Method
                  BLASTX
                  g2492519
NCBI GI
BLAST score
                  523
                  3.0e-53
E value
Match length
                  114
% identity
                  88
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                  7) >gi 1395191 dbj BAA13021 (D86121) 26S proteasome ATPase
                  subunit [Spinacia oleracea]
Seq. No.
                  119686
                  3781 1.R1010
Contig ID
                  g930<del>9</del>52
5'-most EST
                  BLASTN
Method
                  g2760169
NCBI GI
BLAST score
                  149
                   4.0e-78
E value
                  380
Match length
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFB13, complete sequence [Arabidopsis thaliana]
                  119687
Seq. No.
                  3797 1.R1010
Contiq ID
                   jC-a1X22046Q1E1G08b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4220485
BLAST score
                   365
                   9.0e-35
E value
```

E value

4.0e-19

```
% identity
                   (AC006069) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
                   119688
Seq. No.
Contig ID
                   3804_1.R1010
                  LIB24-112-Q1-E1-G1
5'-most EST
                   BLASTX
Method
                   q2136800
NCBI GI
BLAST score
                   182
E value
                   4.0e-13
Match length
                   93
                   47
% identity
                  polyA binding protein II - bovine >gi 1051125 emb CAA62006
NCBI Description
                   (X89969) polyA binding protein II [Bos taurus]
                   119689
Seq. No.
                   3804 2.R1010
Contig ID
                  LIB25-027-Q1-E1-H8
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2136800
BLAST score
                   264
E value
                   1.0e-22
Match length
                  110
% identity
                   54
                  polyA binding protein II - bovine >gi_1051125_emb_CAA62006_
NCBI Description
                   (X89969) polyA binding protein II [Bos taurus]
                   119690
Seq. No.
                   3812 1.R1010
Contig ID
                   jC-alXLIB327435P2b10a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4512675
                   588
BLAST score
E value
                   9.0e-61
Match length
                   165
% identity
                   72
NCBI Description
                  (AC006931) putative citrate synthase [Arabidopsis thaliana]
                   119691
Seq. No.
                   3812 2.R1010
Contig ID
5'-most EST
                  LIB3168-005-P1-K1-E6
                  BLASTX
Method
NCBI GI
                   g4512675
                   451
BLAST score
                   6.0e-45
E value
                   121
Match length
% identity
                   76
                  (AC006931) putative citrate synthase [Arabidopsis thaliana]
NCBI Description
                   119692
Seq. No.
                   3816 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327409P2f11b1
Method
                  BLASTX
NCBI GI
                   g4432860
BLAST score
                   234
```

```
87
Match length
                  57
% identity
                  (AC006300) putative glucose-induced repressor protein
NCBI Description
                   [Arabidopsis thaliana]
                  119693
Seq. No.
                  3816 2.R1010
Contig ID
                  g2748215
5'-most EST
                 · BLASTX
Method
                  g4432860
NCBI GI
BLAST score
                  224
E value
                  2.0e-80
Match length
                  318
                  23
% identity
                  (AC006300) putative glucose-induced repressor protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  119694
                  3824 1.R1010
Contig ID
5'-most EST
                  LIB22-074-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  g2462762
BLAST score
                  1022
E value
                  1.0e-151
Match length
                  296
% identity
                  89
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  119695
Seq. No.
                  3824 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327425P3g09b1
                  BLASTX
Method
                  g2462762
NCBI GI
BLAST score
                   635
                  2.0e-66
E value
Match length
                  125
                  99
% identity
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  119696
Seq. No.
                  3824 4.R1010
Contig ID
5'-most EST
                  jC-atXLIB327428P4g12b2
Method
                  BLASTX
                  g2462763
NCBI GI
BLAST score
                  515
                  2.0e-52
E value
                  102
Match length
                  99
% identity
NCBI Description
                  (AC002292) Highly similar to auxin-induced protein
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  119697
Seq. No.
                  3826 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327424P1e02b2
Method
                  BLASTX
```

Seq. No.

119702

```
NCBI GI
                  q4512699
BLAST score
                  587
                  2.0e-63
E value
Match length
                  178
% identity
                  75
                   (AC006569) putative NADH-ubiquinone oxireductase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  119698
                  3832 1.R1010
Contig ID
                  LIB3234-058-P1-K1-E4
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4158219
BLAST score
                  249
E value
                  3.0e-21
Match length
                  85
% identity
                  64
NCBI Description
                  (Y18623) amylogenin [Oryza sativa]
                  119699
Seq. No.
Contig ID
                  3833 1.R1010
                  jC-atXLIB327402P1a08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4567243
BLAST score
                  369
E value
                  1.0e-36
Match length
                  134
% identity
                  56
NCBI Description
                  (AC007070) putative synaptobrevin protein [Arabidopsis
                  thaliana]
                  119700
Seq. No.
Contig ID
                  3835 1.R1010
5'-most EST
                  jC-atXLIB327416P4f03b1
Method
                  BLASTX
NCBI GI
                  q3193316
BLAST score
                  183
E value
                  2.0e-13
Match length
                  118
% identity
                  39
NCBI Description
                  (AF069299) contains similarity to nucleotide sugar
                  epimerases [Arabidopsis thaliana]
Seq. No.
                  119701
Contig ID
                  3839 1.R1010
5'-most EST
                  LIB3234-041-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q3413718
BLAST score
                  882
E value
                  3.0e-95
Match length
                  168
% identity
                  98
                  (AC004747) alpha-vacuolar processing enzyme [Arabidopsis
NCBI Description
                  thaliana] >gi_3643591 (AC005395) alpha-vacuolar processing
                  enzyme [Arabidopsis thaliana]
```

```
3848 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327409P3h02b1
Method
                   BLASTN
NCBI GI
                  g2392762
BLAST score
                   416
E value
                   0.0e + 00
Match length
                   456
% identity
                   98
NCBI Description
                  Arabidopsis thaliana BAC T32N15 from chromsome III near 54
                  cM, complete sequence
                   119703
Seq. No.
                  3865 1.R1010
Contig ID
                   LIB146-025-Q1-E1-E1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4510385
BLAST score
                   338
E value
                   2.0e-31
Match length
                   97
% identity
                   73
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                   119704
Contig ID
                   3869 1.R1010
5'-most EST
                  LIB146-025-Q1-E1-E2
Method
                  BLASTX
NCBI GI
                   q4220514
BLAST score
                   200
E value
                   2.0e-15
Match length
                   61
% identity
                   57
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                   119705
Seq. No.
                  3872_1.R1010
LIB3234-039-P1-K1-B2
Contig ID
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3132475
BLAST score
                   631
E value
                   6.0e-66
Match length
                   136
% identity
                   88
NCBI Description
                   (AC003096) similar to proline-rich protein [Arabidopsis
                  thaliana]
Seq. No.
                  119706
Contig ID
                   3883 1.R1010
5'-most EST
                  jC-atXLIB327415P2a08b2
Method
                  BLASTN
NCBI GI
                  q3510341
BLAST score
                   239
E value
                   1.0e-131
Match length
                   434
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MFC16, complete sequence [Arabidopsis thaliana]

BLAST score

519

```
Seq. No.
                  119707
                  3895 1.R1010
Contig ID
                  jC-atXLIB327427P2g10b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3915866
BLAST score
                  690
E value
                  1.0e-72
Match length
                  189
                  69
% identity
NCBI Description
                  GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)
                  >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine
                  synthetase [Lupinus luteus]
Seq. No.
                  119708
                  3900 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327411P3b04b1
Method
                  BLASTX
NCBI GI
                  q2062164
BLAST score
                  758
                  3.0e-84
E value
                  166
Match length
% identity
                  96
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
                  119709
Seq. No.
                  3900 2.R1010
Contig ID
5'-most EST
                  LIB3177-070-P1-K1-G7
                  BLASTX
Method
                  q2062164
NCBI GI
BLAST score
                  851
                  2.0e-91
E value
Match length
                  166
% identity
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  119710
Seq. No.
Contig ID
                  3904 1.R1010
5'-most EST
                  jC-atXP95CG12G8T7037d1
Method
                  BLASTX
NCBI GI
                  q2497542
BLAST score
                  45
E value
                  1.0e-36
Match length
                  103
% identity
                  PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR
NCBI Description
                  >gi_629696_pir__S44287 pyruvate kinase, plastid - common
                  tobacco >gi 482938 emb CAA82223 (Z28374) Pyruvate kinase;
                  plastid isozyme [Nicotiana tabacum]
                  119711
Seq. No.
Contig ID
                  3911 1.R1010 .
5'-most EST
                  LIB146-026-Q1-K1-A4
Method
                  BLASTN
NCBI GI
                  q3659491
```

Method

BLASTX

```
E value
                  0.0e + 00
                  623
Match length
                  98
% identity
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                  119712
Seq. No.
                  3914 1.R1010
Contig ID
5'-most EST
                  LIB3168-100-P1-K1-H3
Seq. No.
                  119713
Contig ID
                  3914 2.R1010
5'-most EST
                  LIB3176-039-P1-K1-E2
                  119714
Seq. No.
                  3917 1.R1010
Contig ID
5'-most EST
                  jC-a\(\bar{1}\)XLIB327436P4d07b1
Method
                  BLASTX
                  g2498731
NCBI GI
BLAST score
                  387
E value
                  1.0e-48
Match length
                  164
% identity
                  63
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                  >gi_1362013_pir__S57611 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)
                  zeta-crystallin homologue [Arabidopsis thaliana]
                  119715
Seq. No.
                  3917 2.R1010
Contig ID
                  LIB3234-089-P1-K1-H7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2498731
BLAST score
                  208
E value
                  1.0e-16
Match length
                  77
% identity
                  56
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                  >gi_1362013_pir__S57611 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)
                  zeta-crystallin homologue [Arabidopsis thaliana]
                  119716
Seq. No.
Contig ID
                  3918_1.R1010
                  g906770
5'-most EST
                  BLASTX
Method
                  g2642158
NCBI GI
BLAST score
                  86
                  2.0e-22
E value
Match length
                  154
% identity
                  43
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119717
Contig ID
                  3920_1.R1010
                  LIB3234-070-P1-K1-H5
5'-most EST
```

```
NCBI GI
                  g3024871
BLAST score
                   415
                   9.0e-41
E value
Match length
                   137
% identity
                   57
                  HYPOTHETICAL 77.3 KD PROTEIN SLL0005
NCBI Description
                  >gi 1001579 dbj BAA10206 (D64000) ABC1-like [Synechocystis
                   sp.]
                   119718
Seq. No.
                   3922 1.R1010
Contig ID
                  LIB146-026-Q1-K1-B4
5'-most EST
                   119719
Seq. No.
                  3925 1.R1010
Contig ID
                  LIB3234-076-P1-K1-C11
5'-most EST
                  BLASTN
Method
NCBI GI "
                  g11576
BLAST score
                   116
                   7.0e-59
E value
Match length
                   164
% identity
                   93
                  Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
NCBI Description
                  NADH dehydrogenase and ORF
Seq. No.
                   119720
                   3926 1.R1010
Contig ID
                   jC-atXLIB327409P4h02b1
5'-most EST
Method
                   BLASTX
                  g4206210
NCBI GI
BLAST score
                   889
E value
                   4.0e-96
Match length
                   177
% identity
                   68
                   (AF071527) putative calcium channel [Arabidopsis thaliana]
NCBI Description
                   >qi 4263043 qb AAD15312 (AC005142) putative calcium
                   channel [Arabidopsis thaliana]
                  119721
Seq. No.
                   3928 1.R1010
Contig ID
5'-most EST
                   jC-alXLIB327436P4b11b1
Method
                   BLASTX
NCBI GI
                  g1353352
BLAST score
                   335
                   5.0e-43
E value
Match length
                   132
% identity
                   73
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
                   119722
Seq. No.
                   3928 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327431P2h02a1
Method
                  BLASTX
                  g1353352
NCBI GI
BLAST score
                  890
                  7.0e-96
E value
```

BLAST score

572

```
Match length
                   249
% identity
                   65
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
Seq. No.
                   119723
                   3928_3.R1010
Contig ID
                   LIB3175-058-P1-K1-F1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1353352
BLAST score
                   808
E value
                   3.0e-86
Match length
                   300
                   59
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
                   119724
Seq. No.
                   3929_1.R1010
Contig ID
5'-most EST
                   g2062833
                   BLASTN
Method
NCBI GI
                   q2583106
BLAST score
                   346
                   0.0e + 00
E value
                   497
Match length
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC F4L23 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   119725
Seq. No.
                   3929 2.R1010
Contig ID
5'-most EST
                   jC-aTXLIB327434P3g06b1
Method
                   BLASTX
                   q2583108
NCBI GI
BLAST score
                   1075
E value
                   1.0e-117
                   216
Match length
% identity
                   100
NCBI Description
                   (AC002387) putative surface protein [Arabidopsis thaliana]
                   119726
Seq. No.
                   3929 3.R1010
Contig ID
5'-most EST
                   LIB3177-018-P1-K2-G8
Method
                   BLASTX
NCBI GI
                   q2583108
BLAST score
                   845
                   4.0e-91
E value
Match length
                   221
% identity
                   84
NCBI Description
                  (AC002387) putative surface protein [Arabidopsis thaliana]
                   119727
Seq. No.
                   3933_1.R1010
Contig ID
5'-most EST
                   LIB3234-001-P1-K1-C2
Method
                   BLASTX
                   q3935149
NCBI GI
```

ď.

NCBI GI

```
6.0e-59
E value
Match length
                   204
% identity
                   58
                  (AC005106) T25N20.13 [Arabidopsis thaliana]
NCBI Description
                  119728
Seq. No.
                   3934 1.R1010
Contig ID
                  LIB146-026-Q1-K1-C6
5'-most EST
Method
                  BLASTN
                  q4159704
NCBI GI
BLAST score
                  21
                   9.3e-02
E value
                   416
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MCB17, complete sequence
                  119729
Seq. No.
Contig ID
                   3936 1.R1010
                  jC-atXP10C95K11T7s1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2760172
BLAST score
                  451
E value
                  0.0e + 00
Match length
                  840
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUB3, complete sequence [Arabidopsis thaliana]
                  119730
Seq. No.
Contig ID
                  3937 1.R1010
5'-most EST
                  jC-atXP118C143D19T7057d2
Method
                  BLASTN
NCBI GI
                  q4580745
BLAST score
                  556
E value
                  0.0e + 00
Match length
                  661
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
                  complete sequence
Seq. No.
                  119731
Contig ID
                  3938 1.R1010
5'-most EST
                  LIB3234-087-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  q225279
BLAST score
                  50
E value
                  6.0e-28
Match length
                  93
% identity
                  76
                  rpoC-like ORF 236 [Nicotiana tabacum]
NCBI Description
                  119732
Seq. No.
Contig ID
                  3939 1.R1010
5'-most EST
                  LIB25-047-Q1-E1-C7
Method
                  BLASTN
```

q3047074

5'-most EST

Method

```
BLAST score
                   546
E value
                   0.0e + 00
Match length
                   593
                   98
% identity
NCBI Description Arabidopsis thaliana BAC F21E10
Seq. No.
                  119733
                   3939 2.R1010
Contig ID
5'-most EST
                  LIB146-026-Q1-K1-D12
Method
                  BLASTN
NCBI GI
                   q3047074
BLAST score
                   352
E value
                   0.0e + 00
Match length
                   452
                   95
% identity
                  Arabidopsis thaliana BAC F21E10
NCBI Description
                   119734
Seq. No.
                   3942_1.R1010
Contig ID
                  LIB25-112-Q1-E1-B9
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3702731
BLAST score
                   369
                   0.0e + 00
E value
                   702
Match length
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFC19, complete sequence [Arabidopsis thaliana]
                   119735
Seq. No.
Contig ID
                   3943_1.R1010
5'-most EST
                  LIB146-026-Q1-K1-D6
Method
                  BLASTN
NCBI GI
                  g3133272
BLAST score
                   153
E value
                   1.0e-80
                   219
Match length
% identity
                   95
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T17H7,
                  complete sequence [Arabidopsis thaliana]
                   119736
Seq. No.
Contig ID
                   3948 1.R1010
5'-most EST
                  LIB146-026-Q1-K1-E3
Method
                  BLASTN
NCBI GI
                  q3608126
BLAST score
                   267
E value
                  1.0e-148
Match length
                   429
% identity
                  Arabidopsis thaliana chromosome II BAC T32F12 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  119737
Seq. No.
Contig ID
                  3949 1.R1010
```

jC-atXLIB327429P1f01b2

BLASTX

```
q4455307
NCBI GI
BLAST score
                   405
E value
                   6.0e-39
                   156
Match length
                   54
% identity
NCBI Description
                   (AL035528) methionyl-tRNA synthetase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   119738
                   3949 3.R1010
Contig ID
5'-most EST
                   LIB3168-034-P1-K1-C7
                   119739
Seq. No.
                   3953 1.R1010
Contig ID
5'-most EST
                   LIB3168-013-P1-K1-D4
                   BLASTX
Method
NCBI GI
                   q860891
BLAST score
                   456
                   2.0e-45
E value
                   92
Match length
                   95
% identity
NCBI Description
                   (X87636) PSII cytochome b559 alpha chain [Beta vulgaris]
                   >gi_860897_emb_CAA60972_ (X87637) PSII cytochrome b599
                   alpha chain [Beta vulgaris]
                   119740
Seq. No.
                   3955 1.R1010
Contig ID
5'-most EST
                   q762\overline{9}15
Method
                   BLASTN
                   q4584387
NCBI GI
BLAST score
                   154
                   4.0e-81
E value
Match length
                   424
% identity
                   100
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7
                   (ESSA project)
                   119741
Seq. No.
Contig ID
                   3957 1.R1010
                   LIB3234-079-P1-K1-C6
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2264307
BLAST score
                   246
E value
                   1.0e-136
Match length
                   394
                   91
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MED24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   119742
Contig ID
                   3959 1.R1010
5'-most EST
                   jC-atXLIB327411P3f02a1
Method
                   BLASTN
NCBI GI
                   g2462264
BLAST score
                  -53
E value
                   9.0e-21
Match length
                   53
```

```
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  119743
Seq. No.
                  3960 1.R1010
Contig ID
5'-most EST
                  LIB146-026-Q1-K1-F3
                  BLASTX
Method
                  q4558566
NCBI GI
                  685
BLAST score
E value
                  2.0e-72
Match length
                  131
% identity
                  100
                  (AC007138) putative raffinose synthase or seed imbibition
NCBI Description
                  protein [Arabidopsis thaliana]
                  119744
Seq. No.
Contig ID
                  3961 1.R1010
                  g2748351
5'-most EST
Method
                  BLASTN
                  g3212846
NCBI GI
BLAST score
                  638
E value
                  0.0e + 00
Match length
                  692
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  119745
Seq. No.
                  3961_3.R1010
Contig ID
                  LIB25-050-Q1-E1-B4
5'-most EST
Method
                  BLASTX
                  g119194
NCBI GI
BLAST score
                  658
E value
                  2.0e-98
Match length
                  228
                  87
% identity
                  ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
NCBI Description
                  >gi_81607_pir__S09152 translation elongation factor Tu
                  precursor, chloroplast - Arabidopsis thaliama
                  >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu
                  precursor [Arabidopsis thaliana] >gi 226817 prf 1607332A
                  elongation factor Tu [Arabidopsis thaliana]
                  119746
Seq. No.
                  3961 4.R1010
Contig ID
                  g906<del>9</del>59
5'-most EST
Method .
                  BLASTX
NCBI GI
                  q119194
BLAST score
                  1289
E value
                  1.0e-142
Match length
                  254
                  100
% identity
                  ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
NCBI Description
                  >gi_81607_pir__S09152 translation elongation factor Tu
                  precursor, chloroplast - Arabidopsis thaliana
                  >gi 22565 emb CAA36498 (X52256) elongation factor Tu
                  precursor [Arabidopsis thaliana] >gi 226817_prf__1607332A
```

elongation factor Tu [Arabidopsis thaliana]

```
Seq. No.
                    119747
Contig ID
                    3961 6.R1010
5'-most EST
                    jC-atXLIB327405P2g02b2
Method
                    BLASTX
NCBI GI
                    g119194
BLAST score
                    490
E value
                    2.0e-49
Match length
                    106
% identity
                    88
NCBI Description
                    ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                    >gi 81607 pir S09152 translation elongation factor Tu
                    precursor, chloroplast - Arabidopsis thaliana

>gi_22565_emb_CAA36498_ (X52256) elongation factor Tu

precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A
                    elongation factor Tu [Arabidopsis thaliana]
                    119748
Seq. No.
                    3961_7.R1010
Contig ID
5'-most EST
                    LIB3176-042-P1-K1-G11
Method
                    BLASTX
NCBI GI
                    q2494261
BLAST score
                    326
                    3.0e - 30
E value
                    69
Match length
                    99
% identity
NCBI Description
                    ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                    >gi 99903 pir S21567 translation elongation factor Tu
                    precursor - soybean chloroplast >gi_18776_emb_CAA46864_
                    (X66062) EF-Tu [Glycine max] >gi_448921_prf_1918220A
                    elongation factor Tu [Glycine max]
                    119749
Seq. No.
Contig ID
                    3962 1.R1010
5'-most EST
                    LIB146-026-Q1-K1-F5
Seq. No.
                    119750
Contig ID
                    3963 1.R1010
5'-most EST
                    jC-atXLIB327413P1b10b1
Method
                    BLASTX
NCBI GI
                    g4510383
BLAST score
                    664
E value
                    4.0e-94
Match length
                    262
% identity
NCBI Description
                    (AC007017) unknown protein [Arabidopsis thaliana]
                    119751
Seq. No.
                    3967 1.R1010
Contig ID
5'-most EST
                    LIB3234-058-P1-K1-B4
Method
                    BLASTX
NCBI GI
                    g2493696
BLAST score
                    772
E value
                    6.0e-82
Match length
                    184
% identity
                    82
```

NCBI Description HYPOTHETICAL 21.5 KD PROTEIN (ORF 185) >gi_1480440 (U34204) ORF185; hypothetical 21.4 kD protein [Brassica oleracea]

Seq. No. 119752

Contig ID 3969_1.R1010

5'-most EST LIB3176-024-P1-K1-A6

Method BLASTN
NCBI GI g4388816
BLAST score 280
E value 1.0e-156
Match length 524
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC F9B22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 119753

Contig ID 3973 1.R1010

5'-most EST jC-atXP13C104D22T7048a1

Method BLASTX
NCBI GI g3193301
BLAST score 528
E value 1.0e-53
Match length 179
% identity 64

NCBI Description (AF069298) Arabidopsis putative chloroplast outer envelope

86-like protein T10P11.19 (GB: AC002330) [Arabidopsis

thaliana]

Seq. No. 119754

Contig ID 3973_2.R1010

5'-most EST jC-atXLIB327408P4c05b1

Method BLASTX
NCBI GI g3193301
BLAST score 1358
E value 1.0e-150
Match length 369
% identity 76

NCBI Description (AF069298) Arabidopsis putative chloroplast outer envelope

86-like protein T10P11.19 (GB: AC002330) [Arabidopsis

thaliana]

Seq. No. 119755

Contig ID 3973_3.R1010

5'-most EST LIB3177-059-P1-K1-G1

Method BLASTX
NCBI GI g3193301
BLAST score 501
E value 8.0e-51
Match length 138
% identity 77

NCBI Description (AF069298) Arabidopsis putative chloroplast outer envelope

86-like protein T10P11.19 (GB: AC002330) [Arabidopsis

thaliana]

Seq. No. 119756

Contig ID 3974 1.R1010

5'-most EST jC-atXLIB327422P4a05b1

```
Method
                   BLASTN
NCBI GI
                   g2582640
BLAST score
                   57
                   6.0e-23
E value
Match length
                   77
                   94
% identity
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   119757
Seq. No.
                   3974 2.R1010
Contig ID
                   jC-atXP83CG3E8T7054a1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q1313927
BLAST score
                   53
E value
                   1.0e-20
                   229
Match length
% identity
                   81
NCBI Description B.oleracea mRNA for IFA binding protein (sp10)
Seq. No.
                   119758
                   3979 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327419P4c09b1
Method
                   BLASTX
NCBI GI .
                   q4056432
BLAST score
                   989
E value
                   1.0e-107
                   236
Match length
                   73
% identity
                   (AC005990) Similar to gi_2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig
NCBI Description
                   gb Z97341. ESTs gb T20778 and gb AA586281 come from this
                   gene. [Arabidopsis thaliana]
                   119759
Seq. No.
                   3982 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327430P4b09b1
Method
                   BLASTX
                   q2500378
NCBI GI
BLAST score
                   464
                   4.0e-46
E value
                   95
Match length
% identity
                   92
                   60S RIBOSOMAL PROTEIN L37
NCBI Description
Seq. No.
                   119760
                   3982_3.R1010
Contig ID
                   LIB24-070-Q1-E1-H5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2500378
BLAST score
                   448
                   2.0e-44
E value
                   87
Match length
% identity
                   95
NCBI Description 60S RIBOSOMAL PROTEIN L37
                   119761
Seq. No.
```

```
Contig ID
                   3982 4.R1010 -
5'-most EST
                   jC-atXLIB327401P3a04b2
Method
                   BLASTX
                   g2500378
NCBI GI
                   480
BLAST score
E value
                   4.0e-48
                   89
Match length
                   99
% identity
                  60S RIBOSOMAL PROTEIN L37
NCBI Description
                   119762
Seq. No.
Contig ID
                   3982_5.R1010
5'-most EST
                   jC-atXLIB327426P3f07b1
Method
                   BLASTX
                   q2500378
NCBI GI
                   370
BLAST score
                   2.0e-35
E value
Match length
                   69
                  99
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L37
                  119763
Seq. No.
Contig ID
                  3984 1.R1010
5'-most EST
                   jC-alX22048Q1E1C04b1
                  BLASTX
Method
                                                                    والمعاوي
NCBI GI
                  g1929056
BLAST score
                   464
                   2.0e-46
E value
Match length
                   98
                   90
% identity
                  (Y12090) putative 3,4-dihydroxy-2-butanone kinase
NCBI Description
                   [Lycopersicon esculentum]
Seq. No.
                   119764
Contig ID
                   3985 1.R1010
5'-most EST
                  LIB146-027-Q1-K1-A4
Method
                  BLASTN
                  g12218
NCBI GI
BLAST score
                   224
E value
                  1.0e-123
Match length
                  264
% identity
                  96
NCBI Description Sinapis alba chloroplast trnG gene for transfer RNA-Gly
                  119765
Seq. No.
Contig ID
                   3987_1.R1010
5'-most EST
                   jC-atXP82CG1D12T7b1
Method
                  BLASTX
                  g3024871
NCBI GI
BLAST score
                   506
                   6.0e-51
E value
Match length
                  228
% identity
                   45
NCBI Description
                  HYPOTHETICAL 77.3 KD PROTEIN SLL0005
                  >gi_1001579 dbj BAA10206 (D64000) ABC1-like [Synechocystis
```

sp.]

```
119766
Seq. No.
                   3989 1.R1010
Contig ID
                   jC-atXLIB327419P3h04b2
5'-most EST
                   BLASTX
Method
                   g2558654
NCBI GI
BLAST score
                   788
E value
                   3.0e-84
                   156
Match length
                   100
% identity
NCBI Description
                   (AC002354) No definition line found [Arabidopsis thaliana]
                   119767
Seq. No.
Contig ID
                   3990 1.R1010
5'-most EST
                   jC-atXLIB327421P4a12b1
                   BLASTN
Method
NCBI GI
                   g3047074
BLAST score
                   71
E value
                   2.0e-31
Match length
                   150
                   87
% identity
NCBI Description
                   Arabidopsis thaliana BAC F21E10
                   119768
Seq. No.
Contig ID
                   3991 1.R1010
5'-most EST
                   LIB3175-051-P1-K1-A8
                   BLASTN
Method
                   q3869067
NCBI GI
BLAST score
                   146
E value
                   3.0e-76
Match length
                   532
                   95
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCK7, complete sequence [Arabidopsis thaliana]
                   119769
Seq. No.
Contig ID
                   3992_1.R1010
                   LIB3234-076-P1-K1-D11
5'-most EST
                   119770
Seq. No.
Contig ID
                   3995 1.R1010
                   LIB3168-088-P1-K1-E12
5'-most EST
                   BLASTX
Method
                   q114654
NCBI GI
BLAST score
                   289
                   2.0e-25
E value
                   81
Match length
% identity
NCBI Description
                   ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)
                   >gi 67898 pir LWNTA H+-transporting ATP synthase (EC
                   3.6.1.34) lipid-binding protein - common tobacco
                   chloroplast >gi_11812_emb_CAA77343_ (Z00044) ATPase III
                   subunit [Nicotiana tabacum] >gi_343484 (M10124) ATPase subunit III [Nicotiana tabacum] >gi_224347_prf__1102209A
                   ATPase III, H translocating [Nicotiana sp.]
                   >gi 225272 prf 1211235G ATPase III [Nicotiana tabacum]
```

119771

Seq. No.

5'-most EST

```
3998 1.R1010
Contig ID
5'-most EST
                    LIB3234-015-P1-K1-B8
Method
                    BLASTX
NCBI GI
                    g225280
BLAST score
                    436
E value
                    4.0e-43
Match length
                    96
% identity
                    86
NCBI Description
                    rpoC-like ORF 548 [Nicotiana tabacum]
Seq. No.
                    119772
                    3999 1.R1010
Contig ID
5'-most EST
                    LIB3168-052-P1-K1-F3
Method
                    BLASTX
NCBI GI
                    q133841
BLAST score
                    378
E value
                    6.0e-36
Match length
                    84
% identity
                    92
NCBI Description
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S18 >gi_71016_pir__R3NT18
                    ribosomal protein S18 - common tobacco chloroplast >gi_11851_emb_CAA77371 (Z00044) ribosomal protein S18 [Nicotiana tabacum] >gi_225220_prf__1211235BB ribosomal
                    protein S18 [Nicotiana tabacum]
                    119773
Seq. No.
Contig ID
                    4001 1.R1010
5'-most EST
                    jC-atXLIB327427P4e05b2
                    119774
Seq. No.
                    4001 2.R1010
Contig ID
5'-most EST
                    jC-atXLIB327423P3d04b1
Method
                    BLASTX
NCBI GI
                    q4008544
BLAST score
                    167
E value
                    3.0e-11
Match length
                    104
% identity
                    37
                    (AL034492) putative nucleotide-sugar dehydratase
NCBI Description
                    [Streptomyces coelicolor]
Seq. No.
                    119775
                    4002 1.R1010
Contig ID
                    LIB3234-080-P1-K1-F1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3924604
BLAST score
                    478
                    2.0e-48
E value
Match length
                    98
% identity
                    30
                    (AF069442) putative leucine-rich repeat protein
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    119776
                    4003 1.R1010
Contig ID
```

LIB3234-084-Q1-K1-F3

```
Seq. No.
                  119777
Contig ID
                  4006 1.R1010
5'-most EST
                  jC-atXLIB327425P3h12b1
Method
                  BLASTX
NCBI GI
                  g2982266
                  207
BLAST score
                  1.0e-48
E value
Match length
                  146
% identity
                  73
                  (AF051216) probable fibrillarin [Picea mariana]
NCBI Description
Seq. No.
                  119778
                  4007 1.R1010
Contig ID
                  jC-atXLIB327431P4e03a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3193316
BLAST score
                  966
E value
                  1.0e-104
Match length
                  285
% identity
                  69
NCBI Description
                  (AF069299) contains similarity to nucleotide sugar
                  epimerases [Arabidopsis thaliana]
                  119779
Seq. No.
                  4007 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P3f12b1
Method
                  BLASTX
NCBI GI
                  g3193316
BLAST score
                  736
E value
                  1.0e-77
Match length
                  266
% identity
                  59
NCBI Description
                  (AF069299) contains similarity to nucleotide sugar
                  epimerases [Arabidopsis thaliana]
Seq. No.
                  119780
                  4007 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327425P1g04b1
Method
                  BLASTX
NCBI GI
                  g2583123
BLAST score
                  321
E value
                  3.0e-29
Match length
                  146
% identity
                  53
NCBI Description
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
                  thaliana]
Seq. No.
                  119781
Contig ID
                  4008 2.R1010
5'-most EST
                  LIB3177-072-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q140285
BLAST score
                  207
E value
                  7.0e-16
Match length
                  42
                  95
% identity
NCBI Description HYPOTHETICAL 19 KD PROTEIN (ORF 168)
```

```
119782
 Seq. No.
                    4017 1.R1010
· Contig ID
 5'-most EST
                    LIB146-027-Q1-K1-F1
 Method
                    BLASTN
                    g3659491
 NCBI GI
                    325
 BLAST score
 E value
                    0.0e + 00
 Match length
                    419
 % identity
                    93
                    Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
 NCBI Description
                    1, complete sequence [Arabidopsis thaliana]
                    119783
 Seq. No.
 Contig ID
                    4019 1.R1010
                    jC-atXLIB327418P4e02b1
 5'-most EST
 Method
                    BLASTN
 NCBI GI
                    g4159703
 BLAST score
                    149
 E value
                    9.0e-78
 Match length
                    351
 % identity
                    100
                    Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 NCBI Description
                    K5F14, complete sequence
                    119784
 Seq. No.
                    4019 2.R1010
 Contig ID
 5'-most EST
                    jC-atXP81C240M8T7d1
 Method
                    BLASTN
 NCBI GI
                    g4159703
 BLAST score
                    149
                    6.0e-78
 E value
 Match length
                    169
 % identity
                    100
                    Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 NCBI Description
                    K5F14, complete sequence
                    119785
 Seq. No.
                    4019 3.R1010
 Contig ID
 5'-most EST
                    LIB3234-082-Q1-K1-D5
 Method
                    BLASTX
 NCBI GI
                    q2244797
 BLAST score
                    260
                    3.0e-22
 E value
                    92
 Match length
 % identity
                    57
                    (Z97336) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    119786
 Seq. No.
                    4020 1.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327402P2d01a1
                    BLASTX
 Method
 NCBI GI
                    q4741201
 BLAST score
                    1062
                    1.0e-116
 E value
```

>gi 2924263_emb_CAA77415_ (Z00044) Ycf3 protein [Nicotiana

tabacum]

Match length 246 % identity (AL049746) putative protein [Arabidopsis thaliana] NCBI Description 119787 Seq. No. 4021 1.R1010 Contig ID jC-atXLIB327430P4d09b1 5'-most EST **BLASTX** Method NCBI GI q3243033 BLAST score 223 E value 8.0e-18 Match length 199 32 % identity (AF069765) signal recognition particle 72 [Homo sapiens] NCBI Description >gi 3335650 (AF077019) signal recognition particle 72 [Homo sapiens] Seq. No. 119788 4022_1.R1010 Contig ID 5'-most EST g2047823 Method BLASTN NCBI GI g3510347 BLAST score 396 0.0e + 00E value 456 Match length % identity 97 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana] 119789 Seq. No. 4024 1.R1010 Contig ID 5'-most EST LIB3234-092-P1-K1-H6 Method BLASTX q4406809 NCBI GI BLAST score 162 E value 8.0e-11 100 Match length % identity 44 NCBI Description (AC006201) unknown protein [Arabidopsis thaliana] 119790 Seq. No. 4025 1.R1010 Contig ID LIB146-027-Q1-K1-G2 5'-most EST Method BLASTX NCBI GI q2651310 BLAST score 188

1.0e-48 E value Match length 102 % identity 98

NCBI Description (AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

119791 Seq. No.

4025 2.R1010 Contig ID

jC-atx24066Q1E1E06b1 5'-most EST

BLASTX Method NCBI GI g2651310

```
BLAST score
                  1405
E value
                  1.0e-156
Match length
                  283
                        S. Marie a
                  95
% identity
NCBI Description
                  (AC002336) putative PTR2-B peptide transporter [Arabidopsis
                  thaliana]
                  119792
Seq. No.
Contig ID
                  4029_1.R1010
5'-most EST
                  LIB146-027-Q1-K1-G6
Method
                  BLASTN
NCBI GI
                  g2244829
                  159
BLAST score
                  4.0e-84
E value
Match length
                  249
                  97
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                  119793
Seq. No.
Contig ID
                  4032_1.R1010
5'-most EST
                  jC-atXP89CG6C2T7045d1
Method
                  BLASTX
NCBI GI
                  g1931647
BLAST score
                  1496
E value
                  1.0e-167
Match length
                  348
% identity
                  82
NCBI Description
                  (U95973) endomembrane protein EMP70 precusor isolog
                  [Arabidopsis thaliana]
                  119794
Seq. No.
Contig ID
                  4032_2.R1010
5'-most EST
                  jC-atX25069Q1E1B01b1
Method
                  BLASTN
                  g1931636
NCBI GI
                  273
BLAST score
                  1.0e-152
E value
Match length
                  478
% identity
                  98
NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence
                  119795
Seq. No.
Contig ID
                  4036 1.R1010
5'-most EST
                  g934861
                  119796
Seq. No.
Contig ID
                  4037 1.R1010
5'-most EST
                  LIB23-058-Q1-E1-A9
Method
                  BLASTN
NCBI GI
                  q4467094
BLAST score
                  331
E value
                  0.0e + 00
Match length
                  579
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
```

(ESSA project)

```
119797
  Seq. No.
 Contig ID
                    4039 1.R1010
  5'-most EST
                    LIB3175-064-P1-K1-C8
 Method
                    BLASTN
                    q4510360
 NCBI GI
_ BLAST score
                    360
                    0.0e + 00
 E value
 Match length
                    431
                    100
 % identity
                    Arabidopsis thaliana chromosome II BAC F11F19 genomic
 NCBI Description
                    sequence, complete sequence
                    119798
 Seq. No.
                    4041 1.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327409P1e01b1
 Method
                    BLASTX
 NCBI GI
                    q3128205
 BLAST score
                    211
                    2.0e-28
 E value
 Match length
                    96
                    79
 % identity
 NCBI Description
                    (AC004077) putative pyruvate dehydrogenase complex E1 beta
                    subunit [Arabidopsis thaliana]
 Seq. No.
                    119799
                    4041 2.R1010
 Contig ID
 5'-most EST
                    g2581660
 Method
                    BLASTX
                    q3212869
 NCBI GI
 BLAST score
                    430
                    3.0e-42
 E value
 Match length
                    147
 % identity
                    61
 NCBI Description
                    (AC004005) unknown protein [Arabidopsis thaliana]
                    119800
 Seq. No.
                    4041 4.R1010
 Contig ID
 5'-most EST
                    jC-atXP2C77G11T7066a1
 Method
                    BLASTX
 NCBI GI
                    g3128205
 BLAST score
                    588
                    1.0e-107
 E value
 Match length
                    203
 % identity
                    98
                    (AC004077) putative pyruvate dehydrogenase complex E1 beta
 NCBI Description
                    subunit [Arabidopsis thaliana]
 Seq. No.
                    119801
 Contig ID
                    4041 5.R1010
 5'-most EST
                    jC-atXP104CE7B10T7b1
 Method
                    BLASTX
 NCBI GI
                    g3212869
 BLAST score
                    533
 E value
                    3.0e-54
 Match length
                    111
 % identity
```

91

```
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                   119802
Seq. No.
Contig ID
                   4041 6.R1010
                   jC-atXLIB327409P3d06a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3212869
BLAST score
                   420
E value
                   4.0e-41
Match length
                   89
                   87
% identity
NCBI Description
                   (AC004005) unknown protein [Arabidopsis thaliana]
                   119803
Seq. No.
                   4041 7.R1010
Contig ID
                   jC-a\(\bar{1}\)XLIB327434P1h04b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3212869
BLAST score
                   1286
                   1.0e-142
E value
Match length
                   301
% identity
                   78
NCBI Description
                   (AC004005) unknown protein [Arabidopsis thaliana]
                   119804 --
Seq. No.
                   4041 8.R1010
Contig ID
5'-most EST
                  LIB146-029-Q1-K1-A10
                   BLASTX
Method
                   g3212869
NCBI GI
BLAST score
                   695
                   2.0e-73
E value
Match length
                   143
                   88
% identity
NCBI Description
                   (AC004005) unknown protein [Arabidopsis thaliana]
                   119805
Seq. No.
                   4041 9.R1010
Contig ID
5'-most EST
                   jC-alXLIB327434P1f12b1
Method
                   BLASTX
                   g3212869
NCBI GI
BLAST score
                   784
E value
                   0.0e + 00
Match length
                   387
% identity
                   90
NCBI Description
                   (AC004005) unknown protein [Arabidopsis thaliana]
                   119806
Seq. No.
                   4041_11.R1010
Contig ID
5'-most EST
                   g2759845
Method
                   BLASTX
                   g3212869
NCBI GI
BLAST score
                   536
E value
                   8.0e-55
Match length
                   138
% identity
                   80
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
```

```
119807
Seq. No.
                  4042 1.R1010
Contig ID
                  jC-aTXLIB327405P1d12b2
5'-most EST
Method
                  BLASTX
                  q543632
NCBI GI
BLAST score
                  610
                  3.0e-63
E value
                  163
Match length
% identity
                  68
NCBI Description
                  aldehyde reductase (EC 1.1.1.21), NADPH-dependent -
                  bromegrass >gi_167113 (L12042) aldose reductase-related
                  protein [Bromus inermis]
                  119808
Seq. No.
                  4045 1.R1010
Contig ID
                  jC-atXLIB327414P3g07b1
5'-most EST
Method
                  BLASTX
                  g4567319
NCBI GI
                  927
BLAST score
                  1.0e-113
E value
Match length
                  218
                  94
% identity
NCBI Description
                  (AC005956) putative copper amine oxidase [Arabidopsis
                  thaliana]
                  119809
Seq. No.
Contig ID
                  4046_1.R1010
                  jC-atXLIB327409P3e02b1
5'-most EST
Method
                  BLASTX
                  g4539335
NCBI GI
                  341
BLAST score
                  2.0e-31
E value
Match length
                  154
% identity
                  46
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                  119810
Seq. No.
                  4047 1.R1010
Contig ID
5'-most EST
                  LIB3175-006-P1-K1-C10
                  BLASTX
Method
NCBI GI
                  q940288
BLAST score
                  558
                  7.0e-57
E value
Match length
                  210
                  37
% identity
                  (L43510) protein localized in the nucleoli of pea nuclei;
NCBI Description
                  ORF; putative [Pisum sativum]
Seq. No.
                  119811
Contig ID
                  4049 1.R1010
                  jC-atXP29C137O14T7059d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q549629
BLAST score
                  164
E value
                  6.0e-11
Match length
                  212
```

28

% identity

Match length

127

```
NCBI Description HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REGION
                  >gi 539270 pir__S38147 hypothetical protein YKR070w - yeast
                   (Saccharomyces cerevisiae) >gi 486541 emb CAA82149
                   (Z28295) ORF YKR070w [Saccharomyces cerevisiae]
                  119812
Seq. No.
                  4049_2.R1010
Contig ID
                  g119<del>9</del>986
5'-most EST
                  BLASTX
Method
                  q549629
NCBI GI
BLAST score
                  179
E value
                  5.0e-13
Match length
                  116
% identity
                  35
                  HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REGION
NCBI Description
                  >gi_539270_pir__S38147 hypothetical protein YKR070w - yeast
                   (Saccharomyces cerevisiae) >gi 486541 emb CAA82149
                   (Z28295) ORF YKR070w [Saccharomyces cerevisiae]
                  119813
Seq. No.
                  4053 1.R1010
Contig ID
5'-most EST
                  g1158990
                  BLASTX
Method
NCBI GI
                  g2832643
BLAST score
                  157
                  3.0e-10
E value
Match length
                  102
% identity
NCBI Description
                  (AL021710) hypothetical protein [Arabidopsis thaliana]
                  119814
Seq. No.
                  4053 2.R1010
Contig ID
5'-most EST
                  jC-atXP123C117E9T7060d1
Method
                  BLASTX
                  g2832643
NCBI GI
BLAST score
                  484
E value
                  3.0e-48
                 . 318
Match length
                  39
% identity
NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]
                  119815
Seq. No.
Contig ID
                  4055 1.R1010
5'-most EST
                  LIB35-025-Q1-E1-F6
                  119816
Seq. No.
                  4055_2.R1010
Contig ID
5'-most EST
                  LIB25-063-Q1-E1-G11
Seq. No.
                  119817
Contig ID
                  4056 1.R1010
                  jC-a\overline{t}XP65C209B3T7051d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4204308
BLAST score
                  666
                  7.0e-70
E value
```

Contig ID

```
% identity
                  88
                  (AC003027) lcl prt_seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  119818
                  4057 1.R1010
Contig ID
                  LIB3175-077-P1-K1-F3
5'-most EST
Seq. No.
                  119819
                  4058 1.R1010
Contig ID
5'-most EST
                  jC-atXP73CF3B4T7b1
Method
                  BLASTX
NCBI GI
                  q1652082
BLAST score
                  146
E value
                  4.0e-50
Match length
                  275
% identity
                  44
                  (D90902) UDP-3-0-acyl N-acetylglcosamine deacetylase
NCBI Description
                  [Synechocystis sp.]
                  119820
Seq. No.
Contig ID
                  4058 2.R1010
5'-most EST
                  jC-atXLIB327429P3h10a2
                 BLASTX
Method
                  g1652082
NCBI GI
BLAST score
                  218
                  2.0e-17
E value
Match length
                  72
                  58
% identity
NCBI Description (D90902) UDP-3-0-acyl N-acetylglcosamine deacetylase
                  [Synechocystis sp.]
Seq. No.
                  119821
Contig ID
                  4058 4.R1010
5'-most EST
                  jC-atXLIB327415P4d01b1
                  119822
Seq. No.
Contig ID
                  4058 5.R1010
5'-most EST
                  LIB3168-026-P1-K1-F5
                  119823
Seq. No.
Contig ID
                  4058 6.R1010
5'-most EST
                  g2413578
                  119824
Seq. No.
                  4058_7.R1010
Contig ID
5'-most EST
                  LIB24-001-Q1-E1-C4
Method
                  BLASTN
NCBI GI
                  q2462264
BLAST score
                  52
E value
                  6.0e-20
Match length
                  52
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  119825
```

4058 8.R1010

BLAST score

311

£ 12.

```
5'-most EST
                   jC-atXP13C104N20T7088a1
                                                                            \tau_{\uparrow}=\pm
                   119826
Seq. No.
                   4058 9.R1010
Contig ID
5'-most EST
                   g935843
                   119827
Seq. No.
                   4058 10.R1010
Contig ID
5'-most EST
                   g2446247 ·
Seq. No.
                   119828
Contig ID
                   4059 1.R1010
5'-most EST
                   jC-atXLIB327401P4c07b2
Method
                   BLASTX
NCBI GI
                   q4581156
BLAST score
                   464
E value
                   4.0e-46
Match length
                   98
                   93
% identity
NCBI Description
                  (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
Seq. No.
                   119829
Contig ID
                   4060_1.R1010
5'-most EST
                   LIB3234-006-P1-K1-F6
                   119830
Seq. No.
Contig ID
                   4063 1.R1010
                   LIB3234-077-P1-K1-H5
5'-most EST
                   119831
Seq. No.
                   4067 1.R1010
Contig ID
5'-most EST
                   LIB3175-026-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q4158221
BLAST score
                   630
E value
                   7.0e-66
Match length
                   139
                   80
% identity
NCBI Description (Y18624) reversibly glycosylated polypeptide [Oryza sativa]
                   119832
Seq. No.
                   4068 1.R1010
Contig ID
5'-most EST
                   LIB3176-094-P1-K1-D11
Method
                  BLASTX
                   g4006881
NCBI GI
BLAST score
                   529
E value
                   5.0e-54
Match length
                   132
% identity
                   60
NCBI Description (299707) putative protein [Arabidopsis thaliana]
                   119833
Seq. No.
                   4069 1.R1010
Contig ID
                  LIB3234-048-P1-K1-G2
5'-most EST
Method
                  BLASTN
                   g3659491
NCBI GI
```

Contig ID

5'-most EST

```
1.0e-174
E value
Match length
                   520
                   100
% identity
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                   119834
Seq. No.
                   4072 1.R1010
Contig ID
                   LIB3168-100-P1-K1-E6
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3327922
                   93
BLAST score
                   1.0e-44
E value
                   421
Match length
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC T31E10 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   119835
Seq. No.
                   4072 2.R1010
Contig ID
5'-most EST
                   jC-atX24110Q1E1G02b1
Method
                   BLASTN
NCBI GI
                   q3327922
BLAST score
                   119
                   4.0e-60
E value
Match length
                   446
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC T31E10 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   119836
Seq. No.
                   4074 1.R1010
Contig ID
5'-most EST
                   LIB3234-082-Q1-K1-B3
                   BLASTN
Method
                   g3738313
NCBI GI
BLAST score
                   350
                   0.0e + 00
E value
                   361
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T29E15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   119837
Seq. No.
                   4074_2.R1010
Contig ID
5'-most EST
                   LIB2\overline{3}-054-Q1-E1-G8
Method
                   BLASTX
NCBI GI
                   q3738322
BLAST score
                   403
E value
                   3.0e-39
Match length
                   80
                   100
% identity
                   (AC005170) putative small nuclear ribonucleoprotein
NCBI Description
                   [Arabidopsis thaliana]
                   119838
Seq. No.
```

4074 3.R1010

LIB25-056-Q1-E1-A11

```
Method
                  BLASTX
NCBI GI
                  q3738322
                  389
BLAST score
                  8.0e-38
E value
                  79
Match length
% identity
                  97
                   (AC005170) putative small nuclear ribonucleoprotein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  119839
Contig ID
                  4075 1.R1010
5'-most EST
                  jC-atXP115C248P21T7053d1
                  BLASTX
Method
NCBI GI
                  q4587519
BLAST score
                  964
                  1.0e-104
E value
Match length
                  199
% identity
                  94
                  (AC007060) Strong similarity to F19I3.7 gi_3033380 putative
NCBI Description
                  coatomer epsilon subunit from Arabidopsis Thaliana BAC
                  gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555,
                  gb H76335, gb AA712463, gb W43247, gb T45611, g
Seq. No.
                  119840
Contig ID
                  4075 2.R1010
                  jC-a1XLIB327434P1b06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4587519
                  742
BLAST score
                  8.0e-79
E value
                  145
Match length
% identity
                  100
NCBI Description
                  (AC007060) Strong similarity to F19I3.7 gi_3033380 putative
                  coatomer epsilon subunit from Arabidopsis thaliana BAC
                  gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555,
                  gb H76335, gb AA712463, gb_W43247, gb_T45611, g
                  119841
Seq. No.
Contig ID
                  4076 1.R1010
                  jC-atXLIB327438P4h12b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q282971
BLAST score
                  306
E value
                  2.0e-45
                  261
Match length
% identity
                  chitinase (EC 3.2.1.14) - potato >gi 21495 emb CAA47921
NCBI Description
                   (X67693) endochitinase [Solanum tuberosum]
Seq. No.
                  119842
                  4076 2.R1010
Contig ID
5'-most EST
                  q2747502
                  BLASTX
Method
NCBI GI
                  g974294
BLAST score
                  149
E value
                  3.0e-09
Match length
```

5'-most EST

 $g121\overline{6}922$

```
% identity
NCBI Description
                  (U31309) LP6 [Pinus taeda]
                   119843
Seq. No.
                   4076 3.R1010
Contig ID
                   jC-atXLIB327417P4e01b1
5'-most EST
Method
                   BLASTN
                   g2582640
NCBI GI
BLAST score
                   60
                   8.0e-25
E value
Match length
                   72
                   96
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
Seq. No.
                   119844
                   4080 1.R1010
Contig ID
                  LIB3234-082-Q1-K1-H2
5'-most EST
Seq. No.
                   119845
Contig ID
                   4084 1:R1010
5'-most EST
                   jC-atXLIB327408P1b06b1
Method
                   BLASTX
NCBI GI
                   q1001135
BLAST score
                   223
E value
                   1.0e-17
Match length
                   237
% identity
                  (D64001) acetolactate synthase [Synechocystis sp.]
NCBI Description
                   119846
Seq. No.
Contig ID
                   4087 1.R1010
                   jC-atXLIB327418P3c04b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3461833
BLAST score
                   261
                   3.0e-48
E value
                  96
Match length
                  99
% identity
                  (AC004138) putative expansin [Arabidopsis thaliana]
NCBI Description
                  119847
Seq. No.
Contig ID
                   4090 1.R1010
5'-most EST
                  LIB3177-045-P1-K2-D2
                  BLASTN
Method
                  g22643.07
NCBI GI
                  231
BLAST score
E value
                  1.0e-127
Match length
                  454
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MED24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  119848
                  4091 1.R1010
Contig ID
```

```
Seq. No.
                    119849
                    4095 1.R1010
 Contig ID
                    LIB3234-091-P1-K1-A10
 5'-most EST
                    BLASTN
 Method
 NCBI GI
                    q3449320
 BLAST score
                    320
                    1.0e-180
 E value
 Match length
                    368
 % identity
                    97
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                    MRB17, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    119850
                    4099 1.R1010
 Contig ID
 5'-most EST
                    LIB3234-091-P1-K1-G2
 Seq. No.
                    119851
                    4110 1.R1010
 Contig ID
                    LIB146-029-Q1-K1-H10
 5'-most EST
                    BLASTN
 Method
 NCBI GI
                    q1531761
 BLAST score
                    92
 E value
                    3.0e-44
                    150
 Match length
                    90
 % identity
 NCBI Description A.thaliana gene encoding S-adenosylmethionine decarboxylase
 Seq. No.
                    119852
 Contig ID
                    4112_1.R1010
                    g3449614
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q1351014
 BLAST score
                    247
 E value
                    7.0e-21
 Match length
                    54
 % identity
                    83
                   40S RIBOSOMAL PROTEIN S8 >qi 968902 dbj BAA07207 (D38010)
 NCBI Description
                    ribosomal protein S8 [Oryza sativa]
                    119853
 Seq. No.
                    4112 2.R1010
 Contig ID
 5'-most EST
                    g121\overline{5}928
 Method
                    BLASTX
                    q1498053
 NCBI GI
 BLAST score
                    567
 E value
                    3.0e-58
Match length
                    139
 % identity
                    78
 NCBI Description
                   (U64436) ribosomal protein S8 [Zea mays]
 Seq. No.
                    119854
                    4112 3.R1010
 Contig ID
                    g1158915
 5'-most EST
 Method
                    BLASTX
                    g1498053
 NCBI GI
 BLAST score
                    404
```

3.0e-39

E value

```
Match length
% identity
                  (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                  119855
Seq. No.
                  4113 1.R1010
Contig ID
                  LIB3234-095-P1-K1-G2
5'-most EST
                  BLASTX
Method
                  q3033400
NCBI GI
BLAST score
                  437
E value
                  2.0e-43
Match length
                  120
% identity
                  72
                  (AC004238) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                 .,119856
                  4119_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327418P1a08b1
Method
                  BLASTX
                  q2623962
NCBI GI
BLAST score
                  521
E value
                  9.0e-53
Match length
                  107
% identity
                  93
NCBI Description
                  (Y12540) isocitrate dehydrogenase (NADP+) [Apium
                  graveolens]
                  119857
Seq. No.
                  4119 3.R1010
Contig ID
                  jC-atXP92C246P2T7068d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q169989
BLAST score
                  908
E value
                  3.0e-98
Match length
                  183
% identity
                  94
                  (L12157) NADPH-specific isocitrate dehydrogenase [Glycine
NCBI Description
                  119858
Seq. No.
Contig ID
                  4119 4.R1010
5'-most EST
                  jC-atXP85C241H21T7b1
Method
                  BLASTX
                  g3811007
NCBI GI
BLAST score
                  785
E value
                  9.0e-84
                  188
```

Match length % identity 80

NCBI Description (AB019327) NADP specific isocitrate dehydrogenase [Daucus

carotal

4119 5.R1010

119859 Seq. No. Contig ID

5'-most EST jC-alXLIB327435P2g09b1

Method BLASTX NCBI GI g3811007



```
340
BLAST score
E value
                   1.0e-31
Match length
                   100
% identity
                  72
NCBI Description
                   (AB019327) NADP specific isocitrate dehydrogenase [Daucus
                  carota)
Seq. No.
                   119860
Contig ID
                   4119 6.R1010
                  LIB3175-082-P1-K1-B7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3811007
BLAST score
                  1779
                  0.0e + 00
E value
Match length
                   399
% identity
NCBI Description
                   (AB019327) NADP specific isocitrate dehydrogenase [Daucus
                  carota]
                  119861
Seq. No.
Contig ID
                   4123 1.R1010
5'-most EST
                   jC-atXLIB327409P4a09b1
Method
                  BLASTX
NCBI GI
                  q3107931
BLAST score
                   593
E value
                   2.0e-65
Match length
                  158
% identity
                  77
NCBI Description
                   (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]
Seq. No.
                  119862
                   4123 2.R1010
Contig ID
5'-most EST
                  LIB3234-026-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                   q136739
BLAST score
                   570
E value
                   1.0e-58
Match length
                  167
% identity
                   67
NCBI Description
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
                  PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
                   119863
Seq. No.
Contig ID
                   4126 1.R1010
                  LIB3175-022-P1-K1-A12
5'-most EST
Seq. No.
                  119864
Contig ID
                   4129 1.R1010
5'-most EST
                  LIB3234-039-P1-K1-A1
```

119865 Seq. No. Contig ID 4130 1.R1010 5'-most EST jC-atXP19C109N15T7047a1

Method BLASTX

```
g1169782
NCBI GI
BLAST score
                   1461
E value
                   1.0e-163
Match length
                   304
                   94
% identity
                  FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis
NCBI Description
                   thaliana]
                   119866
Seq. No.
                   4133_1.R1010
Contig ID
5'-most EST
                   935\overline{3}19
Method
                   BLASTX
NCBI GI
                   q4049348
BLAST score
                   1221
E value
                   1.0e-135
Match length
                   232
                   100
% identity
NCBI Description
                  (AL034567) putative protein [Arabidopsis thaliana]
                   119867
Seq. No.
                   4133_2.R1010
Contig ID
5'-most EST
                   jC-atXP32C147D23T7d2
Method
                   BLASTX
NCBI GI
                   g2160158
BLAST score
                   462
                   6.0e-46
E value
Match length
                   185
% identity
                   51
NCBI Description
                   (AC000132) Similar to elongation factor 1-gamma
                   (gb EF1G XENLA). ESTs gb T20564, gb T45940, gb T04527 come
                   from this gene. [Arabidopsis thaliana]
                   119868
Seq. No.
Contig ID
                   4133_3.R1010
5'-most EST
                  LIB3\overline{5}-042-Q1-E1-B9
                   BLASTX
Method
NCBI GI
                   g2160158
BLAST score
                   45
E value
                   5.0e-76
Match length
                   144
                   91
% identity
                   (AC000132) Similar to elongation factor 1-gamma
NCBI Description
                   (gb EF1G XENLA). ESTs gb T20564, gb T45940, gb T04527 come
                   from this gene. [Arabidopsis thaliana]
                   119869
Seq. No.
Contig ID
                   4133_4.R1010
5'-most EST
                   g2749020
Method
                  BLASTX
NCBI GI
                   g4049348
BLAST score
                   579
E value
                   2.0e-59
Match length
                  121
% identity
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
```

119870

Seq. No.

```
Contig ID
                   4133 5.R1010
                  jC-atXLIB327439P3f11b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2160158
BLAST score
                   1274
                  1.0e-171 ·
E value
Match length
                  365
                  84
% identity
                   (AC000132) Similar to elongation factor 1-gamma
NCBI Description
                   (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                  119871
Contig ID
                  4133 6.R1010
5'-most EST
                   jC-atXP78CF4E9T7b1
                  BLASTX
Method
                  g2160158
NCBI GI
BLAST score
                  824
                  3.0e-88
E value
                  190
Match length
                  82
% identity
                   (AC000132) Similar to elongation factor 1-gamma
NCBI Description
                   (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  119872
                  4133_7.R1010
Contig ID
                  LIB3168-066-P1-K1-H11
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2160158
BLAST score
                  517
E value
                  2.0e-52
Match length
                  126
                  79
% identity
NCBI Description
                  (AC000132) Similar to elongation factor 1-gamma
                   (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come
                  from this gene. [Arabidopsis thaliana]
                  119873
Seq. No.
                  4133 8.R1010
Contig ID
5'-most EST
                  g2722245
Method
                  BLASTN
                  g4063735
NCBI GI
BLAST score
                  66
E value
                  1.0e-28
Match length
                  142
                  87
% identity
                  Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5
NCBI Description
                  cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  119874
Contig ID
                  4133 11.R1010
5'-most EST
                  jC-atX24042Q1E1G06b1
Method
                  BLASTX
                  g2160158
NCBI GI
BLAST score
                  204
                  9.0e-16
E value
```

Method

BLASTX

```
Match length
                   39
                   100
% identity
                   (AC000132) Similar to elongation factor 1-gamma
NCBI Description
                   (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come
                   from this gene. [Arabidopsis thaliana]
                  119875
Seq. No.
                   4133 12.R1010
Contig ID
                   g3449755
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2160155
BLAST score
                   33
                   6.0e-09
E value
                   69
Match length
                   90
% identity
                  Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                   119876
Seq. No.
Contig ID
                   4134_1.R1010
                   LIB2\overline{5}-006-Q1-E2-G6
5'-most EST
Method
                   BLASTN
                  g4455262
NCBI GI
BLAST score
                   320
E value
                   1.0e-180
Match length
                   478
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
NCBI Description
                   (ESSAII project)
                   119877
Seq. No.
Contig ID
                   4135 1.R1010
5'-most EST
                   LIB23-027-Q1-E1-E3
Method
                   BLASTX
                  g2809255
NCBI GI
BLAST score
                   798
                  2.0e-85
E value
Match length
                   160
% identity
                   96
                  (AC002560) F21B7.24 [Arabidopsis thaliana]
NCBI Description
                   119878
Seq. No.
                   4137 1.R1010
Contig ID
5'-most EST
                   LIB24-076-Q1-E1-B5
Method
                   BLASTX
                  g3970880
NCBI GI
BLAST score
                   183
E value
                   2.0e-13
Match length
                   106
% identity
                   42
                   (AB015724) nuclear receptor binding factor-1 [Rattus
NCBI Description
                  norvegicus]
                   119879
Seq. No.
Contig ID
                   4138 2.R1010
5'-most EST
                   jC-atXLIB327424P4d08b1
```

Method

```
g3152586
NCBI GI
BLAST score
                  163
E value
                  1.0e-10
Match length
                  43
                  74
% identity
                  (AC002986) YUP8H12R.28 [Arabidopsis thaliana]
NCBI Description
                  119880
Seq. No.
                  4140_1.R1010
Contig ID . .
5'-most EST
                  jC-atXP73C224B6T7d2
Method
                  BLASTX
                  g2827634
NCBI GI
BLAST score
                  701
E value
                  1.0e-73
Match length
                  170
                  82
% identity
                  (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
                  119881
Seq. No.
                  4140_2.R1010
Contig ID
5'-most EST
                  g2762243
                  BLASTN
Method
                  g4678705
NCBI GI
BLAST score
                  142
E value
                  9.0e-74
Match length
                  142
% identity
                  85
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                  (ESSA project)
                  119882
Seq. No.
                  4140 5.R1010
Contig ID
5'-most EST
                  g3449685
Method
                  BLASTN
NCBI GI
                  g4678705
BLAST score
                  407
E value
                  0.0e + 00
Match length
                  411
% identity
                  100 -
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                  (ESSA project)
Seq. No.
                  119883
Contig ID
                  4145 1.R1010
5'-most EST
                  LIB146-030-Q1-K1-D12
Method
                  BLASTX
                  g3859591
NCBI GI
BLAST score
                  336
E value
                  2.0e-31
Match length
                  108
% identity
                  56
                  (AF104919) No definition line found [Arabidopsis thaliana]
NCBI Description
                  119884
Seq. No.
Contig ID
                  4152_1.R1010
5'-most EST
                  LIB3234-025-P1-K1-F11
```

BLASTN

```
NCBI GI
                  q12216
BLAST score
                   355
E value
                   0.0e + 00
Match length
                   668
                   93
% identity
NCBI Description Sinapis alba chloroplast rps16 gene
                  119885
Seq. No.
Contig ID
                   4155 1.R1010
5'-most EST
                  ARABL1-039-Q1-B1-E7
Method
                  BLASTX
NCBI GI
                  q4314370
BLAST score
                   461
E value
                  1.0e-45
Match length
                   130
% identity
                  66
NCBI Description
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
                  119886
Seq. No.
                   4160 1.R1010
Contig ID
5'-most EST
                  LIB3234-092-P1-K1-F10
Seq. No.
                  119887
                  4163 1.R1010
Contig ID
                  LIB146-030-Q1-K1-F7
5'-most EST
Method
                  BLASTN
NCBI GI
                  a3522932
BLAST score
                  379
                  0.0e + 00
E value
                  536
Match length
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  119888
Seq. No.
Contig ID
                  4164 1.R1010
5'-most EST
                  LIB22-041-Q1-E1-C7
Seq. No.
                  119889
                  4167 1.R1010
Contig ID
                  LIB3234-093-P1-K1-E9
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4406766
BLAST score
                  572
                  5.0e-59
E value
                  127
Match length
% identity
                  81
NCBI Description
                  (AC006836) putative flavonol sulfotransferase [Arabidopsis
                  thaliana]
                  119890
Seq. No.
Contig ID
                  4171 1.R1010
5'-most EST
                  LIB146-030-Q1-K1-G5
Seq. No.
                  119891
                  4172 1.R1010
Contig ID
5'-most EST
                  g241\overline{3}901
```

```
Method
                  BLASTX
NCBI GI
                  g2275210
BLAST score
                  823
                  3.0e-88
E value
                  170
Match length
                  94
% identity
                  (AC002337) peptidyl-prolyl cis-trans isomerase isolog
NCBI Description
                  [Arabidopsis thaliana]
                  119892
Seq. No.
Contig ID
                  4172 2.R1010
5'-most EST
                  jC-atXP101CE1H7T7044b1
Method
                  BLASTN
                  q2275194
NCBI GI
BLAST score
                  162
                  1.0e-85
E value
Match length
                  464
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T08I13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  119893
Seq. No.
Contig ID
                  4173_1.R1010
                  LIB3177-068-P1-K1-H12
5'-most EST
Method
                  BLASTX
                  g2894564
NCBI GI
BLAST score
                  209
                  5.0e-37
E value
Match length
                  85
                  95
% identity
                  (AL021890) putative protein [Arabidopsis thaliana]
NCBI Description
                  119894
Seq. No.
Contig ID
                  4173_2.R1010
                  jC-atXLIB327405P3e04b1
5'-most EST
                  BLASTX
Method
                  g4115939
NCBI GI
BLAST score
                  588
E value
                  1.0e-60
Match length
                  134
% identity
                  41
                  (AF118223) contains similarity to Methanobacterium
NCBI Description
                  thermoautotrophicum transcriptional regulator (GB:AE000850)
                  [Arabidopsis thaliana]
                  119895
Seq. No.
Contig ID
                  4173_3.R1010
5'-most EST
                  g635104
Method
                  BLASTN
NCBI GI
                  g2894557
BLAST score
                  258
E value
                  1.0e-143
Match length
                  310
                  96
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T805
NCBI Description
```

(ESSAII project)

```
119896
Seq. No.
Contig ID
                  4176 1.R1010
5'-most EST
                  LIB146-030-Q1-K1-H10
                  119897
Seq. No.
                  4178 1.R1010
Contig ID
                  jC-atXLIB327439P2h03b2
5'-most EST
                  BLASTN
Method
                  q4678705
NCBI GI
BLAST score
                  430
                  0.0e + 00
E value
Match length
                  653
% identity
                  99
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                   (ESSA project)
                  119898
Seq. No.
Contig ID
                  4178 2.R1010
5'-most EST
                  LIB146-030-Q1-K1-H12
Method
                  BLASTN
NCBI GI
                  g4678705
BLAST score
                  324
E value
                  0.0e + 00
Match length
                  356
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
                  (ESSA project)
Seq. No.
                  119899
                  4180 1.R1010
Contig ID
                  jC-aTXLIB327436P1f01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4454032
BLAST score
                  337
E value
                  1.0e-35
Match length
                  134
% identity
                  63
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  119900
Contig ID
                  4180 2.R1010
5'-most EST
                  LIB23-043-Q1-E1-F10
Method
                  BLASTX
NCBI GI
                  g4454032
BLAST score
                  1056
E value
                  1.0e-115
Match length
                  206
                  100
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  119901
                  4181_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327415P1e12b1
Method
                  BLASTX
NCBI GI
                  g3193330
BLAST score
                  297
```

2.0e-26

E value

E value

```
Match length
                   119
                   55
% identity
                   (AF069299) contains similarity to Medicago sativa corC
NCBI Description
                  (GB:L22305) [Arabidopsis thaliana]
Seq. No.
                  119902
Contig ID ...
                   4181 2.R1010
                  jC-atXLIB327409P3f11b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3193330
BLAST score
                   562
E value
                   2.0e-57
Match length
                   203
% identity
                   61
                   (AF069299) contains similarity to Medicago sativa corC
NCBI Description
                   (GB:L22305) [Arabidopsis thaliana]
                  119903
Seq. No.
                   4181_3.R1010
Contig ID
                  g2748331
5'-most EST
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  50
                  8.0e-19
E value
                  73
Match length
% identity
                  95
NCBI Description Cloning vector pSport1, complete cds
                  119904
Seq. No.
                  4181 4.R1010
Contig ID
                  LIB2\overline{4}-065-Q1-E1-A4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3738316
BLAST score
                  162
                  4.0e-11
E value
Match length
                  40
% identity
                  80
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
                  119905
Seq. No.
                  4184_1.R1010
Contig ID
                  LIB23-049-Q1-E1-D8
5'-most EST
Method
                  BLASTX
                  g4105697
NCBI GI
BLAST score
                  1199
                   1.0e-132
E value
Match length
                  234
% identity
                  97
                  (AF049870) thaumatin-like protein [Arabidopsis thaliana]
NCBI Description
                  119906
Seq. No.
                  4185_1.R1010
Contig ID
                  jC-atXLIB327438P4h03b2
5'-most EST
Method
                  BLASTN
NCBI GI
                  q3036791
                  599
BLAST score
                  0.0e + 00
```

Contig ID

```
Match length
                   878
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T19K4
NCBI Description
                   (ESSAII project)
Seq. No.
                   119907
                   4187 1.R1010
Contig ID
                  LIB22-001-Q1-E1-B3
5'-most EST
                  BLASTX
Method
NCBI GI
                   q3337367
BLAST score
                   779
                   4.0e-83
E value
                   205
Match length
                   80
% identity
NCBI Description
                   (AC004481) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   119908
                   4189 1.R1010
Contig ID
                   jC-atXLIB327413P2d04b1
5'-most EST
                   BLASTX
Method
                   q4587989
NCBI GI
BLAST score
                   629
E value
                   1.0e-65
                   121
Match length
                   100
% identity
                   (AF085279) hypothetical Cys-3-His zinc finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   119909
Seq. No.
                   4191 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327438P3h07b1
                   BLASTX
Method
NCBI GI
                   q3287696
BLAST score
                   131
                   6.0e-18
E value
Match length
                   71
% identity
                   (AC003979) Strong similarity to phosphoribosylanthranilate
NCBI Description
                   transferase gb D86180 from Pisum sativum. This ORF may be
                  part of a larger gene that lies in the overlapping region.
                   [Arabidopsis thaliana]
                   119910
Seq. No.
Contig ID
                   4192 1.R1010
5'-most EST
                   jC-atXLIB327423P1a10b1
Method
                   BLASTX
NCBI GI
                   g2795803
BLAST score
                   588
E value
                   2.0e-60
Match length
                   223
                   53
% identity
                   (AC003674) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                   thaliana] >gi 3355491 (AC004218) putative
                  beta-1,3-endoglucanase [Arabidopsis thaliana]
Seq. No.
                   119911
```

4195 1.R1010

```
5'-most EST
                                                      g1216727.
     Method
                                                      BLASTX
      NCBI GI ···
                                                      g4455258
      BLAST score
                                                      657
      E value
                                                      1.0e-68
     Match length
                                                      214
% identity
                                                      55
                                                       (AL035523) acid phosphatase-like protein [Arabidopsis
     NCBI Description
                                                      thaliana]
     Seq. No.
                                                      119912
                                                      4200 1.R1010
      Contig ID
                                                      LIB3175-062-P1-K1-F10
      5'-most EST
     Method
                                                      BLASTN
     NCBI GI
                                                      g3241926
     BLAST score
                                                      201
     E value
                                                      1.0e-109
     Match length
                                                      432
      % identity
                                                      97
                                                     Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
     NCBI Description
                                                      MSG15, complete sequence [Arabidopsis thaliana]
     Seq. No.
                                                      119913
                                                 4202_1.R1010
      Contig ID
                                                      LIB24-011-Q1-E1-A8
      5'-most EST
                                                      BLASTX
     Method
     NCBI GI
                                                      q115486
     BLAST score
                                                      321
     E value
                                                      1.0e-29
     Match length
                                                      126
      % identity
                                                      34
                                                      \label{local_condition} CALMODULIN-2/3/5 > & gi_99671_pir_S22503 \ calmodulin - & calmodulin -
     NCBI Description
                                                     Arabidopsis thaliana >gi_1076437_pir__S53006 calmodulin -
                                                      leaf mustard >gi_2146726_pir__S71513 calmodulin -
                                                      Arabidopsis thaliana >gi_166651 (M38380) calmodulin-2
                                                      [Arabidopsis thaliana] >gi_166653 (M73711) calmodulin-3 [Arabidopsis thaliana] >gi_474183 emb_CAA47690_ (X67273) calmodulin [Arabidopsis thaliana] >gi_497992 (U10150) calmodulin [Brassica napus] >gi_899058 (M88307) calmodulin
                                                      [Brassica juncea] >gi_1183005_dbj_BAA08283 (D45848) calmodulin [Arabidopsis thaliana] >gi_3402706 (AC004261) unknown protein [Arabidopsis thaliana] >gi_3885333
                                                       (AC005623) calmodulin [Arabidopsis thaliana]
                                                      >gi 228407 prf 1803520A calmodulin 2 [Arabidopsis
                                                      thaliana
     Seq. No.
                                                      119914
     Contig ID
                                                      4203 1.R1010
      5'-most EST
                                                      jC-alXLIB327436P2h08b1
     Method
                                                      BLASTX
     NCBI GI
                                                      g1170504
     BLAST score
                                                      719
     E value
                                                      5.0e-76
     Match length
                                                      248
      % identity
                                                      60
                                                     EUKARYOTIC INITIATION FACTOR (ISO) 4F SUBUNIT P82
     NCBI Description
                                                      (IEIF-(ISO)4F P82) >gi 452440 (M95747) initiation factor
```

Method

NCBI GI

E value

BLAST score

BLASTX

485

q1791307

8.0e-49

(iso) 4f p82 subunit [Triticum aestivum] 119915 Seq. No. 4204 1.R1010 Contig ID 5'-most EST jC-atXLIB327410P3b06b1 Method BLASTX NCBI GI g1707011 BLAST score 587 E value 2.0e-60 Match length 108 % identity 100 NCBI Description (U78721) auxin-repressed protein isolog [Arabidopsis thaliana] Seq. No. 119916 4204 2.R1010 Contig ID 5'-most EST q937807 BLASTX Method NCBI GI q1707011 BLAST score 416 1.0e-40 E value Match length 79 % identity 99 (U78721) auxin-repressed protein isolog [Arabidopsis NCBI Description thaliana] Seq. No. 119917 4204 3.R1010 Contig ID $q115\overline{9}478$ 5'-most EST BLASTX Method NCBI GI q1707011 BLAST score 173 E value 2.0e-45 Match length 96 % identity 96 NCBI Description (U78721) auxin-repressed protein isolog [Arabidopsis thaliana] Seq. No. 119918 4205 1.R1010 Contig ID LIB22-001-Q1-E1-D5 5'-most EST BLASTN Method NCBI GI q2832667 BLAST score 415 E value 0.0e + 00450 Match length 99 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project) 119919 Seq. No. 4208 1.R1010 Contig ID 5'-most EST LIB22-001-Q1-E1-D8



```
Match length
                     157
% identity
                     51
NCBI Description
                    (U83501) permease homolog [Arabidopsis thaliana]
Seq. No.
                     119920
                     4210 1.R1010
Contig ID
                     LIB3175-029-P1-K1-C12
5'-most EST
                     BLASTX
Method
NCBI GI
                     q4507703
BLAST score
                     243
                     2.0e-20
E value
                     199
Match length
                     33
% identity
                     tumor suppressing subtransferable candidate 1
NCBI Description
                     >gi_2655037_gb_AAC51911_ (AF019952) tumor suppressing STF
                     cDNA 1 [Homo sapiens]
Seq. No.
                     119921
                     4211 1.R1010
Contig ID
                     jC-atXLIB327403P3h06b2
5'-most EST
Method
                     BLASTX
NCBI GI
                     g120667
BLAST score
                     1521
E value
                     1.0e-169
Match length
                     338
% identity
NCBI Description
                    GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                    >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
thaliana >gi_166706 (M64116) cystolic
                     glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                     thaliana] >gi 166710 (M64119) glyceraldehyde-3-phosphate
                     dehydrogenase [Arabidopsis thaliana]
Seq. No.
                     119922
                     4211 2.R1010
Contiq ID
5'-most EST
                     jC-atXLIB327423P2b08b1
Method
                     BLASTX
                     g120667
NCBI GI
BLAST score
                     1002
                     1.0e-109
E value
                     200
Match length
% identity
                     98
NCBI Description
                    GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                    >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
thaliana >gi_166706 (M64116) cystolic
                     glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                     thaliana] >gi 166710 (M64119) glyceraldehyde-3-phosphate
                     dehydrogenase [Arabidopsis thaliana]
```

Seq. No. 119923 Contig ID 4211_3.R1010

5'-most EST jC-atXLIB327413P1e10b1

Method BLASTX NCBI GI g120667 BLAST score 754

```
4.0e-80
E value
Match length
                  194
% identity
                  78
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 81622 pir__JQ1287 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                  thaliana >gi 166706 (M64116) cystolic
                  glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                  thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate
                  dehydrogenase [Arabidopsis thaliana]
                  119924
Seq. No.
Contig ID
                  4211 4.R1010
5'-most EST
                  jC-atXLIB327414P2c03b1
Method
                  BLASTX
                  g120675
NCBI GI
BLAST score
                  478
                  7.0e-48
E value
Match length
                  136
% identity
                  71
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                  >qi 21143 emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis
                  alba]
                  119925
Seq. No.
                  4211 5.R1010
Contig ID
                  LIB3234-058-P1-K1-D5
5'-most EST
Method
                  BLASTX
                  g120667
NCBI GI
BLAST score
                  806
                  3.0e-91
E value
Match length
                  235
% identity
                  79
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis -
                  thaliana >gi 166706 (M64116) cystolic
                  glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                  thaliana] >gi 166710 (M64119) glyceraldehyde-3-phosphate
                  dehydrogenase [Arabidopsis thaliana]
                  119926
Seq. No.
Contig ID
                  4211_7.R1010
5'-most EST
                  LIB3175-029-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g120667
BLAST score
                  477
E value
                  5.0e-48
Match length
                  107
% identity
                  87
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                  thaliana >gi 166706 (M64116) cystolic
```

glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis

NCBI GI

g4503527

```
Seq. No.
                   119927
                   4211 8.R1010
 Contig ID
 5'-most EST
                   ARABL1-040-Q1-B1-C9
 Method
                   BLASTX
                   q120675
 NCBI GI
 BLAST score
                    454
                    4.0e-45
. E value
 Match length
                   106
 % identity
                   82
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 NCBI Description
                   \verb|>gi_66011_pir\_DEIS3C glyceraldehyde-3-phosphate|\\
                   dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                   >gi 21143 emb CAA27844 (X04301) GAPDH (aa 1-338) [Sinapis
                   119928
 Seq. No.
                   4213_1.R1010
 Contig ID
                   LIB22-013-Q1-E1-D4
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   g2935525
 BLAST score
                   172
                    3.0e-12
 E value
                   89
 Match length
                   52
 % identity
 NCBI Description (AF049067) cytochrome P450 [Pinus radiata]
                   119929
 Seq. No.
                   4215 1.R1010
 Contig ID
                   LIB2\overline{2}-060-Q1-E1-D12
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   g1707021
 BLAST score
                    51
                    1.0e-62
 E value
 Match length
                    135
 % identity
                    85
                   (U78721) Ubiquitin-conjugating enzyme, E2-16kD isolog
 NCBI Description
                    [Arabidopsis thaliana]
                    119930
 Seq. No.
                   4216 1.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327439P1a09b2
 Method
                   BLASTX
                   g4006893
 NCBI GI
 BLAST score
                    729
 E value
                   2.0e-77
 Match length
                    138
 % identity
                    100
                   (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
 NCBI Description
                   119931
 Seq. No.
                    4217 1.R1010
 Contig ID
                   jC-atXLIB327418P4c11b1
 5'-most EST
 Method
                   BLASTX
```

thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate

dehydrogenase [Arabidopsis thaliana]

```
BLAST score
                  432
                  2.0e-42
E value
Match length
                  197
% identity
                  42
                  UNKNOWN >gi_1778051 (U62583) Prt1 homolog [Homo sapiens]
NCBI Description
                  119932
Seq. No.
                  4217 2.R1010
Contig ID
                  jC-aTXLIB327419P2h03b2
5'-most EST
                  BLASTX
Method
                  g4503527
NCBI GI
                  276
BLAST score
                  5.0e-24
E value
Match length
                  186
                  37
% identity
                  UNKNOWN >gi 1778051 (U62583) Prt1 homolog [Homo sapiens]
NCBI Description
                  119933
Seq. No.
                  4220 1.R1010
Contig ID
                  LIB22-001-Q1-E1-F4
5'-most EST
                  BLASTN
Method
                  g3449323
NCBI GI
BLAST score
                  234
                  1.0e-128
E value
Match length
                   442
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MZA15, complete sequence [Arabidopsis thaliana]
                  119934
Seq. No.
                   4222 1.R1010
Contig ID
                  ARABL1-031-Q1-B1-C10
5'-most EST
                  BLASTX
Method
                  g2894598
NCBI GI
                   659
BLAST score
                   4.0e-69
E value
                  170
Match length
                  78
% identity
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119935
                   4223 1.R1010
Contig ID
                   q2597276
5'-most EST
                  BLASTN
Method
                   g3695372
NCBI GI
BLAST score
                   771
                   0.0e+00
E value
                   876
Match length
                   99
% identity
NCBI Description Arabidopsis thaliana BAC F1104
Seq. No.
                   119936
                  4226_1.R1010
Contig ID
                  LIB24-116-Q1-E1-D11
5'-most EST
                   119937
Seq. No.
Contig ID
                   4226 2.R1010
```

```
5'-most EST
                  LIB3175-015-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   q4263507
BLAST score
                   215
E value
                   5.0e-17
Match length
                   177
% identity
                   31 ∉
                  (AC004044) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   119938
                   4229 1.R1010
Contig ID
                   LIB22-001-Q1-E1-G5
5'-most EST
Seq. No.
                   119939
                   4230 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327439P3a06b2
Method
                   BLASTN
NCBI GI
                   q4587582
BLAST score
                   431
E value
                   0.0e + 00
Match length
                   431
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T16B14 genomic
                  sequence, complete sequence
                  119940
Seq. No.
Contig ID
                   4232_1.R1010
                  LIB22-082-01-E2-C10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4539335
BLAST score
                   909
E value
                   3.0e-98
Match length
                   299
% identity
                   60
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                  119941
Seq. No.
Contig ID
                   4235 1.R1010
5'-most EST
                   iC-atXLIB327413P4c08b1
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                   64
E value
                   4.0e-27
Match length
                  72
% identity
                  97
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  119942
Contig ID
                  4235 2.R1010
5'-most EST
                  q1216737
Method
                  BLASTX
NCBI GI
                  q2688824
BLAST score
                  90
E value
                  5.0e-17
Match length
                  67
% identity
                  76
```

Contig ID

```
NCBI Description (U93273) putative auxin-repressed protein [Prunus
                  armeniaca]
                  119943
Seq. No.
                  4235 3.R1010
Contig ID
5'-most EST
                  g2576654
                  BLASTX
Method
                  q2688824
NCBI GI
BLAST score
                  204
E value
                  8.0e-21
Match length
                  99
% identity
                  63
                  (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                  armeniaca]
Seq. No.
                  119944
                  4235_5.R1010
Contig ID
                  g937343
5'-most EST
                  BLASTX
Method
                  q2688824
NCBI GI
                  244
BLAST score
E value
                  2.0e-20
Match length
                  69
                  72
% identity
                  (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                  armeniaca]
                  119945
Seq. No.
                  4235_6.R1010
Contig ID
5'-most EST
                  g2757494
                  BLASTX
Method
                  q2688824
NCBI GI
BLAST score
                  230
                   4.0e-19
E value
Match length
                  65
% identity
                  72
                  (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                  armeniaca]
Seq. No.
                  119946
                  4235_9.R1010
Contig ID
5'-most EST
                  ARABL1-043-Q1-B1-G1
                  119947
Seq. No.
                   4236_1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327408P1h02b1
                  BLASTN
Method
NCBI GI
                  g3046851
                   658
BLAST score
E value
                   0.0e + 00
                   689
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIJ24, complete sequence [Arabidopsis thaliana]
                  119948
Seq. No.
```

4237_1.R1010

E value

2.0e-46

```
LIB22-001-Q1-E1-H7
5'-most EST
Method
                   BLASTN,
NCBI GI
                   g4538895
BLAST score
                    75
E value
                   7.0e-34
Match length
                   191
% identity
                   85
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8
NCBI Description
                    (ESSA project)
                   119949
Seq. No.
                    4238 1.R1010
Contig ID
                   LIB22-001-Q1-E1-H8
5'-most EST
Method
                   BLASTX
                   q4191789
NCBI GI
BLAST score
                    443
                   1.0e-48
E value
Match length
                   183
% identity
                    65
                    (AC005917) putative transmembrane transport protein
NCBI Description
                    [Arabidopsis thaliana]
                    119950
Seq. No.
                    4243 1.R1010
Contig ID
5'-most EST
                    jC-alXLIB327434P3e05a1
Method
                   BLASTX
NCBI GI
                   q3287862
BLAST score
                    465
                    2.0e-46
E value
                   85
Match length
                    100
% identity
NCBI Description
                   PUTATIVE TRYPSIN INHIBITOR T01024.27 PRECURSOR >gi 2289007
                    (AC002335) trypsin inhibitor 2 precursor isolog
                    [Arabidopsis thaliana]
                    119951
Seq. No.
                    4243 3.R1010
Contig ID
                    jC-atXLIB327409P1b11b1
5'-most EST
                                                                          . /-
                   BLASTX
Method
                   g1708577
NCBI GI
BLAST score
                    187
                    9.0e-14
E value
Match length
                    63
% identity
                   TRYPSIN INHIBITOR 2 PRECURSOR (MTI-2)
NCBI Description
                   >gi_2129818_pir__S65661 trypsin inhibitor 2 - white mustard
>gi_1054853_emb_CAA58994 (X84208) trypsin inhibitor 2
                    [\overline{\text{Sinapis alba}}] > \overline{\text{gi } 2791356} \text{ emb } CAA76116} (Y16190) trypsin
                    inhibitor 2 [Sinapis alba]
                   119952
Seq. No.
                    4243 4.R1010
Contig ID
5'-most EST
                    jC-alXLIB327434P4e07a1
Method
                   BLASTX
NCBI GI
                   q3287862
BLAST score
                    465
```

Match length

122

```
85
Match length
% identity
                   100
                  PUTATIVE TRYPSIN INHIBITOR T01024.27 PRECURSOR >qi 2289007
NCBI Description
                   (AC002335) trypsin inhibitor 2 precursor isolog
                   [Arabidopsis thaliana]
                   119953
Seq. No.
                   4245_1.R1010
Contig ID
                   g2747755
5'-most EST
                                                                         . . -
Method
                  BLASTX
NCBI GI
                   g2244792
BLAST score
                   1092
E value
                   1.0e-119
Match length
                   264
% identity
                  78
                  (Z97336) ankyrin homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  119954
Contig ID
                   4246 1.R1010
5'-most EST
                   g2747542
Method
                  BLASTX
NCBI GI
                  q1780755
BLAST score
                   210
E value
                   2.0e-16
Match length
                  122
                   42
% identity
NCBI Description
                  (D61380) DJ-1 protein [Homo sapiens]
Seq. No.
                  119955
                   4246 2.R1010
Contig ID
5'-most EST
                   jC-atXP31C146L15T7d2
Method
                   BLASTX
NCBI GI
                   q2499005
                   308
BLAST score
                   2.0e-27
E value
Match length
                   276
                   39 🖫
% identity
                  4-METHYL-5 (B-HYDROXYETHYL) -THIAZOLE MONOPHOSPHATE
NCBI Description
                  BIOSYNTHESIS ENZYME >gi_1100872 (U34923) ThiJ [Escherichia
                  coli] >gi_1773108 (U82664)
                   4-methyl-\overline{5} (b-hydroxyethyl) -thiazole monophosphate
                  biosynthesis protein [Escherichia coli] >gi 1786626
                   (AE000148) 4-methyl-5(beta-hydroxyethyl)-thiazole
                  monophosphate synthesis [Escherichia coli]
                  119956
Seq. No.
                   4246_3.R1010
Contig ID
5'-most EST
                  g906083
Seq. No.
                  119957
                  4246 5.R1010
Contig ID
5'-most EST
                  jC-atXLIB327438P2d12a1
Method
                  BLASTX
NCBI GI
                  g2291156
BLAST score
                  110
E value
                  5.0e-10
```

```
% identity
                   36
                   (AF016418) No definition line found [Caenorhabditis
NCBI Description
                  elegans]
                  119958
Seq. No.
                   4247 1.R1010
Contig ID
                  jC-atXLIB327410P1f07b1
5'-most EST
                  BLASTX
Method
                  q3088646
NCBI GI
BLAST score
                   492
E value
                   2.0e-49
Match length
                   187
                   56
% identity
                   (AF056493) pectin methylesterase [Pisum sativum]
NCBI Description
                  >qi 3426335 (AF081457) pectin methylesterase [Pisum
                   satīvum]
                  119959
Seq. No.
                   4247 2.R1010
Contig ID
5'-most EST
                  g757680
                  BLASTX
Method
NCBI GI
                  g1279600
BLAST score
                  894
                  2.0e-96
E value
                   289 ...
Match length
% identity
                   63
                  (Z71753) pectin methylesterase [Nicotiana plumbaginifolia]
NCBI Description
Seq. No.
                   119960
                  4247 3.R1010
Contig ID
                   jC-atXLIB327414P4h09b2
5'-most EST
                  BLASTN
Method
NCBI GI
                  q2582640
                   69
BLAST score
E value
                   4.0e-30
Match length
                   77
                   97
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   119961
Seq. No.
                   4248 1.R1010
Contig ID
                  jC-atXP31C146I21T7d2
5'-most EST
Method
                  BLASTX
NCBI GI
                   q127041
BLAST score
                   1625
                  0.0e + 00
E value
Match length
                   327
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 81647 pir JN0131 methionine adenosyltransferase (EC
                   2.5.1.6) - Arabidopsis thaliana >gi 166872 (M55077)
                  S-adenosylmethionine synthetase [Arabidopsis thaliana]
                  119962
Seq. No.
Contig ID
                  4248 2.R1010
```

```
5'-most EST
                   iC-atXP123C117D21T7028d1
                   BLASTX
Method
                   g127045
NCBI GI
                   751
BLAST score
                   9.0e-80
E value
Match length
                   165
                   87
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                   >gi_99756_pir__JQ0410 methionine adenosyltransferase (EC
                   2.5.1.6) \overline{2} - Arabidopsis thaliana >gi 166874 (M33217)
                   S-adenosylmethionine synthetase (sam-2) [Arabidopsis
                   thaliana] >gi_4558554_gb_AAD22647.1_AC007138_11 (AC007138)
                   S-adenosylmethionine synthase 2 [Arabidopsis thaliana]
Seq. No.
                   119963
                   4248 3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327418P4b12b1
                   BLASTX
Method
                   q127045
NCBI GI
                   963
BLAST score
E value
                   1.0e-104
Match length
                   185
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                   >gi 99756 pir__JQ0410 methionine adenosyltransferase (EC
                   2.5.1.6) \overline{2} - Arabidopsis thaliana >gi 166874 (M33217)
                   S-adenosylmethionine synthetase (sam-\overline{2}) [Arabidopsis
                   thaliana] >gi 4558554_gb AAD22647.1_AC007138 11 (AC007138)
                   S-adenosylmethionine synthase 2 [Arabidopsis thaliana]
Seq. No.
                   119964
                   4248 4.R1010
Contig ID
                   jC-atXLIB327432P2a12b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g127041
BLAST score
                   605
E value
                   8.0e-63
Match length
                   114
                   100
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi 81647 pir JN0131 methionine adenosyltransferase (EC
                   2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077)
                   S-adenosylmethionine synthetase [Arabidopsis thaliana]
Seq. No.
                   119965
                   4248 10.R1010
Contig ID
                   q2748140
5'-most EST
Method
                   BLASTX
                   q1346520
NCBI GI
BLAST score
                   206
E value
                   3.0e-52
Match length
                   122
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
NCBI Description
```

```
>gi 790978 emb CAA56590 (X80362) S-adenosyl-L-methionine
                  synthetase [Brassica juncea]
                  119966
Seq. No.
                  4248 12.R1010
Contig ID
5'-most EST
                  jC-atXLIB327438P4e06a2
                  BLASTX
Method
                  g127041
NCBI GI
BLAST score
                  552
                  1.0e-56
E value
Match length
                  106
% identity
                  99
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 81647 pir JN0131 methionine adenosyltransferase (EC
                  2.5.1.6) - Arabidopsis thaliana >gi 166872 (M55077)
                  S-adenosylmethionine synthetase [Arabidopsis thaliana]
                  119967
Seq. No.
                  4248 16.R1010
Contig ID
5'-most EST
                  jC-atXLIB327438P4e06b2
                  BLASTX
Method
                  g127,041
NCBI GI
BLAST score
                  314
                  7.0e-29
E value
Match length
                  61
                  95
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 81647 pir JN0131 methionine adenosyltransferase (EC
                  2.5.1.6) - Arabidopsis thaliana >gi 166872 (M55077)
                  S-adenosylmethionine synthetase [Arabidopsis thaliana]
                  119968
Seq. No.
                  4250 1.R1010
Contig ID
                  jC-atXP123C117C18T7067d1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g2462264
BLAST score
                  49
                  5.0e-18
E value
Match length
                  53
% identity
                  98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  119969
Seq. No.
                  4250 2.R1010
Contig ID
5'-most EST
                  jC-aTXP124C118N4T7d1
Method
                  BLASTN
NCBI GI
                  g2477521
BLAST score
                  41
E value
                  2.0e-13
Match length
                  506
% identity
                  14
                  Arabidopsis thaliana chromosome I BAC F22K20 genomic
NCBI Description
```

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)

sequence, complete sequence [Arabidopsis thaliana]

BLAST score

```
119970
  Seq. No.
                     4250 4.R1010
  Contig ID
                     LIB2\overline{2}-043-Q1-E1-D1
  5'-most EST
                     BLASTN
  Method
  NCBI GI
                     g2477521
  BLAST score
                     35
                     1.0e-09
· · E value
  Match length
                     1026
                     15
  % identity
                     Arabidopsis thaliana chromosome I BAC F22K20 genomic
  NCBI Description
                     sequence, complete sequence [Arabidopsis thaliana]
                     119971
  Seq. No.
                     4250 5.R1010
  Contig ID
                     q241\overline{3}239
  5'-most EST
  Seq. No.
                      119972
                      4252 1.R1010
  Contig ID
                     LIB3234-086-Q1-K1-A10
  5'-most EST
                     BLASTX
  Method
                      q2829894
  NCBI GI
  BLAST score
                      417
  E value
                      3.0e-40
                      398
  Match length
  % identity
                      59
                     (AC002311) Unknown protein [Arabidopsis thaliana]
NCBI Description
                      119973
  Seq. No.
                      4253 1.R1010
  Contig ID
  5'-most EST
                      jC-atXLIB327413P1a02b1
                      BLASTN
  Method
                      q2582640
  NCBI GI
  BLAST score
                      51
                      2.0e-19
  E value
  Match length
                      67
   % identity
                      94
                      Arabidopsis thaliana mRNA for arginine/serine-rich splicing
  NCBI Description
                      factor, RSp40
   Seq. No.
                      119974
                      4255 1.R1010
   Contig ID
                      jC-atXLIB327438P4h05b2
   5'-most EST
                      BLASTN
  Method
   NCBI GI
                      q2582640
   BLAST score
                      65
                      6.0e-28
   E value
                      65
  Match length
   % identity
                      100
                      Arabidopsis thaliana mRNA for arginine/serine-rich splicing
   NCBI Description
                      factor, RSp40
                      119975
   Seq. No.
                      4256 1.R1010
   Contig ID
                      jC-atXLIB327404P1e05b1
   5'-most EST
   Method
                      BLASTN
                      q3985952
   NCBI GI
```

Contig ID

```
E value
                   7.0e-29
Match length
                   199
% identity
                   86
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MRC8, complete sequence [Arabidopsis thaliana]
                   119976
Seq. No...
                   4258 1.R1010
Contig ID
5'-most EST
                   LIB3177-088-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g2494144
BLAST score
                   200
                   2.0e-15
E value
Match length
                   68
% identity
                   68
NCBI Description
                   (AC002329) predicted leucine-rich protein [Arabidopsis
                   119977
Seq. No.
                   4260 1.R1010
Contig ID
5'-most EST
                  LIB3176-099-P1-K1-E10
Method
                  BLASTN
NCBI GI
                   q4755185
BLAST score
                   328
E value
                   0.0e + 00
Match length
                   817
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F5G3 genomic
                   sequence, complete sequence
Seq. No.
                   119978
Contig ID
                   4261 1.R1010
5'-most EST
                  LIB22-002-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                   g2245060
BLAST score
                   368
E value
                   4.0e-35
Match length
                   76
% identity
                   99
NCBI Description
                  (Z97342) allergen homolog [Arabidopsis thaliana]
Seq. No.
                   119979
                   4262_1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327404P4b04b1
Method
                   BLASTX
NCBI GI
                   g2501578
BLAST score
                   1426
E value
                   1.0e-158
Match length
                   309
% identity
                   91
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__$60047
NCBI Description
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                  119980
Seq. No.
```

4264 1.R1010

```
5'-most EST
                   jC-alXLIB327434P1e03b1
Method
                   BLASTN
                   g4559319
NCBI GI
BLAST score
                   440
                   0.0e + 00
E value
Match length
                   469
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC F14N22 genomic
NCBI Description
                  sequence, complete sequence
                   119981
Seq. No.
Contig ID
                   4267_1.R1010
                   jC-atXLIB327437P2d11a1
5'-most EST
Method
                  BLASTX
                  q3212866
NCBI GI
BLAST score
                   222
E value
                  1.0e-18
Match length
                  168
                   39
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                  119982
Seq. No.
Contig ID
                   4267_2.R1010
5'-most EST
                   jC-atXLIB327438P3h09b1
Method
                  BLASTX
NCBI GI
                   g3212866
BLAST score
                   200
E value
                   4.0e-15
Match length
                  147
% identity
                   34
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
                  119983
Seq. No.
                   4267 4.R1010
Contig ID
5'-most EST
                  jC-atXLIB327437P2d11b1
                  119984
Seq. No.
                   4269 1.R1010
Contig ID
5'-most EST
                   jC-atXP86CG9G7T7d2
Method
                  BLASTX
                   q419789
NCBI GI
BLAST score
                   731
                   2.0e-77
E value
Match length
                   216
% identity
                   65
NCBI Description hypothetical protein - potato
Seq. No.
                  119985
                  4269_2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327428P1e08b2
Method
                  BLASTX
                  a419789
NCBI GI
BLAST score
                   394
                   5.0e-38
E value
Match length
                  155
% identity
                  53
NCBI Description hypothetical protein - potato
```

% identity

```
119986
  Seq. No.
                     4272 1.R1010
  Contig ID
  5'-most EST
                     jC-atXP44C170I8T7092a1
                     BLASTX
  Method
  NCBI GI
                     g2213626
  BLAST score
                     213
  E value
                     1.0e-16
  Match length
                     95
  % identity
                     43
  NCBI Description
                     (AC000103) F21J9.18 [Arabidopsis thaliana]
                     119987
  Seq. No.
                     4272 2.R1010
  Contig ID
  5'-most EST
                     jC-alX24085Q1E1H11b1
                     BLASTN
  Method
  NCBI GI
                     q3985958
  BLAST score
                     222
  E value
                     1.0e-121
                                       ...
  Match length
                     733
                     97
  % identity
  NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                     119988
                     4272 4.R1010
  Contig ID
                     jC-alXLIB327436P4g04b1
  5'-most EST
  Method
                     BLASTN
  NCBI GI
                     q3985958
  BLAST score
                     67
  E value
                     5.0e-29
  Match length
                     243
  % identity
                     88
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
  NCBI Description
                    MZN1, complete sequence [Arabidopsis thaliana]
                     119989
  Seq. No. -
  Contig ID
                     4272 5.R1010
  5'-most EST
                     q937562
  Method
                     BLASTN
  NCBI GI
                     g3985958
  BLAST score
                     66
  E value
                     2.0e-28
  Match length
                     322
                     86
  % identity
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
  NCBI Description
                    MZN1, complete sequence [Arabidopsis thaliana]
  Seq. No.
                     119990
  Contig ID
                     4275 1.R1010
  5'-most EST
                     jC-atXLIB327420P4e10b1
  Method
                     BLASTX
                     g2252857
  NCBI GI
  BLAST score
                     327
  E value
                     4.0e-30
  Match length
                     103
```

\1 ·

```
(AF013294) similar to acidic ribosomal protein pl
NCBI Description
                  [Arabidopsis thaliana]
                  119991
Seq. No.
                  4280 1.R1010
Contig ID
                  LIB22-002-Q1-E1-D5
5'-most EST
                  BLASTN
Method
                  g975645
NCBI GI
BLAST score
                  37
                  3.0e-11
E value
Match length
                  37
                  100
% identity
NCBI Description A.thaliana cor47 gene
                  119992
Seq. No.
                  4281 1.R1010
Contig ID
                  jC-atXP79C240B3T7d2
5'-most EST
Method
                  BLASTX
                  g1321924
NCBI GI
BLAST score
                  367
E value
                  7.0e-35
Match length
                  115
% identity
                  61
                  (X92205) NAM [Petunia x hybrida]
NCBI Description
Seq. No.
                  119993
                  4281 2.R1010
Contig ID
                  jC-atXP34C151G21T7d1
5'-most EST
Method
                  BLASTX
                  g1321924
NCBI GI
BLAST score
                  216
E value
                  2.0e-18
                  106
Match length
% identity
                  47
                  (X92205) NAM [Petunia x hybrida]
NCBI Description
                  119994
Seq. No.
                  4282 1.R1010
Contig ID
                  LIB22-002-Q1-E1-D8
5'-most EST
                  119995
Seq. No.
                  4283 1.R1010
Contig ID
                  LIB22-002-Q1-E1-E1
5'-most EST
                  119996
Seq. No.
                  4290 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327404P2c01b1
                  BLASTX
Method
NCBI GI
                  q113116
BLAST score
                  569
                  2.0e-58
E value
Match length
                  168
% identity
                  61
NCBI Description ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME)
                  >gi 111396 pir A35007 ATP citrate (pro-S)-lyase (EC
                  4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase
```

[Rattus norvegicus]

```
119997
Seq. No.
                  4292 1.R1010
Contig ID
5'-most EST
                  LIB3176-042-P1-K1-G1
                  BLASTX
Method
NCBI GI
                  q2827550
BLAST score
                  105
                  3.0e-22
E value
Match length
                  96
% identity
                  29
NCBI Description
                  (ALO21635) leucine rich repeat receptor kinase-like protein
                  [Arabidopsis thaliana]
                  119998
Seq. No.
                  4297 1.R1010
Contig ID
5'-most EST
                  LIB3175-051-P1-K1-H11
Method
                  BLASTX
                  q2760320
NCBI GI
                  534
BLAST score
                  1.0e-104
E value
                  203
Match length
% identity
                  95
NCBI Description
                  (AC002130) F1N21.4 [Arabidopsis thaliana]
                  119999
Seq. No.
                  4297 2.R1010
Contig ID
                  q2758069
5'-most EST
Method
                  BLASTX
                  q2760320
NCBI GI
BLAST score
                  399
                  8.0e-39
E value
Match length
                  109
% identity
                  80
NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana]
Seq. No.
                  120000
                  4301_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P1a12b2
Method
                  BLASTN
NCBI GI
                  a3941523
BLAST score
                  44
E value
                  2.0e-15
Match length
                  56
% identity
                  96
NCBI Description
                  Arabidopsis thaliana putative transcription factor (MYB92)
                  mRNA, complete cds
Seq. No.
                  120001
Contig ID
                  4304 1.R1010
5'-most EST
                  jC-atXP41C162N8T7d1
                  BLASTX
Method
NCBI GI
                  q2781394
BLAST score
                  247
E value .
                  7.0e-21
Match length
                  112
% identity
NCBI Description (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
```

```
120002
Seq. No.
                   4309 1.R1010
Contig ID
5'-most EST
                   jC-atXP37C159C4T7d2
Method
                  BLASTX
                  q3236246
NCBI GI
BLAST score
                   276
                   5.0e-24
E value
Match length
                   66
% identity
                  76
NCBI Description
                  (AC004684) putative expansin protein [Arabidopsis thaliana]
                  120003
Seq. No.
                  4309 2.R1010
Contig ID
                  LIB3177-014-P1-K2-D1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1041706
BLAST score
                  94
E value
                  5.0e-61
Match length
                  143
% identity
                  78
NCBI Description
                  (U30480) expansin At-EXP6 [Arabidopsis thaliana]
Seq. No.
                  120004
                  4311 1.R1010
Contig ID
                  jC-atXLIB327412P3h02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2511693
BLAST score
                  310
E value
                   4.0e-28
Match length
                  155
% identity
                  45
NCBI Description
                  (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
Seq. No.
                  120005
                  4311 2.R1010
Contig ID
                  LIB22-059-Q1-E1-F3
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3451077
BLAST score
                  291
E value
                  5.0e-26
Match length
                  113
% identity
                  51
NCBI Description
                   (AL031326) cysteine proteinase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  120006
                  4311_3.R1010
Contig ID
5'-most EST
                  LIB22-081-Q1-E2-F4
Method
                  BLASTX
NCBI GI
                  q1172873
BLAST score
                  344
E value
                  4.0e-32
Match length
                  167
% identity
                  49
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
NCBI Description
```

drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A

precursor - Arabidopsis thaliana >gi 435619 dbj BAA02374 (D13043) thiol protease [Arabidopsis thaliana]

120007 Seq. No. 4312 1.R1010 Contig ID LIB22-003-Q1-E1-F7 5'-most EST Method BLASTX q4490732 NCBI GI

BLAST score 1823 E value 0.0e + 00Match length 380 % identity 91

NCBI Description (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like

protein [Arabidopsis thaliana]

Seq. No. 120008

4312 2.R1010 Contig ID

jC-atXLIB327418P2a06b2 5'-most EST

Method BLASTX NCBI GI q3986198 BLAST score 259 E value 5.0e-70 Match length 277 % identity 49

(AB015618) phosphoenolpyruvate carboxykinase NCBI Description

[Rhodopseudomonas palustris]

Seq. No. 120009

4312 3.R1010 Contig ID

5'-most EST LIB3176-009-P1-K2-E9

Method BLASTX NCBI GI q4490732 BLAST score 305 E value 1.0e-56 Match length 152 % identity 80

NCBI Description (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like

protein [Arabidopsis thaliana]

120010 Seq. No. 4312 4.R1010 Contig ID 5'-most EST $q498\overline{4}64$ Method BLASTX NCBI GI q4490732 BLAST score 766 E value 1.0e-81

Match length 189 % identity 80

NCBI Description (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like

protein [Arabidopsis thaliana]

Seq. No. 120011

4312_5.R1010 Contig ID 5'-most EST g2048233 Method BLASTX NCBI GI q4490732

BLAST score 375

BLAST score

```
8.0e-36
E value
                   86
Match length
                   86
% identity
                   (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                   protein [Arabidopsis thaliana]
                   120012
Seq. No.
                   4313 1.R1010
Contig ID
5'-most EST
                   jC-atXP8C92O4T7s1
                   BLASTN
Method
                   q3869065
NCBI GI
BLAST score
                   366
                   0.0e + 00
E value
                   457
Match length
                   98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K24M7, complete sequence [Arabidopsis thaliana]
                   120013
Seq. No.
                   4314 1.R1010
Contig ID
5'-most EST
                   LIB22-002-Q1-E1-G6
Method
                   BLASTX
NCBI GI
                   g2213583
BLAST score
                   771
                   2.0e-90
E value
Match length
                   186
% identity
                   94
                  (AC000348) T7N9.3 [Arabidopsis thaliana]
NCBI Description
                   120014
Seq. No.
                   4315 1.R1010
Contig ID
5'-most EST
                   jC-atXP32C147P24T7d2
Method
                   BLASTX
NCBI GI
                   g3080427
BLAST score
                   86
E value
                   1.0e-68
Match length
                   201
% identity
                   69 ·
                   (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                   120015
Seq. No.
                   4315 2.R1010
Contig ID
5'-most EST
                   jC-atXP94CG11A12T7b1
Method
                   BLASTX
NCBI GI
                   g3047104
BLAST score
                   270
E value
                  1.0e-23
Match length
                  96
% identity
                   57
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                  120016
Seq. No.
                   4316 1.R1010
Contig ID
5'-most EST
                  g2749102
                  BLASTN
Method
NCBI GI
                  g2264311
```

```
E value
                   0.0e + 00
                   588
Match length
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MLN1, complete sequence [Arabidopsis thaliana]
                   120017
Seq. No.
                   4318 1.R1010
Contig ID
                   jC-atXP73CF3A3T7b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g320608
BLAST score
                   1061
                   1.0e-116
E value
                   214
Match length
                   37
% identity
                   ubiquitin precursor - wild oat >gi 15989 emb CAA49200
NCBI Description
                   (X69422) tetraubiquitin [Avena fatua] >gi 777758 (L41658)
                   polyubiquitin [Saccharum sp.]
                   120018
Seq. No.
                   4318 2.R1010
Contig ID
5'-most EST
                   jC-atXP73C223E2T7b1
Method
                   BLASTX
                   q70642
NCBI GI
                   997
BLAST score
                   1.0e-108
E value
                   205
Match length
% identity
                   ubiquitin precursor - Arabidopsis thaliana
NCBI Description
                   >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382)
                   [Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi_226499_prf__1515347A
                   poly-ubiquitin [Arabidopsis thaliana]
Seq. No.
                   120019
Contig ID
                   4318 3.R1010
                   jC-atXLIB327428P4h05b2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q421929
BLAST score
                   350
                   1.0e-110
E value
                   232
Match length
% identity
                   ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156)
NCBI Description
                   ubiquitin [Lycopersicon esculentum]
                   120020
Seq. No.
Contig ID
                   4318 5.R1010
5'-most EST
                   jC-atXLIB327440P1g02a1
Method
                   BLASTX
NCBI GI
                   g70642
BLAST score
                   616
E value
                   5.0e-64
Match length
                   126
% identity
                   21
                   ubiquitin precursor - Arabidopsis thaliana
NCBI Description
                   >gi_17678_emb_CAA31331 (X12853) polyubiquitin (AA 1 - 382)
```

Contig ID

5'-most EST

```
[Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi_226499 prf_1515347A
                    poly-ubiquitin [Arabidopsis thaliana]
Seq. No.
                    120021
                    4318 6.R1010
Contig ID
5'-most EST
                    g907069
Method
                    BLASTX
NCBI GI
                    g1076678
BLAST score
                    380
E value
                    2.0e-36
Match length
                    79
% identity
                    97
NCBI Description
                    ubiquitin / ribosomal protein S27a - potato (fragment)
                    120022
Seq. No.
                    4318 9.R1010
Contig ID
                    LIB22-056-Q1-E1-A3
5'-most EST
Method
                    BLASTX
NCBI GI
                    q3603456
BLAST score
                    490
E value
                    2.0e-49
Match length
                    123
% identity
                    26
                    (AF088848) polyubiquitin [Capsicum chinense]
NCBI Description
                    120023
Seq. No.
Contig ID
                    4318 11.R1010
5'-most EST
                    jC-atXLIB327421P1e04b1
                    BLASTX
Method
NCBI GI
                    q70642
BLAST score
                    559
E value
                    2.0e-57
Match length
                    116
% identity
NCBI Description
                    ubiquitin precursor - Arabidopsis thaliana
                    >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382)
                    [Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi_226499_prf__1515347A
                    poly-ubiquitin [Arabidopsis thaliana]
                    120024
Seq. No.
Contig ID
                    4321 1.R1010
5'-most EST
                    jC-atXP11C97G5T7010d1
Method
                    BLASTN
NCBI GI
                    q3800746
BLAST score
                    50
E value
                    8.0e-19
Match length
                    50
% identity
NCBI Description
                    Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,
                    complete cds
                    120025 -
Seq. No.
```

4321_2.R1010

LIB3177-041-P1-K2-F12

```
Seq. No.
                   120026
                   4322 1.R1010
Contig ID
                   LIB22-002-Q1-E1-H4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4587571
BLAST score
                   573
                   4.0e-59
E value
Match length
                   154
% identity
                   73
                   (AC006550) Belongs to the PF 01027 Uncharacterized protein
NCBI Description
                   family UPF0005 with 7 transmembrane domains. [Arabidopsis
                   thaliana]
                   120027
Seq. No.
                   4323 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327420P4b11b1
Method
                   BLASTX
NCBI GI
                   g2341034
BLAST score
                   1645
E value
                   0.0e + 00
Match length
                   332
% identity
                   97
NCBI Description
                   (AC000104) F19P19.13 [Arabidopsis thaliana]
                   120028
Seq. No.
                   4323 8.R1010
Contig ID
5'-most EST
                   q2757532
Method
                   BLASTX
                   g2341034
NCBI GI
BLAST score
                   342
E value
                   9.0e-32
Match length
                   202
% identity
                   48
NCBI Description
                   (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                   120029
                   4323 10.R1010
Contig ID
5'-most EST
                   g2747970
Method
                  BLASTX
                   g2341034
NCBI GI
BLAST score
                   283
E value
                   5.0e-25
Match length
                   55
% identity
                   98
NCBI Description
                  (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                   120030
                   4323 11.R1010
Contig ID
                  LIB3177-008-P1-K2-D3
5'-most EST
Seq. No.
                   120031
                   4323 12.R1010
Contig ID
                  LIB3176-121-P2-K1-G5
5'-most EST
Method
                  BLASTX
                  g2341034
NCBI GI
BLAST score
                   404
```

2.0e-40

E value

% identity

```
Match length
                  104
% identity
                  86
                  (AC000104) F19P19.13 [Arabidopsis thaliana]
NCBI Description
                  120032
Seq. No.
                  4323 15.R1010
Contig ID
                  LIB24-116-Q1-E1-A4
5'-most EST
                  BLASTN
Method
                  q2341023
NCBI GI
BLAST score
                  111
E value
                  3.0e-55
Match length
                  162
                  100
% identity
                  Sequence of BAC F19P19 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                  120033
Seq. No.
                  4323 17.R1010
Contig ID
                  LIB3177-098-P1-K1-D8
5'-most EST
                  120034
Seq. No.
Contig ID
                  4326 1.R1010
5'-most EST
                  LIB22-080-Q1-E2-A1
                  BLASTN
Method
                  q4589439
NCBI GI
                   355
BLAST score
                  0.0e + 00
E value
Match length
                   391
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQM1, complete sequence
                   120035
Seq. No.
                   4327 1.R1010
Contig ID
                  LIB22-002-Q1-E1-H9
5'-most EST
Method
                   BLASTX
                   q4455210
NCBI GI
                   170
BLAST score
E value
                   3.0e-24
                   113
Match length
% identity
                   (AL035440) putative aspartate-tRNA ligase [Arabidopsis
NCBI Description
                   thaliana]
                   120036
Seq. No.
                   4331_1.R1010
Contig ID
5'-most EST
                   LIB23-069-Q1-E1-E7
                   120037
Seq. No.
Contig ID
                   4332 1.R1010
                   jC-atXLIB327439P2b07b2
5'-most EST
                   BLASTN
Method
NCBI GI
                   g4115930
BLAST score
                   414
E value
                   0.0e + 00
Match length
                   471
```

```
NCBI Description Arabidopsis thaliana BAC T4B21
                  120038
Seq. No.
                  4333 1.R1010
Contig ID
                  jC-atXLIB327439P2b08b2
5'-most EST
Method
                  BLASTX
                  q4128133
NCBI GI
                  230
BLAST score
                  7.0e-19
E value
Match length
                  102
% identity
                  44
                  (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
NCBI Description
                  120039
Seq. No.
                  4334 1.R1010
Contig ID
5'-most EST
                  jC-atXP104CE10B3T7b1
Method
                  BLASTX
                  q4586449
NCBI GI
                  254
BLAST score
                  2.0e-21
E value
                  47
Match length
% identity
                  (AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]
NCBI Description
Seq. No.
                  120040
                  4334 2.R1010
Contig ID
                  LIB23-025-Q1-E1-F4
5'-most EST
Method
                  BLASTX
                  q4586449
NCBI GI
                   328
BLAST score
                   4.0e-31
E value
                   72
Match length
% identity
                  80
                  (AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]
NCBI Description
                   120041
Seq. No.
                   4336 1.R1010
Contig ID
5'-most EST
                   jC-atXP74C225E24T7054d1
Method
                   BLASTX
                   q2245093
NCBI GI
BLAST score
                   516
                   1.0e-108
E value
                   250
Match length
% identity
                   (Z97343) membrane channel protein [Arabidopsis thaliana]
NCBI Description
                   120042
Seq. No.
Contig ID
                   4344 1.R1010
5'-most EST
                   jC-atXLIB327433P1d04b1
Method
                   BLASTX
NCBI GI
                   q2160166
BLAST score
                   1929
E value
                   0.0e+00
Match length
                   449
% identity
                   85
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
```

```
120043
Seq. No.
                  4345_1.R1010
Contig ID
5'-most EST
                   g16821
Method
                  BLASTX
                   g4406756
NCBI GI
BLAST score
                   224
                   2.0e-18
E value
Match length
                  113
                   44
% identity
                   (AC006836) putative integral membrane protein A3
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  120044
                   4346 1.R1010
Contig ID
                  jC-atXLIB327416P1c07b1
5'-most EST
                  BLASTX
Method
                  g3641252
NCBI GI
BLAST score
                   601
                  2.0e-62
E value
                  145
Match length
                  79
% identity
                   (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                  domestica]
                  120045
Seq. No.
                   4346 2.R1010
Contig ID
                  LIB22-003-Q1-E1-C1
5'-most EST
                  BLASTX
Method
                  g3641252
NCBI GI
BLAST score
                   421
                   4.0e-41
E value
                  189
Match length
                   47
% identity
                  (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                  domestica]
                  120046
Seq. No.
Contig ID
                   4348 1.R1010
5'-most EST
                   jC-atXLIB327423P1a10a1
Method
                  BLASTX
NCBI GI
                  q1706551
BLAST score
                   338
E value
                  3.0e - 31
Match length
                  137
% identity
                  47
                  GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR
NCBI Description
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1,3-ENDOGLUCANASE) >gi_924953 (U30323) beta
                   1,3-glucanase [Triticum aestivum]
Seq. No.
                  120047
                  4348 2.R1010
Contig ID
5'-most EST
                   jC-atXP89C245D4T7040d1
Method
                  BLASTX
NCBI GI
                  g2795803
                  709
BLAST score
                  9.0e-75
E value
```

```
234
Match length
% identity
                   43
NCBI Description
                   (ACO03674) putative beta-1,3-endoglucanase [Arabidopsis
                   thaliana] >gi 3355491 (AC004218) putative
                   beta-1,3-endoglucanase [Arabidopsis thaliana]
                   120048
Seq. No.
                   4350 1.R1010
Contig ID
5'-most EST
                   jC-alXLIB327435P4d06a1
Method
                   BLASTN
NCBI GI
                   q2182287
BLAST score
                   283
E value
                   1.0e-158
Match length
                   322
% identity
                   97
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC T7N9,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   120049
                   4353 1.R1010
Contig ID
5'-most EST
                   q241\overline{4}014
Method
                   BLASTX
NCBI GI
                   g1931639
BLAST score
                   198
                   5.0e-15
E value
Match length
                   82
                   48
% identity
                   (U95973) lysophospholipase isolog [Arabidopsis thaliana]
NCBI Description
                   120050
Seq. No.
                   4353 2.R1010
Contig ID
5'-most EST
                   LIB3176-092-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g1931639
BLAST score
                   225
E value
                   3.0e-18
Match length
                   88
% identity
                   (U95973) lysophospholipase isolog [Arabidopsis thaliana]
NCBI Description
                   120051
Seq. No.
                   4353 3.R1010
Contig ID
5'-most EST
                   LIB3176-021-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g1931639
BLAST score
                   356
E value
                   2.0e-33
Match length
                   191
% identity
                   38
                  (U95973) lysophospholipase isolog [Arabidopsis thaliana]
NCBI Description
                   120052
Seq. No.
                   4354 1.R1010
Contig ID
                   LIB2\overline{3}-067-Q1-E1-B11
5'-most EST
                   120053
Seq. No.
                   4355 1.R1010
Contig ID
```

```
5'-most EST
                   jC-alXLIB327436P1h11b1
Method
                   BLASTX
                   g2500497
NCBI GI
BLAST score
                   361
E value
                   5.0e - 34
Match length
                   81
% identity
                   81
                   40S RIBOSOMAL PROTEIN S21 >gi 1419372_emb_CAA67225.1_
NCBI Description
                   (X98656) ribosomal protein S21 [Zea mays]
                   120054
Seq. No.
Contig ID
                   4355_2.R1010
                   g272\overline{3}128
5'-most EST
Method
                   BLASTN
                   q4581161
NCBI GI
BLAST score
                   209
E value
                   1.0e-114
Match length
                   500
% identity
                   35
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20G20 genomic
                   sequence, complete sequence
Seq. No.
                   120055
Contig ID
                 4355_3.R1010
                   g2758568
5'-most EST
Method
                  BLASTN
NCBI GI
                   g4581161
BLAST score
                   293
E value
                   1.0e-164
Match length
                   495
% identity '
                   39
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20G20 genomic
                   sequence, complete sequence
                   120056
Seq. No.
                   4355_5.R1010
Contig ID
                   g905775
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4581161
BLAST score
                   139
                   5.0e-72
E value
                   472
Match length
                   37
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20G20 genomic
                   sequence, complete sequence
                   120057
Seq. No.
Contig ID
                   4355 6.R1010
                   q1149447
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4581161
BLAST score
                   158
E value
                   2.0e-83
Match length
                   446
% identity
                   31
                  Arabidopsis thaliana chromosome II BAC T20G20 genomic
NCBI Description
                   sequence, complete sequence
```

```
Seq. No.
                    120058
                    4355_7.R1010
 Contig ID
 5'-most EST
                    q957703
                    BLASTN
 Method
 NCBI GI
                    g4581161
 BLAST score
                    69
 E value
                    2.0e-30
 Match length
                    251
 % identity
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC T20G20 genomic
                   sequence, complete sequence
                    120059
 Seq. No.
 Contig ID
                    4357 2.R1010 -
 5'-most EST
                    jC-atX35019Q1E1D0330b1
 Method
                    BLASTN
 NCBI GI
                    q2264317
 BLAST score
                    451
                    0.0e + 00
 E value
                    455
Match length
 % identity
                    100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MUG13, complete sequence [Arabidopsis thaliana]
                    120060
 Seq. No.
 Contig ID
                    4359 1.R1010
 5'-most EST
                   LIB3176-054-P1-K1-G4
                    BLASTX
Method
NCBI GI
                    q2827711
BLAST score
                    605
E value
                    5.0e-63
Match length
                    141
                    82
 % identity
NCBI Description
                    (AL021684) oxoglutarate dehydrogenase - like protein
                    [Arabidopsis thaliana]
                    120061
Seq. No.
 Contig ID
                    4360 1.R1010
.5'-most EST
                    q2763350
 Method
                   BLASTX
NCBI GI
                    g4490309
BLAST score
                    454
 E value
                    3.0e-45
Match length
                    89
                    99
 % identity
NCBI Description
                    (AL035678) peroxidase ATP17a-like protein [Arabidopsis
                    thaliana]
Seq. No.
                    120062
                   4361_1.R1010
 Contig ID
                   LIB25-031-Q1-E1-F2
 5'-most EST
Method
                   BLASTN
NCBI GI
                    g3176701
BLAST score
                   189
E value
                    1.0e-102
Match length
                    423
```

5'-most EST

q1217117

```
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC T20K24 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   120063
                   4363_1.R1010
Contig ID
                   g272\overline{2}714
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2062155
BLAST score
                   553
E value
                   1.0e-56
Match length
                   114
% identity
                   99
NCBI Description
                   (AC001645) mitochondrial processing peptidase alpha subunit
                  precusor isolog [Arabidopsis thaliana]
Seq. No.
                   120064
                   4363 2.R1010
Contig ID
5'-most EST
                   LIB3176-071-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   q4220446
BLAST score
                   847
E value
                   6.0e-91
Match length
                   198
% identity
                   86
                   (AC006216) Strong similarity to gi_2062155 T02004.2
NCBI Description
                  mitochondrial processing peptidase alpha subunit precusor
                   isolog from Arabidopsis thaliana BAC gb_AC001645. ESTs
                   gb Z18504 and gb AA395715 come from this gene. [Arabidopsis
                   thaliana]
                   120065
Seq. No.
Contig ID
                   4364 1.R1010
5'-most EST
                   LIB2\overline{3}-011-Q1-E1-H5
Method
                   BLASTX
NCBI GI
                   g3250696
BLAST score
                   198
E value
                   4.0e-15
Match length
                   70
% identity
                   26
NCBI Description
                   (AL024486) putative protein [Arabidopsis thaliana]
                   120066
Seq. No.
Contig ID
                   4366 1.R1010
5'-most EST
                   jC-atXLIB327417P1e10a1
Method
                   BLASTX
NCBI GI
                   q4406768
BLAST score
                   225
E value
                   3.0e-60
Match length
                   250
                   47
% identity
NCBI Description
                   (AC006836) putative flavonol sulfotransferase [Arabidopsis
                  thaliana]
Seq. No.
                  120067
                  4366_3.R1010
Contig ID
```

```
Method
                  BLASTX
NCBI GI
                  q285286
BLAST score
                  269
E value
                  2.0e-23
Match length
                  117
% identity
                  44
NCBI Description flavonol 4'-sulfotransferase - Flaveria chloraefolia
Seq. No.
                  120068
                  4367 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P1d03b2
Method
                  BLASTX
NCBI GI
                  q2576361
BLAST score
                  545
E value
                  8.0e-56
Match length
                  114
% identity
                  87
                  (U39782) lysine and histidine specific transporter
NCBI Description
                  [Arabidopsis thaliana]
                  120069
Seq. No.
Contig ID
                  4368 1.R1010
                  jC-atXLIB327432P2b04b2
5'-most EST
                  BLASTX
Method
                  q2494113
NCBI GI ·
BLAST score
                  859
                  1.0e-92
E value
Match length
                  200
                  82
% identity
                  (AC002376) Strong similarity to Musa pectate lyase
NCBI Description
                  (gb X92943). ESTs gb AA042458, gb ATTS4502, gb N38552 come
                  from this gene. [Arabidopsis thaliana]
                  120070
Seq. No.
Contig ID
                  4368 2.R1010
5'-most EST
                  LIB3175-077-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q2494113
BLAST score
                  731
E value
                  1.0e-77
Match length
                  131
                  100
% identity
NCBI Description
                  (AC002376) Strong similarity to Musa pectate lyase
                   (gb X92943). ESTs gb AA042458, gb ATTS4502, gb N38552 come
                  from this gene. [Arabidopsis thaliana]
                  120071
Seq. No.
Contig ID
                  4369 1.R1010
5'-most EST
                  jC-atXLIB327439P2d04b2
Method
                  BLASTX
NCBI GI
                  q4204300
BLAST score
                  298
E value
                  7.0e-27
Match length
                  136
% identity
                  51
```

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

```
120072
   Seq. No.
                     4370 1.R1010
   Contig ID
                     jC-atXLIB327418P3a10b1
  5'-most EST
                     BLASTX
   Method
                     g2145358
   NCBI GI
   BLAST score
                     183
   E value
                     5.0e-54
                     124
   Match length
                     79
   % identity
                     (Y10922) HD-Zip protein [Arabidopsis thaliana]
   NCBI Description
                     120073
   Seq. No.
   Contig ID
                     4372 1.R1010
   5'-most EST
                     jC-atXLIB327413P1h04b1
   Method
                     BLASTX
   NCBI GI
                     q1730512
   BLAST score
                     1803
   E value
                     0.0e + 00
   Match length
                     399
                     91
   % identity
                     PHOSPHOGLYCERATE KINASE, CHLOROPLAST
   NCBI Description
                     >gi 2129669 pir S71368 phosphoglycerate kinase -
                     Arabidopsis thaliana (fragment) >gi 1022805 (U37701)
                     phosphoglycerate kinase [Arabidopsis thaliana]
                     120074
   Seq. No.
                     4372 2.R1010
   Contig ID
   5'-most EST
                     LIB3175-027-P1-K1-C11
   Method
                     BLASTX
                     g3738261
   NCBI GI
   BLAST score
                     351
                     6.0e-33
   E value
   Match length
                     139
   % identity
                     (AB018412) chloroplast phosphoglycerate kinase [Populus
   NCBI Description
                     nigra]
                     120075
Seq. No.
   Contig ID
                     4372 3.R1010
                     jC-aTXP13C103P17T7030a1
   5'-most EST
   Method
                     BLASTX
   NCBI GI
                     g1730512
   BLAST score
                     556
   E value
                     5.0e-69
   Match length
                     172
                     85
   % identity
                     PHOSPHOGLYCERATE KINASE, CHLOROPLAST
   NCBI Description
                     >gi_2129669_pir__S71368 phosphoglycerate kinase -
                     Arabidopsis thaliana (fragment) >gi_1022805 (U37701)
                     phosphoglycerate kinase [Arabidopsis thaliana]
                     120076
   Seq. No.
   Contig ID
                     4372 5.R1010
                     LIB3176-069-P1-K1-F9
   5'-most EST
   Seq. No.
                     120077
   Contig ID
                     4372 7.R1010
```

```
5'-most EST
                  jC-atXP38C159H9T7s2
Method
                  BLASTX
                  g2129668
NCBI GI
BLAST score
                  503
E value
                  6.0e-51
Match length
                  113
% identity
                  88
                  phosphoglycerate kinase - Arabidopsis thaliana (fragment)
NCBI Description
                  >qi 1022803 (U37700) phosphoglycerate kinase [Arabidopsis
                  thalianal
                  120078
Seq. No.
                  4373 1.R1010
Contig ID
5'-most EST
                  jC-atX22069Q1E1H04b1
Seq. No.
                  120079
                  4376 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P1d12b2
Method
                  BLASTN
NCBI GI
                  q4584531
BLAST score
                  481
E value
                  0.0e + 00
Match length
                  816
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8
NCBI Description
                   (ESSA project)
Seq. No.
                  120080
                  4379 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327416P3c08b1
Method
                  BLASTX
NCBI GI
                  g1778093
BLAST score
                  396
E value
                  2.0e-38
Match length
                  114
% identity
                  70
NCBI Description
                  (U64902) putative sugar transporter; member of major
                  facilitative superfamily; integral membrane protein [Beta
                  vulgaris]
Seq. No.
                  120081
Contig ID
                  4381 1.R1010
5'-most EST
                  jC-atXP60C197H18T7073d1
Method
                  BLASTX
NCBI GI
                  q542200
BLAST score
                  560
E value
                  3.0e-57
Match length
                  245
% identity
                  46
NCBI Description
                  hypothetical protein - garden asparagus
                  >gi_452714 emb CAA54526_ (X77320) unknown [Asparagus
                  officinalis]
Seq. No.
                  120082
                  4381 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327413P2d10b1
Method
                  BLASTX
```

```
NCBI GI
                  q542200
BLAST score
                   156
                   1.0e-41
E value
                   146
Match length
% identity
                   57
                  hypothetical protein - garden asparagus
NCBI Description
                  >gi 452714 emb CAA54526 (X77320) unknown [Asparagus
                  officinalis]
                  120083
Seq. No.
                  4382 1.R1010
Contig ID
                  jC-atXLIB327439P3d11b2
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4220643
BLAST score
                  387
E value
                  0.0e + 00
Match length
                   421
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120084
                  4383 1.R1010
Contig ID
                  LIB3175-061-P1-K1-H7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2829913
BLAST score
                  633
                  2.0e-66
E value
Match length
                  134
% identity
                  90
                   (AC002291) putative carboxyphosphonoenolpyruvate mutase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  120085
                  4384 1.R1010
Contig ID
5'-most EST
                  jC-atX22003Q1E1G04b1
Seq. No.
                  120086
                  4386 1.R1010
Contig ID
                  LIB22-003-Q1-E1-G4
5'-most EST
                  BLASTN
Method
NCBI GI
                  q4415928
BLAST score
                  661
E value
                  0.0e + 00
                  802
Match length
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13A10 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  120087
Seq. No.
                  4388 1.R1010
Contig ID
                  LIB22-070-Q1-E1-E3
5'-most EST
                  BLASTX
Method
                  g2388710
NCBI GI
BLAST score
                  435
E value
                  5.0e-43
Match length
                  118
```

5'-most EST

```
% identity
                    69
                    (AF017150) betaine aldehyde dehydrogenase [Amaranthus
NCBI Description
                    hypochondriacus]...
 Seq. No.
                    120088
                    4392 1.R1010
 Contig ID
 5'-most EST
                    jC-atX22003Q1E1H12b1
                    120089
 Seq. No.
                    4394 1.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327439P2e11b2
 Method
                    BLASTX
 NCBI GI
                    q2739386
 BLAST score
                    388
 E value
                    2.0e-37
 Match length
                    140
 % identity
                    59
                   (AC002505) unknown protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    120090
                    4395 1.R1010
 Contig ID
 5'-most EST
                    q3868965
 Method
                    BLASTX
                    g4006829
 NCBI GI
                    147
 BLAST score
                    1.0e-23
 E value
                    105
 Match length
 % identity
                    59
 NCBI Description
                    (AC005970) putative protein kinase [Arabidopsis thaliana]
                    120091
 Seq. No.
                    4397 1.R1010
 Contig ID
                    jC-atXLIB327418P4f02b1
 5'-most EST
                    BLASTN
 Method
 NCBI GI
                    q3212102
 BLAST score
                    385
                    0.0e + 00
 E value
 Match length
                    437
 % identity
                    98
                   Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
 NCBI Description
                    complete sequence [Arabidopsis thaliana]
                    120092
 Seq. No.
 Contig ID
                    4399 1.R1010
                    jC-atX22004Q1E1H08a1
 5'-most EST
 Method
                    BLASTN
 NCBI GI
                    q3449326
 BLAST score
                    497
                    0.0e + 00
 E value
 Match length
                    504
                    100
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 NCBI Description
                    K19M22, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    120093
                    4399 3.R1010
 Contig ID
```

jC-atXLIB327439P1e09b2

```
BLASTN
Method
                   q2582640
NCBI GI
                   61
BLAST score
                   4.0e-25
E value
Match length
                   76
                   96
% identity
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   120094
Seq. No.
                   4399 4.R1010
Contig ID
                   q371\overline{9}201
5'-most EST
                   BLASTX
Method
                   g2493493
NCBI GI
                   597
BLAST score
E value
                   2.0e-61
                   275
Match length
% identity
                   44
                   SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1)
NCBI Description
                   >gi_619352_bbs_153538 CP-MII.1=serine carboxypeptidase
                   [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324
                   120095
Seq. No.
                   4403 1.R1010
Contig ID
                   jC-atXLIB327439P1b06b2
5'-most EST
Method
                   BLASTX
                   g1703478
NCBI GI
                   802
BLAST score
                   6.0e-86
E value
                   158
Match length
% identity
                   (U40566) ubiquitin activating enzyme 2 [Arabidopsis
NCBI Description
                   thaliana]
                   120096
Seq. No.
                   4408 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327439P1b08b2
Method
                   BLASTX
NCBI GI
                   q4033431
                   676
BLAST score
                   3.0e-71
E value
Match length
                   157
% identity
                   87
                   PROBABLE PYRUVATE KINASE, CYTOSOLIC ISOZYME (PK)
NCBI Description
                   >qi 2982467 emb CAA18231 (AL022223) pyruvate kinase like
                   protein [Arabidopsis thaliana]
                   120097
Seq. No.
                   4409 1.R1010
Contig ID
                   LIB22-045-Q1-E1-D10
5'-most EST
Method
                   BLASTX
                   g1335862
NCBI GI
BLAST score
                   317
                   4.0e-29
E value
                   81
Match length
% identity
                   80
```

```
NCBI Description (U42608) clathrin heavy chain [Glycine max]
                   120098
Seq. No.
                   4410 1.R1010
Contig ID
5'-most EST
                   LIB3176-106-P1-K1-F10
                   BLASTN
Method
                   q4757409
NCBI GI
BLAST score
                   742
E value
                   0.0e + 00
Match length
                   2516
% identity
                   86
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MVC8, complete sequence
                   120099
Seq. No.
                   4410 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327439P1b09b2
Method
                   BLASTN
NCBI GI
                   q4757409
BLAST score
                   77
E value
                   8.0e-35
Match length
                   708
% identity
                   78
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MVC8, complete sequence
                   120100
Seq. No.
                   4410 6.R1010
Contig ID
5'-most EST
                   q241\overline{4}016
                   BLASTN
Method
NCBI GI
                   q4757409
BLAST score
                   211
E value
                   1.0e-115
Match length
                   297
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MVC8, complete sequence
                   120101
Seq. No.
                   4411_1.R1010
Contiq ID
5'-most EST
                   LIB22-004-Q1-E1-A8
Method
                   BLASTX
NCBI GI
                   q4262226
BLAST score
                   279
E value
                   3.0e-24
Match length
                   136
% identity
                   43
NCBI Description
                  (AC006200) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   120102
Contig ID
                   4413_1.R1010
5'-most EST
                  LIB35-044-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                   q136251
BLAST score
                   1453
E value
                   1.0e-162
Match length
                   306
```

NCBI GI

```
% identity
                  92
                  TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR
NCBI Description
                  >gi_99767_pir__A31393 tryptophan synthase (EC 4.2.1.20)
                  beta chain - Arabidopsis thaliana >gi_166892 (M23872)
                  tryptophan synthase beta subunit [Arabidopsis thaliana]
                  120103
Seq. No.
                  4414_1.R1010
Contig ID
                  LIB3176-069-P1-K1-C10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4335723
BLAST score
                  701
                  7.0e-74
E value
                  172
Match length
% identity
                  (AC006248) putative thioredoxin M [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  120104
Contig ID
                  4416 1.R1010
5'-most EST
                  jC-a1X24075Q1E1F12b1
Method
                  BLASTX
NCBI GI
                  q1839188
BLAST score
                  1350
E value
                  1.0e-150
Match length
                  279
                  96
% identity
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]
Seq. No.
                  120105
                  4417 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327402P4c12b1
Method
                  BLASTX
NCBI GI
                  q3927825
                  889
BLAST score
                  5.0e-96
E value
Match length
                  183
% identity
                  93
                  (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                  [Arabidopsis thaliana]
                  120106
Seq. No.
                  4418 1.R1010
Contig ID
5'-most EST
                  jC-atX24041Q1E1C12a1
Method
                  BLASTX
NCBI GI
                  q4455223
BLAST score
                  1536
                  1.0e-171
E value
Match length
                  363
% identity
                  83
NCBI Description
                  (AL035440) putative DNA binding protein [Arabidopsis
                  thalianal
                  120107
Seq. No.
Contig ID
                  4418_2.R1010
5'-most EST
                  jC-atXLIB327431P2g05a1
Method
                  BLASTX
```

g4455223

```
1048
BLAST score
                  1.0e-114
E value
                  204
Match length
                  52
% identity
                  (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  120108
Seq. No.
                  4419 1.R1010
Contig ID
                  jC-atXLIB327439P3b04b2
5'-most EST
                  BLASTN
Method
                  q3250673
NCBI GI
                  471
BLAST score
                  0.0e + 00
E value
                  690
Match length
% identity
                  98
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5
NCBI Description
                  (ESSAII project)
                  120109
Seq. No.
                  4427 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327430P1h04b1
Method
                  BLASTX
                  q1169451
NCBI GI
                  328
BLAST score
E value
                  2.0e-30
Match length
                  116
% identity
                  53
                  PROBABLE GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE A6 PRECURSOR
NCBI Description
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1, 3-ENDOGLUCANASE) >gi_322510_pir__S31906
                  beta-1,3-glucanase homolog - Arabidopsis thaliana
                  >gi 22677 emb CAA49853 (X70409) A6 [Arabidopsis thaliana]
                  >gi 2244764 emb CAB10187 (Z97335) AMP-binding protein
                  [Arabidopsis thaliana]
                  120110
Seq. No.
                  4434 1.R1010
Contig ID
                  jC-atXLIB327414P1f02a1
5'-most EST
Method
                  BLASTX
                  g3763932
NCBI GI
BLAST score
                  1001
                  1.0e-109
E value
                  236
Match length
                  80
% identity
                  (AC004450) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  120111
Seq. No.
                  4434 2.R1010
Contig ID
                  LIB25-020-Q1-E1-G6
5'-most EST
Method
                  BLASTX
                  g3763932
NCBI GI
BLAST score
                  233
E value
                  3.0e-19
                  72
Match length
% identity
                  61
NCBI Description (AC004450) putative protein kinase [Arabidopsis thaliana]
```

```
120112
Seq. No.
                  4435 1.R1010
Contig ID
                  jC-atXP118C145D18T7060a1
5'-most EST
Method
                  BLASTX
                  g1172635
NCBI GI
                  713
BLAST score
                  2.0e-75
E value
Match length
                  157
                  90
% identity
                  26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 2) >gi 556558 dbj BAA04615 (D17789) rice
                  homologue of Tat binding protein [Oryza sativa]
                  120113
Seq. No.
                  4435 2.R1010
Contig ID
                  LIB3175-079-P1-K1-C2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4580460
BLAST score
                  1190
                  1.0e-161
E value
Match length
                  362
% identity
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                  thaliana]
                  120114
Seq. No.
                  4435 3.R1010
Contig ID
                  g2047926
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1172635
BLAST score
                  226
E value
                  2.0e-18
Match length
                  60
% identity
                  77
                  26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice
                  homologue of Tat binding protein [Oryza sativa]
                  120115
Seq. No.
                  4435 4.R1010
Contig ID
5'-most EST
                  jC-atXP38C158I11T7d1
                  BLASTX
Method
NCBI GI
                  q4580460
BLAST score
                  552
                  9.0e-57
E value
Match length
                  123
% identity
NCBI Description
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
                  thaliana]
                  120116
Seq. No.
                  4436 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327424P4d11b1
Method
                  BLASTX
NCBI GI
                  g4586254
BLAST score
                  353
```

Method

```
E value
                    2.0e-56
 Match length
                    155
                    77
 % identity
                   (AL049640) auxilin-like protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                    120117
                    4440 1.R1010
 Contig ID
                    jC-atXP5C89K8T7049a1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g2252859
 BLAST score
                    630
 E value
                    1.0e-65
 Match length
                    155
 % identity
                    54
                    (AF013294) No definition line found [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    120118
                    4440 2.R1010
 Contig ID
                    jC-a\overline{t}XP79C239E9T7d2
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g2252859
 BLAST score
                    1137
 E value
                    1.0e-125
 Match length
                    243
 % identity
                    88
                   (AF013294) No definition line found [Arabidopsis thaliana]
 NCBI Description
                    120119
 Seq. No.
                    4441 1.R1010
 Contig ID
                    LIB25-082-Q1-E1-C6
 5'-most EST
 Method
                    BLASTX
                    q584825
 NCBI GI
 BLAST score
                    655
 E value
                    4.0e-68
 Match length
                    151
 % identity
                    79
                   B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
 NCBI Description
                    >gi 297889_emb_CAA51078 (X72385) B2 protein [Daucus
                    carota]
 Seq. No.
                    120120
                    4441 2.R1010
 Contig ID
                    jC-aTXLIB327423P4f02b1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q584825
 BLAST score
                    405
                    4.0e-39
 E value
 Match length
                    133
 % identity
                    64
 NCBI Description
                   B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
                    >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                    carota]
 Seq. No.
                    120121
 Contig ID
                    4441_3.R1010
 5'-most EST
                    LIB3175-082-P1-K1-A9
```

BLASTX

E value

5.0e-19

```
NCBI GI
                    g1351408
BLAST score
                    572
                    7.0e-59
E value
Match length
                    138
% identity
                    73
                    VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
NCBI Description
                    >gi_1076563_pir__S51117 cystein proteinase - sweet orange
                    >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by
similarity) [Citrus sinensis] >gi_1588548_prf__2208463A
                    vascular processing protease [Citrus sinensis]
Seq. No.
                    120122
                    4441 4.R1010
Contig ID
                    LIB3175-063-P1-K1-E9
5'-most EST
Method
                    BLASTX
NCBI GI
                    g1351411
BLAST score
                    440
E value
                    1.0e-43
Match length
                    146
% identity
NCBI Description
                   VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) (PROTEINASE B)
                    >gi_1076553_pir__S49175 cysteine proteinase precursor -
                    spring vetch >gi_2129906_pir__S68984 cysteine proteinase precursor - spring vetch >gi_510358_emb_CAA84383_ (Z34899)
                    cysteine proteinase [Vicia sativa]
                    120123
Seq. No.
Contig ID
                    4442 1.R1010
5'-most EST
                    jC-atXLIB327429P1d03b2
Method
                    BLASTX
NCBI GI
                    q3213227
BLAST score
                    228
E value
                    2.0e-18
Match length,
                    152
% identity
NCBI Description
                    (AF035209) putative v-SNARE Vtila [Mus musculus]
                    >gi 3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]
Seq. No.
                    120124
                    4442 3.R1010
Contia ID
5'-most EST
                    jC-atXLIB327409P3g03b1
Method
                    BLASTN
NCBI GI
                    q2582640
BLAST score
                    68
E value
                    1.0e-29
Match length
                    75
                    99
% identity
NCBI Description
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                    factor, RSp40
Seq. No.
                    120125
Contig ID
                    4443 1.R1010
5'-most EST
                    jC-atXLIB327414P4b10a2
Method
                    BLASTX
NCBI GI
                    g4503515
BLAST score
                    231
```

Match length

```
Match length
                   94
% identity
                   54
                  UNKNOWN >gi 2351380 (U54559) translation initiation factor
NCBI Description
                  eIF3 p40 subunit [Homo sapiens]
Seq. No.
                   120126
                   4444 1.R1010
Contig ID
                  LIB22-019-Q1-E1-B10
5'-most EST
Method
                  BLASTN
                  q3766106
NCBI GI
BLAST score
                   224
                   1.0e-123
E value
                   386
Match length
% identity
                   98
                  Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                   120127
Seq. No.
                   4445 1.R1010
Contig ID
                  LIB22-004-Q1-E1-D8
5'-most EST
Seq. No.
                  120128
                   4449 1.R1010
Contig ID
                  LIB25-079-Q1-E1-F4
5'-most EST
Method
                  BLASTN
NCBI GI
                  q3643588
BLAST score
                  184
E value
                   5.0e-99
Match length
                   416
% identity
                   96
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   120129
                   4452 1.R1010
Contig ID
                   jC-atXLIB327411P1d05b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  56
                  4.0e-22
E value
                  72
Match length
                   96
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  120130
                   4452 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327422P1b12b1
Seq. No.
                  120131
                   4455 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327439P1d04b2
Method
                  BLASTX
NCBI GI
                  g4567278
BLAST score
                  826
E value
                  9.0e-89
```

```
% identity
                  100
                   (AC006841) putative anthracycline associated resistance ARX
NCBI Description
                  protein [Arabidopsis thaliana]
                  120132
Seq. No.
Contig ID
                  4457 1.R1010
                  jC-aTXLIB327439P1d05b2
5'-most EST
                  BLASTX
Method
                  q1170939
NCBI GI
BLAST score
                  1056
E value
                  1.0e-115
Match length
                  212
                  93
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                  >gi_1084408_pir__S46540 methionine adenosyltransferase (EC
                  2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743)
                  S-adenosyl-L-methionine synthetase [Lycopersicon
                  esculentum]
                  120133
Seq. No.
Contig ID
                  4460 1.R1010
5'-most EST
                  g2758457
Methød
                  BLASTX
                  g2245087
NCBI GI
                  328
BLAST score
                  2.0e-30
E value
Match length
                  153
% identity
                  44
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
                  120134
Seq. No.
                  4462 1.R1010
Contig ID
5'-most EST
                  LIB22-004-Q1-E1-F12
Method
                  BLASTX
NCBI GI
                  q549975
BLAST score
                  389
E value
                  2.0e-37
Match length
                  100
% identity
                  (U12858) nucleosome assembly protein I-like protein;
NCBI Description
                  similar to mouse nap I, PIR Accession Number JS0707
                   [Arabidopsis thaliana]
                  120135
Seq. No.
                  4466 1.R1010
Contig ID
5'-most EST
                  LIB24-075-Q1-E1-C9
Method
                  BLASTX
NCBI GI
                  q1799787
BLAST score
                  287
E value
                  1.0e-25
Match length
                  134
                  46
% identity
NCBI Description
                  (D90868) OXALYL-COA DECARBOXYLASE (EC 4.1.1.8).
                   [Escherichia coli]
```

13200

120136

Seq. No.

```
Contig ID
                  4467 1.R1010
                  jC-atXLIB327439P1d02b2
5'-most EST
                   BLASTX
Method
                   q2827717
NCBI GI
                   309
BLAST score
E value
                   4.0e-28
                   74
Match length
                   81
% identity
NCBI Description
                   (AL021684) phosphoenolpyruvate carboxykinase (ATP) - like
                  protein [Arabidopsis thaliana]
Seq. No.
                   120137
Contig ID
                   4468 1.R1010
5'-most EST
                   jC-atXP74C223N10T7091d1
                  BLASTX
Method
NCBI GI
                   g2244819
BLAST score
                   375
                   2.0e-54
E value
                   197
Match length
% identity
                   45
NCBI Description
                  (Z97336) germin type 2 [Arabidopsis thaliana]
Seq. No.
                  120138
                  4468 2.R1010
Contig ID
                  LIB22-004-Q1-E1-F8
5'-most EST
                  BLASTX
Method
                  a2244819
NCBI GI
BLAST score
                   368
                   3.0e-35
E value
                  107
Match length
                   69
% identity
                  (Z97336) germin type 2 [Arabidopsis thaliana]
NCBI Description
                   120139
Seq. No.
Contig ID
                   4472 1.R1010
                  jC-atXLIB327409P4g06b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3785991
BLAST score
                   1408
E value
                   1.0e-156
Match length
                   338
% identity
NCBI Description
                  (AC005560) putative MAP kinase [Arabidopsis thaliana]
                   120140
Seq. No.
                   4472 3.R1010
Contig ID
5'-most EST
                  g2723010
Method
                  BLASTX
NCBI GI
                   g3785991
BLAST score
                   347
E value
                   1.0e-125
Match length
                   250
% identity
                   91
NCBI Description (AC005560) putative MAP kinase [Arabidopsis thaliana]
                  120141
Seq. No.
                   4473 1.R1010
Contig ID
```

```
5'-most EST
                   jC-atXLIB327410P1b01b1
                                                        - 11
                   120142
Seq. No.
                   4476 1.R1010
Contig ID
                  LIB22-027-Q1-E1-A10
5'-most EST
Method
                  BLASTN
                   g16473
NCBI GI
                   472
BLAST score
                   0.0e + 00
E value
Match length
                   507
% identity
                   98
                  Arabidopsis thaliana 25S-18S ribosomal DNA spacer
NCBI Description
Seq. No.
                   120143
                   4476 3.R1010
Contig ID
5'-most EST
                   g2748677
Method
                  BLASTN
                   q16472
NCBI GI
BLAST score
                   308
                  1.0e-173
E value
                   351
Match length
% identity
                   98
                  A.thaliana rRNA repeat unit, most frequent IGR type
NCBI Description
                   120144 . . .
Seq. No.
                   4477 1.R1010
Contig ID
                   jC-atXLIB327414P2d11a1
5'-most EST
Method
                   BLASTN
                   q3241920
NCBI GI
BLAST score
                   557
                   0.0e + 00
E value
Match length
                   667
% identity
                   97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAE1, complete sequence [Arabidopsis thaliana]
                   120145
Seq. No.
                   4477 2.R1010
Contig ID
5'-most EST
                   LIB22-004-Q1-E1-G7
Method
                   BLASTX
NCBI GI
                   g3608261
BLAST score
                   314
E value
                   2.0e-28
Match length
                   84
                   64
% identity
NCBI Description
                  (AB017564) dof zinc finger protein [Arabidopsis thaliana]
Seq. No.
                   120146
                   4478 1.R1010
Contig ID
                  jC-atX22003Q1E1G11b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3128134
BLAST score
                   398
E value
                  0.0e+00.
Match length
                   406
% identity
                   100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
```

K18G13, complete sequence [Arabidopsis thaliana] Seq. No. 120147 4479 1.R1010 Contig ID 5'-most EST jC-atXLIB327409P3e11b1 Method BLASTN g2264306 NCBI GI 728 BLAST score E value 0.0e + 00728 Match length % identity 100 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MBK5, complete sequence [Arabidopsis thaliana] 120148 Seq. No. 4480 1.R1010 Contig ID jC-atXLIB327421P3c12b1 5'-most EST Method BLASTX NCBI GI g3122673 BLAST score 993 E value 1.0e-108 Match length 204 % identity 92 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ NCBI Description (297341) ribosomal protein [Arabidopsis thaliana] Seq. No. 120149 4482 1.R1010 Contig ID jC-atXLIB327420P4g06b1 5'-most EST Method BLASTN NCBI GI g4691223 BLAST score 175 2.0e-93 E value Match length 350 % identity 100 Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 NCBI Description (ESSA project) 120150 Seq. No. 4482 2.R1010 Contig ID jC-atXLIB327439P1e12b2 5'-most EST Method BLASTX NCBI GI q4678935 BLAST score 963 1.0e-104 E value Match length 224 % identity 84 (AL049711) putative protein [Arabidopsis thaliana] NCBI Description 120151 Seq. No. 4482 3.R1010 Contig ID jC-atXLIB327432P4a07b1 5'-most EST BLASTX Method NCBI GI g4678935

419

98

5.0e-41

BLAST score

Match length

E value

NCBI GI

```
% identity
  NCBI Description (AL049711) putative protein [Arabidopsis thaliana]
                    120152
  Seq. No.
                     4483 1.R1010
  Contig ID
                    jC-atXLIB327410P2a07b1
  5'-most EST
                    BLASTX
  Method
                    g1256509
  NCBI GI
                    1012
  BLAST score
                     1.0e-110
  E value
  Match length
                     252
  % identity
  NCBI Description (X92943) pectate lyase [Musa acuminata]
                     120153
  Seq. No.
                     4484 1.R1010
  Contig ID
                     jC-atXLIB327439P1e08b2
  5'-most EST
                     BLASTN
  Method
                     g4454447
  NCBI GI
                     193
  BLAST score
                     1.0e-104
  E value
  Match length
                     471
  % identity
                     100
                    Arabidopsis thaliana chromosome II BAC F5H14 genomic
  NCBI Description
                     sequence, complete sequence [Arabidopsis thaliana]
                     120154
  Seq. No.
                     4485 1.R1010
  Contig ID
                     jC-atXLIB327439P2e08b2
  5'-most EST
                     BLASTX
  Method
                     g1170094
  NCBI GI
                     335
  BLAST score
  E value
                     3.0e-31
                     114
  Match length
  % identity
                     59
                     GLUTATHIONE S-TRANSFERASE (CLASS-PHI) (25 KD AUXIN-BINDING
  NCBI Description
                     PROTEIN) >gi 860956 emb CAA55039_ (X78203) glutathione
                     transferase [Hyoscyamus muticus]
                     120155
  Seq. No.
                     4485 2.R1010
  Contig ID
                     jC-atXLIB327409P3g07b1
  5'-most EST
                     BLASTX
  Method
                     g1170094
  NCBI GI
  BLAST score
                     236
  E value
                     1.0e-19
· · Match length
                     81
  % identity
                     56
                     GLUTATHIONE S-TRANSFERASE (CLASS-PHI) (25 KD AUXIN-BINDING
  NCBI Description
                     PROTEIN) >gi 860956 emb CAA55039_ (X78203) glutathione
                     transferase [Hyoscyamus muticus]
                     120156
  Seq. No.
                     4488 1.R1010
  Contig ID
                     jC-atXP96C249I21T7b1
  5'-most EST
                     BLASTN
  Method
```

q4589436

```
BLAST score
                  60
E value
                  7.0e-25
Match length
                  85
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MPA22, complete sequence
                  120157
Seq. No.
                  4489 1.R1010
Contig ID
                  jC-atXLIB327439P2e10b2
5'-most EST
Method
                  BLASTX
                  q4006918
NCBI GI
BLAST score
                  487
                  8.0e-49
E value
Match length
                  115
% identity
                  87
                  (Z99708) peroxidase like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  120158
                  4491 1.R1010
Contig ID
5'-most EST
                  jC-atXP65C206L22T7065d1
Method
                  BLASTX
NCBI GI
                  g2062161
BLAST score
                  1376
E value
                  1.0e-153
                  295
Match length
% identity
                  89
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  120159
Seq. No.
                  4491 2.R1010
Contig ID
                  jC-atXP112C127L18T7d2
5'-most EST
Method
                  BLASTX
                  q3738092
NCBI GI
                  1560
BLAST score
                  1.0e-174
E value
Match length
                  356
% identity
                  90
                  (AC005617) similar to glyoxysomal malate dehydrogenase
NCBI Description
                  [Arabidopsis thaliana]
                  120160
Seq. No.
                  4491 4.R1010
Contig ID
                  jC-atXLIB327410P4h01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2062158
BLAST score
                  1431
                  1.0e-159
E value
                  298
Match length
                  92
% identity
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  120161
Seq. No.
Contig ID
                  4491 5.R1010
```

g1158723

5'-most EST

```
Method
                  BLASTX
NCBI GI
                  g2062161
                  575
BLAST score
                  3.0e-59
E value
                  196
Match length
% identity
                  65
                  (ACO01645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  120162
Seq. No.
                  4491 7.R1010
Contig ID
5'-most EST
                  jC-alXLIB327436P2e09a1
Method
                  BLASTX
                  g3738092
NCBI GI
BLAST score
                  235
                  2.0e-19
E value
                  47
Match length
                  98
% identity
                  (AC005617) similar to glyoxysomal malate dehydrogenase
NCBI Description
                  [Arabidopsis thaliana]
                  120163
Seq. No.
Contig ID
                  4491 9.R1010
5'-most EST
                  LIB3176-009-P1-K3-B1
                  BLASTX
Method
                  g2062161
NCBI GI
BLAST score
                  146
                  3.0e-09
E value
Match length
                  27
                  100
% identity
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  120164
Seq. No.
                  4491 20.R1010
Contig ID
5'-most EST
                  LIB3176-122-P2-K1-H11
Method
                  BLASTX
                  g3738092
NCBI GI
BLAST score
                  297
E value
                  7.0e-27
Match length
                  61
                  92
% identity
                  (AC005617) similar to glyoxysomal malate dehydrogenase
NCBI Description
                  [Arabidopsis thaliana]
                  120165
Seq. No.
Contig ID
                  4493_1.R1010
                  jC-aTXLIB327439P2b05b2
5'-most EST
Method
                  BLASTX
                  g4585977
NCBI GI
                  377
BLAST score
                  5.0e-36
E value
Match length
                  126
                  59
% identity
                  (AC005287) Unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

Method

BLASTX

```
Contig ID
                  4495 1.R1010
                  jC-atXP83CG3F12T7055a1
5'-most EST
                  120167
Seq. No.
                  4495 2.R1010
Contig ID
                  LIB3168-034-P1-K1-C5
5'-most EST
                  120168
Seq. No.
Contig ID
                  4500 1.R1010
5'-most EST
                  jC-atXLIB327411P2f12b1
Method
                  BLASTX
NCBI GI
                  q3608137
BLAST score
                   605
                  1.0e-62
E value
Match length
                  214
                   60
% identity
                  (AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
                  120169
Seq. No.
                  4508 1.R1010
Contig ID
                  jC-atX24029Q1E1G05b1
5'-most EST
Method
                  BLASTX
                  g3056597
NCBI GI
BLAST score
                  176
                  2.0e-12
E value
Match length
                  194
                  31
% identity
NCBI Description
                  (AC004255) T1F9.18 [Arabidopsis thaliana]
                  120170
Seq. No.
Contig ID
                   4510 1.R1010
5'-most EST
                  LIB22-005-Q1-E1-B8
Method
                  BLASTN
                  q2924651
NCBI GI
BLAST score
                   46
E value
                  1.0e-16
Match length
                  187
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2A18, complete sequence [Arabidopsis thaliana]
                  120171
Seq. No.
Contig ID
                   4513 1.R1010
                  LIB24-008-Q1-E1-H8
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4589414
BLAST score
                  294
E value
                  1.0e-164
Match length
                   413
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                  K14B15, complete sequence
Seq. No.
                  120172
                  4514 1.R1010
Contig ID
                  LIB22-005-Q1-E1-C12
5'-most EST
```

Contig ID

5'-most EST

```
g2388570
NCBI GI
BLAST score
                  421
                  2.0e-41
E value
Match length
                  130
                  71
%: identity
                  (AC000098) YUP8H12.12 [Arabidopsis thaliana]
NCBI Description
                  120173
Seq. No.
                  4517 1.R1010
Contig ID
                  LIB24-079-Q1-E1-C9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2497539
BLAST score
                  511
                  2.0e-56
E value
Match length
                  200
                  59
% identity
                  PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703
NCBI Description
                  (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]
                  120174
Seq. No.
Contig ID
                  4524_1.R1010
5'-most EST
                  LIB22-005-Q1-E1-D12
Method
                  BLASTN
                  q2623294
NCBI GI
                  398
BLAST score
                  0.0e + 00
E value
                   414
Match length
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC T20B5 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                   120175
Seq. No.
                   4526 1.R1010
Contig ID
                   jC-atXLIB327439P1c12b2
5'-most EST
                  BLASTN
Method
NCBI GI
                   q4587641
BLAST score
                   615
                   0.0e + 00
E value
Match length
                   623
                   100
% identity
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   120176
                   4527 1.R1010
Contig ID
5'-most EST
                  LIB3168-086-P1-K1-C4
Method
                  BLASTX
NCBI GI
                   q2894599
BLAST score
                   532
E value
                   5.0e-54
Match length
                   163
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   120177
Seq. No.
```

4527 2.R1010

g1216543

```
Method
                   BLASTN
                   q4757678
NCBI GI
                   342
BLAST score
                   0.0e + 00
E value
                   448
Match length
% identity
                   95
                   Arabidopsis thaliana chromosome I BAC F9H16 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   120178
Contig ID
                   4528 1.R1010
                   LIB25-021-Q1-E1-F5
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4033431
BLAST score
                   478
E value
                   4.0e-48
Match length
                   102
                   93
% identity
                   PROBABLE PYRUVATE KINASE, CYTOSOLIC ISOZYME (PK) >gi_2982467_emb_CAA18231_ (AL022223) pyruvate kinase like
NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   120179
                   4532_1.R1010
Contig ID
                   jC-atXLIB327413P1c09b1
5'-most EST
Method
                   BLASTN
                   g4159704
NCBI GI
BLAST score
                   423
                   0.0e + 00
E value
                   423
Match length
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MCB17, complete sequence
                   120180
Seq. No.
Contig ID
                   4532 2.R1010
                   g1159397
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4159704
BLAST score
                   521
E value
                   0.0e + 00
Match length
                   533
                   99
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MCB17, complete sequence
                   120181
Seq. No.
Contig ID
                   4534 1.R1010
5'-most EST
                   LIB23-037-Q1-E1-D3
Method
                   BLASTX
NCBI GI
                   q2914706
BLAST score
                   353
E value
                   2.0e-33
Match length
                   93
% identity
                   66
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]
```

BLAST score

184

```
120182
Seq. No.
                  4539 1.R1010
Contig ID
                  LIB22-005-Q1-E1-E7
5'-most EST
                   120183
Seq. No.
Contig ID
                   4540 1.R1010
                  jC-a\overline{t}XLIB327407P1f01b2
5'-most EST
Method
                  BLASTX
                   g4835247
NCBI GI
BLAST score
                   742
E value
                  2.0e-78
Match length
                  176
% identity
                   81
                  (ALO49862) putative tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                  120184
Seq. No.
Contig ID
                   4541 1.R1010
                  LIB3176-054-P1-K1-G3
5'-most EST
Method
                  BLASTX
NCBI GI
                   g1931640
BLAST score
                   382
                   1.0e-36
E value
Match length
                   144
% identity
                   53
                  (U95973) Serine carboxypeptidase isolog [Arabidopsis
NCBI Description
                  thaliana]
                  120185
Seq. No.
Contig ID
                   4542 1.R1010
5'-most EST
                  LIB22-005-Q1-E1-F1
                  BLASTX
Method
                  g1363484
NCBI GI
BLAST score
                   479
E value
                   7.0e-48
                   116
Match length
% identity
                   84
NCBI Description
                  IAA13 protein - Arabidopsis thaliana >gi_972929 (U18415)
                   IAA13 [Arabidopsis thaliana] >gi 2459414 (AC002332) auxin
                   inducible protein, IAA13 [Arabidopsis thaliana]
                   120186
Seq. No.
                   4546 1.R1010
Contig ID
5'-most EST
                  LIB22-005-Q1-E1-F2
Method
                  BLASTX
NCBI GI
                  g2921445
BLAST score
                   149
                   3.0e-09
E value
                   115
Match length
                   38
% identity
                  (AF037257) ES2 protein [Drosophila melanogaster]
NCBI Description
                  120187
Seq. No.
Contig ID
                   4549 1.R1010
5'-most EST
                  LIB3176-065-P1-K1-H2
Method
                  BLASTX
                  g4335737
NCBI GI
```

```
E value
                   3.0e-13
Match length
                   130
% identity
                   25
                   (AC006248) putative serine/threonine kinase [Arabidopsis
NCBI Description
                   thaliana]
                   120188
Seq. No.
                   4549 2.R1010
Contig ID
5'-most EST
                   g1159312
Method
                   BLASTX
NCBI GI
                   q4567208
BLAST score
                   314
                   2.0e-28
E value
Match length
                   112
% identity
                   58
NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]
Seq. No.
                   120189
                   4551 1.R1010
Contig ID
5'-most EST
                   q315473
Method
                   BLASTN
NCBI GI
                   q3128142
BLAST score
                   211
E value
                   1.0e-115
Match length
                   438
% identity
                   99
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MQN23, complete sequence [Arabidopsis thaliana]
Seq. No.
                   120190
                   4552 1.R1010
Contig ID
5'-most EST
                   LIB3175-075-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g3287691
BLAST score
                   475
                   3.0e-47
E value
Match length
                   180 -
% identity
                   58
                   (AC003979) Contains similarity to RING zinc finger protein
NCBI Description
                   gb X95455 from Gallus gallus. [Arabidopsis thaliana]
                   120191
Seq. No.
                   4553 1.R1010
Contig ID
5'-most EST
                   jC-a\(\bar{1}\)XLIB327436P2c11b1
Method
                   BLASTX
                   g114421
NCBI GI
BLAST score
                   1531
E value
                   0.0e + 00
Match length
                   515
% identity
                   85
                   ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_82133_pir__A24355 H+-transporting ATP synthase (EC
3.6.1.34) beta-1 chain, mitochondrial - curled-leaved
                   tobacco >gi 19685 emb CAA26620 (X02868) ATP synthase beta
                   subunit [Nicotiana plumbaginifolia]
```

Seq. No.

```
Contig ID
                   4553 2.R1010
                   jC-atXLIB327407P4h03b1
5'-most EST
                   BLASTX
Method
                   q3893822
NCBI GI
BLAST score
                   662
E value
                   3.0e-69
                   136
Match length
                   94
% identity
NCBI Description
                   (U96498) ATPase beta subunit [Nicotiana sylvestris]
Seq. No.
                   120193
                   4553 3.R1010
Contig ID
5'-most EST
                   LIB22-010-Q1-E1-A8
                   BLASTX
Method
NCBI GI
                   q231586
BLAST score
                   319
E value
                   3.0e-29
Match length
                   169
                   48
% identity
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_82027_pir__S20504 H+-transporting ATP synthase (EC
                   3.6\overline{.}1.34) beta chain, mitochondrial - Para rubber tree
                   >gi 18831 emb CAA41401_ (X58498) mitochondrial ATP synthase
                   beta-subunit [Hevea brasiliensis]
                   120194
Seq. No.
Contig ID
                   4553 4.R1010
5'-most EST
                   jC-atXLIB327428P4c06a2
                   BLASTX
Method
NCBI GI
                   q114421
BLAST score
                   175
E value
                   3.0e-12
Match length
                   35
                   94
% identity
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi 82133 pir__A24355 H+-transporting ATP synthase (EC
                   3.6.1.34) beta-1 chain, mitochondrial - curled-leaved
                   tobacco >gi 19685 emb CAA26620 (X02868) ATP synthase beta
                   subunit [Nicotiana plumbaginifolia]
Seq. No.
                   120195
Contig ID
                   4553 6.R1010
5'-most EST
                   jC-atX35039Q1E1E02a1
Method
                   BLASTX
NCBI GI
                   g2116558
BLAST score
                   253
E value
                   1.0e-21
Match length
                   60
% identity
                   83
                  (AB003549) F1 ATPase [Pisum sativum]
NCBI Description
                   120196
Seq. No.
                   4557 1.R1010
Contig ID
                   jC-a1XLIB327436P4b06b1
5'-most EST
                  BLASTN
Method
                  g2582640
NCBI GI
```

BLAST score

```
E value
                   1:0e-21
                   59
Match length
                   98
% identity
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   120197
Seq. No.
                   4557 2.R1010
Contig ID
                   LIB24-096-Q1-E1-G7
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4586107
                   745
BLAST score
                   5.0e-79
E value
                   286
Match length
% identity
                   38
                   (ALO49638) putative disease resistance protein [Arabidopsis
NCBI Description
                   thaliana]
                   120198
Seq. No.
                   4560 1.R1010
Contig ID
5'-most EST
                   LIB25-113-Q1-E1-D11
Method
                   BLASTX
NCBI GI
                   g2832674
BLAST score
                   1352
                   1.0e-150
E value
Match length
                   310
% identity
                   89
                   (AL021712) fibrillin precursor-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   120199
Seq. No.
Contig ID
                   4560 2.R1010
                   jC-atXLIB327420P4e06b1
5'-most EST
Method
                   BLASTX
                   g3377825
NCBI GI
                   745
BLAST score
                   3.0e-79
E value
Match length
                   148
                   99
% identity
                   (AF075598) contains similarity to fibrillins [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   120200
                   4561 1.R1010
Contig ID
                   g3450514
5'-most EST
Method
                   BLASTX
                   q3834312
NCBI GI
BLAST score
                   762
E value
                   5.0e-81
                   156
Match length
                   90
% identity
                   (AC005679) Strong similarity to glycoprotein EP1 gb_L16983
NCBI Description
                   Daucus carota and a member of S locus glycoprotein family
                   PF_00954. ESTs gb_AA067487, gb_Z35737, gb_Z30815, gb_Z35350, gb_AA713171, gb_AI100553, gb_Z34248,
```

gb AA728536, gb Z30816 an

NCBI GI

```
Seq. No.
                  120201
                  4561 2.R1010
Contig ID
                  jC-atXLIB327408P3c11a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3834328
BLAST score
                  688
E value
                  2.0e-72
Match length
                  142
% identity
                  89
NCBI Description
                  (AC005679) Strong similarity to glycoprotein EP1 gb L16983
                  Daucus carota and a member of S locus glycoprotein family
                  PF 00954. [Arabidopsis thaliana]
                  120202
Seq. No.
                  4562 1.R1010
Contia ID
5'-most EST
                  jC-atXLIB327433P1c05b1
Method
                  BLASTN
NCBI GI
                  q3702439
BLAST score
                  62
E value
                  4.0e-26
Match length
                  289
% identity
                  86
NCBI Description
                  Human DNA sequence from clone 415G2 on chromosome 22
                  Contains synapsin IIIa exon 1, EST and GSS, complete
                  sequence [Homo sapiens]
                  120203
Seq. No.
                  4564 1.R1010
Contig ID
5'-most EST
                  LIB3176-039-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q2558654
BLAST score
                  848
E value
                  2.0e-91
Match length
                  166
% identity
                  57
NCBI Description
                  (AC002354) No definition line found [Arabidopsis thaliana]
Seq. No.
                  120204
                  4566 1.R1010
Contig ID
5'-most EST
                  jC-atXP63C2O3J14T7s2
                  120205
Seq. No.
Contig ID
                  4567 1.R1010
5'-most EST
                  jC-atXLIB327439P2e07b2
Method
                  BLASTX
NCBI GI
                  g2244752
BLAST score
                  495
E value
                  5.0e-50
Match length
                  142
% identity
                  69
NCBI Description
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
                  120206
Seq. No.
Contig ID
                  4569 1.R1010
                  jC-atXLIB327439P2e04b2
5'-most EST
                  BLASTN
Method
```

g2582640

5'-most EST

g1159087

```
BLAST score
                   57
                   3.0e-23
E value
Match length
                  73 🚎 🛴
                   96
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   120207
Seq. No.
                   4570 1.R1010
Contig ID
5'-most EST
                   LIB2\overline{2}-005-Q1-E1-H4
Method
                  BLASTN
                  g4757399
NCBI GI
                   320
BLAST score
                   1.0e-180
E value
Match length
                   324
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MEE13, complete sequence
                  120208
Seq. No.
                   4573_1.R1010
Contig ID
5'-most EST
                  ARABL1-038-Q1-B1-B11
Method
                  BLASTN
NCBI GI
                  g3355463
BLAST score
                   269
E value
                   1.0e-149
Match length
                   493
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F12L6 genomic
                  sequence; complete sequence [Arabidopsis thaliana]
                  120209
Seq. No.
Contig ID
                   4573_2.R1010
                  LIB3175-027-P1-K1-E3
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3355463
                   223
BLAST score
E value
                   1.0e-122
Match length
                   530
% identity
                   99
                  Arabidopsis thaliana chromosome II BAC F12L6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   120210
                   4578_1.R1010
Contig ID
                  jC-aTXP39C161G19T7d1
5'-most EST
Method
                   BLASTX
NCBI GI
                  g1934756
BLAST score
                   1481
E value
                   1.0e-169
                   326
Match length
% identity
                  89
                  (Y12459) cytosolic glutamine synthetase [Brassica napus]
NCBI Description
Seq. No.
                  120211
                  4578 2.R1010
Contig ID
```

```
₹, •
Method
                  BLASTX
NCBI GI
                  q228455
BLAST score
                  865
                  4.0e-93
E value
                  162
Match length
% identity
                  100
NCBI Description Gln synthetase [Arabidopsis thaliana]
                  120212
Seq. No.
                  4578 3.R1010
Contig ID
5'-most EST
                  jC-alXLIB327435P2a05a1
Method
                  BLASTX
NCBI GI
                  q1084350
BLAST score
                   714
E value
                   1.0e-75
Match length
                   143
% identity
                   91
                  glutamate--ammonia ligase (EC 6.3.1.2) - rape
NCBI Description
                  >gi 599656 emb CAA58118.1_ (X82997) glutamate--ammonia
                  ligase [Brassica napus]
Seq. No.
                   120213
                   4578 4.R1010
Contig ID
5'-most EST
                   jC-atXLIB327420P1e04a1
                  BLASTX
Method
NCBI GI
                  q228454
BLAST score
                  889
E value
                   6.0e-96
Match length
                   167
                   99
% identity
                  Gln synthetase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120214
                   4578 5.R1010
Contig ID
5'-most EST
                   q957650
Method
                  BLASTX
NCBI GI
                   q481914
BLAST score
                   561
E value
                   1.0e-57
Match length
                   129
                   82
% identity
                  glutamate--ammonia ligase (EC 6.3.1.2) - rape
NCBI Description
                   >gi 436422 emb CAA54151.1 (X76736) glutamine [Brassica
                   napus]
                   120215
Seq. No.
Contig ID
                   4578 6.R1010
                   jC-atXP4C88D20T7059a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q228454
BLAST score
                   295
                   5.0e-47
E value
                   107
Match length
% identity
                   91
NCBI Description Gln synthetase [Arabidopsis thaliana]
```

Seq. No.

Method

BLASTN

```
Contig ID
                   4580 1.R1010
                   jC-atXP108C157L12T7043d1
5'-most EST
Method
                   BLASTX
                   q3834309
NCBI GI
                   1515
BLAST score
E value
                   1.0e-169
                   281
Match length
% identity
                   (AC005679) Strong similarity to glycoprotein EP1 gb_L16983
NCBI Description
                  Daucus carota and a member of S locus glycoprotein \overline{f}amily
                   PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and
                   gb W43262 come from this gene. [Arabidopsis thaliana]
                   120217
Seq. No.
                   4580 2.R1010
Contiq ID
5'-most EST
                  jC-atXLIB327409P1h01b1
Method
                   BLASTX
                  q3834309
NCBI GI
                   1132
BLAST score
                   1.0e-124
E value
                   225
Match length
% identity
                   96
NCBI Description
                   (AC005679) Strong similarity to glycoprotein EP1 gb_L16983
                   Daucus carota and a member of S locus glycoprotein family
                   PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and
                  gb W43262 come from this gene. [Arabidopsis thaliana]
                  120218
Seq. No.
                   4580 3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327439P1b04b2
                  BLASTX
Method
NCBI GI
                  q3834309
BLAST score
                   646
                   2.0e-67
E value
Match length
                   176
% identity
                   (AC005679) Strong similarity to glycoprotein EP1 gb_L16983
NCBI Description
                   Daucus carota and a member of S locus glycoprotein family
                   PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and
                   gb W43262 come from this gene. [Arabidopsis thaliana]
                   120219
Seq. No.
Contig ID
                   4584 1.R1010
5'-most EST
                  jC-atXLIB327439P2b04b2
Method
                  BLASTX
NCBI GI
                  q3885328
BLAST score
                   335
E value
                   3.0e - 31
Match length
                   87
% identity
                  75
NCBI Description
                   (AC005623) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   120220
                   4587 1.R1010
Contig ID
                  g936<del>3</del>51
5'-most EST
```

Seq. No.

120225

```
NCBI GI
                  q4159709
BLAST score
                  306
E value
                  1.0e-171
                  705
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLN21, complete sequence
                  120221
Seq. No.
                  4590 1.R1010
Contig ID
5'-most EST
                  jC-atXP89C244P22T7083d1
                  BLASTX
Method
                  g2281629
NCBI GI
BLAST score
                  766
                  2.0e-81
E value
                  143
Match length
% identity
                  100
NCBI Description
                  (AF003095) AP2 domain containing protein RAP2.2
                  [Arabidopsis thaliana]
                  120222
Seq. No.
                  4590 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P4b06b1
Method
                  BLASTX
NCBI GI
                  g2281629
BLAST score
                  899
E value
                  7.0e-97
Match length
                  214
% identity
                  80
NCBI Description
                  (AF003095) AP2 domain containing protein RAP2.2
                  [Arabidopsis thaliana]
                  120223
Seq. No.
                  4590 3.R1010
Contig ID
5'-most EST
                  LIB3234-022-P1-K1-H9
Method
                  BLASTN
NCBI GI " '
                  g4159709
BLAST score
                  336
E value
                  0.0e+00
Match length
                  376
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MLN21, complete sequence
Seq. No.
                  120224
Contig ID
                  4592 1.R1010
5'-most EST
                  g937699
Method
                  BLASTN
NCBI GI
                  g4490717
BLAST score
                  188
E value
                  1.0e-101
Match length
                  515
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
                  project)
```

```
Contig ID
                   4593 1.R1010
                  LIB22-006-Q1-E1-B7
5'-most EST
                   BLASTN
Method
                   q4589418
NCBI GI
                   715
BLAST score
E value
                   0.0e + 00
                   842
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21G20, complete sequence
Seq. No.
                   120226
Contig ID
                   4597 1.R1010
5'-most EST
                   jC-atXLIB327432P3b04b1
                   BLASTX
Method
NCBI GI
                   g2160156
BLAST score
                   413
                   2.0e-40
E value
                   95
Match length
                   83
% identity
                   (AC000132) Strong similarity to S. pombe leucyl-tRNA
NCBI Description
                   synthetase (gb Z73100). [Arabidopsis thaliana]
Seq. No.
                   120227
                   4599 1.R1010
Contig ID
                   jC-atx22006Q1E1C04b1 ·
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4325346
                   851
BLAST score
                   1.0e-91
E value
                   184
Match length
                   92
% identity
NCBI Description
                   (AF128393) similar to N-ethylmaleimide sensitive fusion
                   proteins; contains similarity to ATPases (Pfam: PF00004,
                   Score=307.7, E=1.4e-88n N=1) [Arabidopsis thaliana]
                   120228
Seq. No.
                   4600 1.R1010
Contig ID
5'-most EST
                   jC-atXP89CG6E1T7054d1
                   BLASTN
Method
NCBI GI
                   q4753195
BLAST score
                   51
                   2.0e-19
E value
Match length
                   196
                  89
% identity
                  Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5
NCBI Description
                  cM, complete sequence
Seq. No.
                   120229
Contig ID
                   4600 2.R1010
5'-most EST
                  LIB3176-018-P1-K1-H1
Method
                  BLASTN
NCBI GI
                   g4753195
BLAST score
                   51
E value
                  1.0e-19
Match length
                   122
% identity
                   92
```

```
NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5
                  cM, complete sequence
                  120230
Seq. No.
                  4603 1.R1010
Contig ID
5'-most EST
                  jC-atXP114C229O11T7s1
Method
                  BLASTX
                  g1170555
NCBI GI
BLAST score
                  237
E value
                  4.0e-21
Match length
                  158
% identity
                  44
                  MYO-INOSITOL 4-O-METHYLTRANSFERASE >gi_282822_pir__$22696
NCBI Description
                  methyltransferase - common ice plant >gi_167262 (M87340)
                  myo-inositol O-methyl transferase [Mesembryanthemum
                  crystallinum] >gi 1488237 (U63634) inositol
                  methyltransferase [Mesembryanthemum crystallinum]
                  120231
Seq. No.
                  4603_2.R1010
Contig ID
5'-most EST
                  g2047392
                  BLASTX
Method
NCBI GI
                  g4104224 .
BLAST score
                  47
E value
                  2.0e-12
Match length
                  103
% identity
                  46
                  (AF033540) caffeic acid O-methyltransferase; LPOMT3 [Lolium
NCBI Description
                  perenne]
                  120232
Seq. No.
                  4604 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327417P3f08b1
Method
                  BLASTX
NCBI GI
                  g4512683
BLAST score
                  1301
E value
                  1.0e-144
Match length
                  255
                  99
% identity
NCBI Description
                  (AC006931) putative lipase [Arabidopsis thaliana]
                  >gi 4559323 gb AAD22985.1 AC007087 4 (AC007087) putative
                  lipase [Arabidopsis thaliana]
                  120233
Seq. No.
                  4606_1.R1010
Contig ID
                  g2597489
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4559380
BLAST score
                  662
E value
                  1.0e-69
Match length
                  129
% identity
                  100
                  (AC006526) putative auxin-responsive GH3 protein
NCBI Description
                  [Arabidopsis thaliana]
                  120234
Seq. No.
```

4607_1.R1010

Contig ID

E value

1.0e-97

```
5'-most EST
                   jC-atX22011Q1K1D03b1
                   BLASTX
Method
 NCBI GI
                   a2827555
 BLAST score
                   506
                   3.0e-51
 E value
 Match length
                   102
                   61
 % identity
                   (ALO21635) Translation factor EF-1 alpha - like protein
 NCBI Description
                   [Arabidopsis thaliana]
 Seq. No.
                   120235
 Contig ID
                   4609 1.R1010
 5'-most EST
                   LIB3177-081-P1-K1-G8
                   BLASTX
 Method
 NCBI GI
                   q4558661
 BLAST score
                   559
 E value
                   2.0e-57
                   176
 Match length
 % identity
                   71
                   (AC007063) putative malate oxidoreductase (NAD)
 NCBI Description
                   [Arabidopsis thaliana]
                  , 120236
 Seq. No.
                   4612 1.R1010
 Contig ID
 5'-most EST
                   LIB22-006-Q1-E1-D3
                   120237
 Seq. No.
 Contig ID
                   4614 1.R1010
                   LIB3176-069-P1-K1-A2
 5'-most EST
                   BLASTN
Method
 NCBI GI
                   q2832689
 BLAST score
                   328
 E value
                   0.0e + 00
                   449
Match length
 % identity
                   43
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21
                   (ESSAII project)
                   120238
 Seq. No.
                   4614_3.R1010
 Contig ID
 5'-most EST
                   LIB22-054-Q1-E2-F12
 Method
                   BLASTN
 NCBI GI
                   g2832689
 BLAST score
                   249
 E value
                   1.0e-138
 Match length
                   390
                   45
 % identity
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21
                   (ESSAII project)
                   120239
 Seq. No.
 Contig ID
                   4615 1.R1010
                   jC-atXP115C248F7T7059d1
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   g3107931
 BLAST score
                   905
```

Contig ID

```
Match length
                  201
% identity
                   (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]
NCBI Description
                  120240
Seq. No.
                  4615 2.R1010 ·
Contig ID
                  LIB3168-023-P1-K1-H12
5'-most EST
                  BLASTX
Method
                  g2117937
NCBI GI
BLAST score
                  1219
E value
                  1.0e-134
Match length
                  315
% identity
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                  barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
                  120241
Seq. No.
                  4615 4.R1010
Contig ID
5'-most EST
                  q2048468
                  BLASTX
Method
NCBI GI
                  q136739
BLAST: score
                  143
                  1.0e-08
E value
Match length
                  81
% identity
                  64
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                  PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                  120242
                  4616 1.R1010
Contig ID
                  jC-atXP87CG10F2T7b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2924652
BLAST score
                  438
E value
                  0.0e + 00
                  449
Match length
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9L2, complete sequence [Arabidopsis thaliana]
                  120243
Seq. No.
                  4617 1.R1010
Contig ID
                  jC-atXLIB327413P4h06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2723496
BLAST score
                  225
E value
                  7.0e-18
Match length
                  245
                  27
% identity
                  (AB009972) beta-1,4-xylosidase [Aspergillus oryzae]
NCBI Description
                  120244
Seq. No.
```

4617 2.R1010

5'-most EST

```
5'-most EST
                  iC-atXLIB327429Pla04b2
Method
                  BLASTX
                  q2181180
NCBI GI
BLAST score
                  226
E value
                  5.0e-21
Match length
                  229
% identity
                  30
                  (284377) xylosidase [Aspergillus niger]
NCBI Description
Seq. No.
                  120245
                  4617 3.R1010
Contig ID
                  jC-atXLIB327437P2c06b2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2181180
BLAST score
                  481
E value
                  7.0e-48
Match length
                  348
% identity
                  34
NCBI Description
                  (Z84377) xylosidase [Aspergillus niger]
Seq. No.
                  120246
Contig ID
                  4617 4.R1010
                  LIB25-051-Q1-E1-C5
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4235093
BLAST score
                  387
E value
                  6.0e-37
Match length
                  196
% identity
                  41
NCBI Description (AF108944) beta-xylosidase [Aspergillus niger]
Seq. No.
                  120247
                  4617 6.R1010
Contig ID
                  LIB35-046-Q1-E1-H10
5'-most EST
                  BLASTX
Method
NCBI GI .
                  g2181180
BLAST score
                  366
E value
                  8.0e-35
Match length
                  156
% identity
                  45
                  (Z84377) xylosidase [Aspergillus niger]
NCBI Description
Seq. No.
                  120248
Contig ID
                  4618 1.R1010
                  LIB24-051-Q1-E1-D7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4582468
BLAST score
                  664
E value
                  1.0e-69
                  169
Match length
% identity
                  83
                  (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                  C-terminal domain [Arabidopsis thaliana]
                  120249
Seq. No.
Contig ID
                  4618 2.R1010
```

jC-atXLIB327440P1g12a1

```
Method
                  BLASTX
NCBI GI
                  q4582468
BLAST score
                  1113
E value
                  1.0e-122
Match length
                  248
% identity
                  90
                  (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                  C-terminal domain [Arabidopsis thaliana]
Seq. No.
                  120250
                  4619 1.R1010
Contig ID
                  LIB25-063-Q1-E1-G6
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2864615
BLAST score
                  383
E value
                  6.0e-37
Match length
                  83
                  95
% identity
NCBI Description
                  (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                  120251
                  4621_1.R1010
Contig ID
5'-most EST
                  LIB25-014-Q1-E1-A5
Method
                  BLASTN
NCBI GI
                  q3869064
BLAST score
                  196
E value
                  1.0e-106
Match length
                  372
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K1013, complete sequence [Arabidopsis thaliana]
                  120252
Seq. No.
Contig ID
                  4622 1.R1010
5'-most EST
                  jC-atX22006Q1E1E05b1
Method
                  BLASTN
NCBI GI
                  g2618683
BLAST score
                  274
E value
                  1.0e-152
Match length
                  411
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC T32G6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  120253
Seq. No.
                  4623 1.R1010
Contig ID
5'-most EST
                  LIB3176-071-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q3319355
BLAST score
                  1012
E value
                  1.0e-110
                  215
Match length
% identity
                  99
                  (AF077407) similar to chaperonin containing TCP-1 complex
NCBI Description
                  gamma chain [Arabidopsis thaliana]
```

Seq. No.

NCBI GI

q510876

```
Contig ID
                   4624 1.R1010
                   jC-atXP37C158A5T7d2
5'-most EST
                  BLASTN
Method
                  g531828
NCBI GI
                   55
BLAST score
E value
                   9.0e-22
                   97
Match length
                  96
% identity
NCBI Description Cloning vector pSport1, complete cds
                   120255
Seq. No.
Contig ID
                   4627 1.R1010
                   jC-alXLIB327435P4a11b1
5'-most EST
                  BLASTX
Method
                  a2708745
NCBI GI
                   449
BLAST score
E value
                   2.0e-44
                  153
Match length
                   60
% identity
                   (AC003952) putative calcium-dependent ser/thr protein
NCBI Description
                  kinase [Arabidopsis thaliana]
Seq. No.
                  120256
                  4628_1.R1010
Contig ID
                  LIB22-006-Q1-E1-E7
5'-most EST
                  120257
Seq. No.
Contig ID
                  4629 1.R1010
                  LIB3234-058-P1-K1-E1
5'-most EST
                   120258
Seq. No.
                   4630 1.R1010
Contig ID
5'-most EST
                  LIB22-071-Q1-E1-B6
                   BLASTX
Method
NCBI GI
                   q4581139
BLAST score
                   731
                  1.0e-77
E value
                  159
Match length
% identity
                   57 .
NCBI Description (AC006919) putative ABC transporter [Arabidopsis thaliana]
                   120259
Seq. No.
                   4635 1.R1010
Contig ID
5'-most EST
                  LIB3176-099-P1-K1-F10
                  BLASTX
Method
                   q4239891
NCBI GI
BLAST score :
                   1930
E value
                  0.0e + 00
                   441
Match length
% identity
                  83
NCBI Description
                  (AB016804) NADP-malic enzyme [Aloe arborescens]
                   120260
Seq. No.
                   4635 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P1h08b1
Method
                  BLASTX
```

```
BLAST score
                   113
 E value
                   2.0e-33
 Match length
                   152
 % identity
                   62
                   (X80051) NADP dependent malic enzyme [Phaseolus vulgaris]
 NCBI Description
                   120261
 Seq. No.
                   4635_4.R1010
 Contig ID
                   jC-atXP114C231J18T7d1
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   g510876
 BLAST score
                   956
 E value
                   1.0e-103
 Match length
                   226
 % identity
                   82
 NCBI Description (X80051) NADP dependent malic enzyme [Phaseolus vulgaris]
                   120262
 Seq. No.
                   4635 5.R1010
 Contig ID
 5'-most EST
                   g1269528
                   BLASTX
 Method
                   g1561774
 NCBI GI
 BLAST score
                   543
 E value
                   1.0e-55
Match length
                   157
 % identity
                   69
 NCBI Description (U67426) malate dehydrogenase [Vitis vinifera]
                   120263
 Seq. No.
                   4636 1.R1010
 Contig ID
 5'-most EST
                   LIB22-006-Q1-E1-F3
                   BLASTX
Method
 NCBI GI
                   g2104535
 BLAST score
                   445
                   3.0e-44
 E value
 Match length
                   118
 % identity
                   75
 NCBI Description (AF001308) T10M13.13 [Arabidopsis thaliana]
 Seq. No.
                   120264
                   4640 1.R1010
 Contig ID
                   LIB22-006-Q1-E1-F7
 5'-most EST
                   120265
 Seq. No.
 Contig ID
                   4641_1.R1010
5'-most EST
                   jC-atXLIB327439P2d10b2
                   120266
 Seq. No.
 Contig ID
                   4642_1.R1010
                   jC-atXLIB327439P2d11b2
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   q136739
 BLAST score
                   403
                   4.0e-39
 E value
 Match length
                   129
 % identity
                   64
                   UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
 NCBI Description
```

```
PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU
                   UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                   potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose
                   pyrophosphorylase precursor [Solanum tuberosum]
                   120267
Seq. No.
                   4644 1.R1010
Contig ID
                   jC-atXLIB327430P2h09b1
 5'-most EST
Method
                   BLASTN
                   q4589430
NCBI GI
                   132
BLAST score
                   1.0e-67
E value
                   649
Match length
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MLD14, complete sequence
                   120268
Seq. No.
                   4646 1.R1010
 Contig ID
 5'-most EST
                   LIB22-006-Q1-E1-G12
Method
                   BLASTX
NCBI GI
                   q4468979
                   406
BLAST score
                   1.0e-39
E value
Match length
                   86
% identity
                   87
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]
                   120269
Seq. No.
                   4648 1.R1010
Contig ID
 5'-most EST
                   jC-atX24061Q1E1C06b1
Method
                   BLASTX
                   q3668069
NCBI GI
BLAST score
                   359
                   4.0e-34
E value
Match length
                   111
                   62
 % identity
NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
                   120270
 Seq. No.
                   4649 1.R1010
Contig ID
 5'-most EST
                   jC-atXLIB327418P4f05b1
Method
                   BLASTX
                   g4220533
NCBI GI
BLAST score
                   589
                   9.0e-61
E value
                   132
Match length
                   93
 % identity
                   (AL035356) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
                   120271
Seq. No.
                   4649 2.R1010
 Contig ID
 5'-most EST
                   jC-atXLIB327431P4a02a1
                   BLASTX
Method
                   g4220533
NCBI GI
```

BLAST score

% identity

71

```
E value
                  1.0e-155
Match length
                  313
% identity
                  89
                   (AL035356) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  120272
                  4650 1.R1010
Contig ID
                  LIB22-006-Q1-E1-G5
5'-most EST
                  120273
Seq. No.
                  4652 1.R1010
Contig ID
                  LIB2\overline{2}-039-Q1-E1-D8
5'-most EST
                  BLASTX
Method
                  g2829871
NCBI GI
BLAST score
                  232
E value
                  3.0e-19
Match length
                  85
% identity
                  58
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  120274
                  4653 1.R1010
Contig ID
                  jC-atXLIB327439P3d08b2
5'-most EST
                  120275
Seq. No.
                  4654 1.R1010
Contig ID
                  LIB3168-051-P1-K1-B10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3367573
BLAST score
                  546
E value
                  3.0e-56
Match length
                  110
% identity
                  95
                  (AL031135) homeodomain - like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  120276
                  4655 1.R1010
Contig ID
                  jC-atX22080Q1E1A08b1
5'-most EST
Method
                  BLASTN
                  g1050427
NCBI GI
BLAST score
                  505
                  0.0e+00
E value
Match length
                  505
% identity
                  100
NCBI Description A.thaliana mRNA for an exon from SNAP25A protein
Seq. No.
                  120277
                  4656 1.R1010
Contig ID
5'-most EST
                  LIB3176-104-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2880051
BLAST score
                  348
E value
                  9.0e-33
Match length
                  101
```

```
NCBI Description (AC002340) putative protein kinase [Arabidopsis thaliana]
                  120278
Seq. No.
                  4656 4.R1010
Contig ID
5'-most EST
                  LIB24-053-Q1-E2-A12
Method
                  BLASTN
                  q2880038
NCBI GI
BLAST score
                  45
E value
                  4.0e-16
Match length
                  149
% identity
                  87
                  Arabidopsis thaliana chromosome II BAC T11J7 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  120279
Seq. No.
                  4657 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327412P2b01b1
Method
                  BLASTN
NCBI GI
                  g3869074
BLAST score
                  775
E value
                  0.0e + 00
Match length
                  807
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MMI9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120280
Contig ID
                  4658 1.R1010
5'-most EST
                  jC-atXLIB327439P1e04b2
Seq. No.
                  120281
Contig ID
                  4661_1.R1010
5'-most EST
                  LIB22-006-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  q2829871
BLAST score
                  1158
E value
                  1.0e-127
Match length
                  229
% identity
                  97
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  120282
Contig ID
                  4662 1.R1010
5'-most EST
                  jC-atXLIB327409P2f10b1
                  120283
Seq. No.
Contig ID
                  4662 2.R1010
5'-most EST
                  jC-atXLIB327440P1c04b1
Method
                  BLASTN
NCBI GI
                  q1245938
BLAST score
                  36
E value
                  2.0e-10
Match length
                  36
% identity
                  62
NCBI Description
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
```

heart atrium, mRNA, 2998 nt]

Match length

249

```
120284
Seq. No.
                  4662_3.R1010
Contig ID
                  jC-atX22014Q1E1G02a1
5'-most EST
                  120285
Seq. No.
                  4669_1.R1010
Contig ID
                  jC-atXLIB327431P1a06b1
5'-most EST
                  BLASTN
Method
                  g4510323
NCBI GI
BLAST score
                  295
E value
                  1.0e-165
Match length
                  468
                  100
% identity
NCBI Description
                  Arabidopsis thaliana BAC T7B11 from chromosome IV near 10
                  cM, complete sequence
Seq. No.
                  120286
                  4675 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327428P1a05b2
Method
                  BLASTX
NCBI GI
                  g1518540
BLAST score
                  1763
E value
                  0.0e+00
Match length
                  477
% identity
                  91
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
                  120287
Seq. No.
Contig ID
                  4675 3.R1010
                  jC-atXP125C159B10T7d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1518540
BLAST score
                  773
                  2.0e-82
E value
Match length
                  160
% identity
                  88
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
Seq. No.
                  120288
                  4675 4.R1010
Contig ID ·
                  LIB3176-063-P1-K1-F7
5'-most EST
Method
                  BLASTX
                  g1518540
NCBI GI
BLAST score
                  643
                  4.0e-67
E value
Match length
                  137
% identity
                  93
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                  120289
                  4675_5.R1010
Contig ID
                  LIB3177-025-P1-K2-A3
5'-most EST
                  BLASTX
Method
                  q1518540
NCBI GI
                                                                ٠.
BLAST score
                  494
                  1.0e-100
E value
```

```
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                  120290
Seq. No.
Contig ID
                  4676 1.R1010
5'-most EST
                  LIB23-069-Q1-E1-H9
Method
                  BLASTX
                  g4455192
NCBI GI
                  1544
BLAST score
E value
                  1.0e-172
Match length
                  313
% identity
                  96
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  120291
Seq. No.
Contig ID
                  4677 1.R1010
                  jC-atXLIB327439P2f05b2
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4185120
BLAST score
                  410
                  0.0e+00
E value
Match length
                  454
% identity
                  97
                  Arabidopsis thaliana chromosome 1 BAC F5F19 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  120292
Seq. No.
Contig ID
                  4679_1.R1010
                  LIB35-015-Q1-E1-D6
5'-most EST
Method
                  BLASTN
                  g4589435
NCBI GI
BLAST score
                  334
E value
                  0.0e+00
Match length
                  386
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MOE17, complete sequence
                  120293
Seq. No.
                  4680 1.R1010
Contig ID
5'-most EST
                  LIB22-007-Q1-E1-B5
Seq. No.
                  120294
Contig ID
                  4682 1.R1010
                  jC-atXLIB327411P1f06b1
5'-most EST
                  BLASTX
Method
                  q2160168
NCBI GI
BLAST score
                  751
                  6.0e-80
E value
Match length
                  142
                  99
% identity
                  (AC000132) Strong similarity to R. communis
NCBI Description
                  phosphoglycerate mutase (gb X70652). ESTs
                  gb T41853, gb T76648 come from this gene. [Arabidopsis
                  thaliana]
```

120295

Seq. No.

```
Contig ID
                  4683 1.R1010
                  jC-atXLIB327439P1f04b2
5'-most EST
                  BLASTN
Method
                  q4159712
NCBI GI
BLAST score
                  652
E value
                  0.0e + 00
Match length
                  846
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
Seq. No.
                  120296
Contig ID
                  4684 1.R1010
5'-most EST
                  jC-atXLIB327439P1f10b2
Method
                  BLASTX
NCBI GI
                  q1216391
BLAST score
                  335
E value
                  4.0e-31
Match length
                  142
                  45
% identity
NCBI Description
                  (U39319) myrosinase-associated protein [Brassica napus]
                  >gi_1589010_prf__2209432B myrosinase-associated
                  protein:ISOTYPE=4 [Brassica napus]
                  120297
Seq. No.
                  4687 1.R1010
Contig ID
5'-most EST
                  ARABL1-022-Q1-B1-A11
Method
                  BLASTX
NCBI GI
                  q4586255
BLAST score
                  707
E value
                  1.0e-74
Match length
                  138
% identity
                  100
NCBI Description
                  (AL049640) putative protein [Arabidopsis thaliana]
Seq. No.
                  120298
                  4688 1.R1010
Contig ID
5'-most EST
                  LIB3175-035-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q1458245
BLAST score
                  233
E value
                  9.0e-42
Match length
                  333
% identity
                  34
                  (U64834) coded for by C. elegans cDNA cml7al; coded for by
NCBI Description
                  C. elegans cDNA cm7g1; coded for by C. elegans cDNA
                  CEMSE26F; similar to methyltransferases [Caenorhabditis
                  elegans]
Seq. No.
                  120299
                  4688_3.R1010
Contig ID
5'-most EST
                  q2763241
Method
                  BLASTN
NCBI GI
                  g3869069
BLAST score
                  77
                  4.0e-35
E value
Match length
                  351
```

```
% identity
                  88
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                 . MEB5, complete sequence [Arabidopsis thaliana]
                  120300
Seq. No.
                  4688 4.R1010
Contig ID
                  jC-aTX22074Q1E1F03b1
5'-most EST
                  BLASTN
Method
                  g3869069
NCBI GI
BLAST score
                  217
                  1.0e-119
E value
Match length
                  381
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MEB5, complete sequence [Arabidopsis thaliana]
                  120301
Seq. No.
                  4689 1.R1010
Contig ID
                  jC-atXLIB327439P1f11b2
5'-most EST
                  BLASTX
Method
                  g2062169
NCBI GI
BLAST score
                  85
E value
                  6.9e-02
Match length
                  88
                  37
% identity
                  (ACO01645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                  thaliana]
                  120302
Seq. No.
                  4689 2.R1010
Contig ID
                  LIB3177-042-P1-K2-A9
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1514643
BLAST score
                  202
                  5.0e-15
E value
                  429
Match length
% identity
                  17
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
Seq. No.
                  120303
                  4689 4.R1010
Contig ID
                  jC-a1X22082Q1E2C06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2062169
                  400
BLAST score
E value
                  3.0e-43
Match length
                  118
% identity
                  71
                  (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                  thaliana]
                  120304
Seq. No.
                  4691_1.R1010
Contig ID
                  LIB25-086-Q1-E1-G7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4503521
BLAST score
                  254
```

```
2.0e-43
E value
Match length
                  196
% identity
                 51
                  murine mammary tumor integration site 6 (oncogene homolog)
NCBI Description
                  >gi 2498490 sp Q64252 INT6 MOUSE VIRAL INTEGRATION SITE
                  PROTEIN INT-6 >gi 185\overline{4}579 (L35556) Int-6 [Mus musculus]
                  >gi 2114363 (U62962) similar to mouse Int-6 [Homo sapiens]
                  >gi 2351382 (U54562) eIF3-p48 [Homo sapiens] >gi 2688818
                   (U85947) Int-6 [Homo sapiens] >gi 2695701 (U94175) mammary
                  tumor-associated protein INT6 [Homo sapiens]
                  120305
Seq. No.
                  4692 1.R1010
Contig ID
                  LIB24-058-Q1-E1-B10
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4468993
                  576
BLAST score
                  2.0e-59
E value
Match length
                  109
% identity
                  100
NCBI Description
                  (AL035605) putative protein [Arabidopsis thaliana]
Seq. No.
                  120306
                  4692 2.R1010
Contig ID
                  LIB23-003-Q1-E1-F11
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4539340
BLAST score
                  321
E value
                  8.0e-30
Match length
                  60
% identity
                  100
NCBI Description
                  (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                  120307
                  4698 1.R1010
Contig ID
                  jC-atXLIB327439P2g06b2
5'-most EST
Method
                  BLASTX
                  g2498731
·NCBI GI
                  490
BLAST score
                  2.0e-49
E value
Match length
                  134
% identity
                  69
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                  >gi 1362013 pir S57611 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi 886428 emb CAA89838 (Z49768)
                  zeta-crystallin homologue [Arabidopsis thaliana]
                  120308
Seq. No.
                  4698 2.R1010
Contig ID
                  LIB3176-042-P1-K1-C2
5'-most EST
                  BLASTX
Method
                  g2498732
NCBI GI
BLAST score
                  196
E value
                  7.0e-29
Match length
                  105
% identity
                  62
NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2
```

Method

NCBI GI

BLAST score

BLASTN g2264315

220

```
Arabidopsis thaliana >gi_886430_emb_CAA89262_ (Z49268)
                  zeta-crystallin homologue [Arabidopsis thaliana]
                  120309
Seq. No.
                  4699 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P2g07b2
                  BLASTX
Method
                  g3785991
NCBI GI
BLAST score
                  710
                  5.0e-75
E value
Match length
                  177
% identity
                  85
                  (AC005560) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
                  120310
Seq. No.
                  4699 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P1e03a2
                  BLASTN
Method
                  g3785968
NCBI GI
BLAST score
                  307
                  1.0e-172
E value
Match length
                  397
% identity
                  97
                  Arabidopsis thaliana chromosome II BAC F2I9 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  120311
Seq. No.
Contig ID
                  4700 1.R1010
5'-most EST
                  jC-atXLIB327439P2g04b2
Method
                  BLASTN
NCBI GI
                  g2582640
BLAST score
                  64
E value
                  3.0e-27
                  75
Match length
                  97
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  120312
Seq. No.
                  4701 1.R1010
Contig ID
5'-most EST
                  jC-atX22008Q1E1E10b1
Method
                  BLASTN
NCBI GI
                  g3985952
BLAST score
                  157
                  6.0e-83
E value
Match length
                  345
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MRC8, complete sequence [Arabidopsis thaliana]
                  120313
Seq. No.
Contig ID
                  4705_1.R1010
                  LIB23-022-Q2-E1-B8
5'-most EST
```

>gi_1362014_pir__S57612 zeta-crystallin homolog -

```
1.0e-120
E value
Match length
                  316
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRN17, complete sequence [Arabidopsis thaliana]
                  120314
Seq. No.
                  4706 1.R1010
Contig ID
                  jC-atXP11C98K18T7069d1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3169883
BLAST score
                  460
                  1.0e-67
E value
                  234
Match length
% identity
                  61
                  (AF033194) dehydroguinate dehydratase/shikimate:NADP
NCBI Description
                  oxidoreductase [Lycopersicon esculentum] >gi 3169888
                  (AF034411) dehydroquinate dehydratase/shikimate:NADP
                  oxidoreductase [Lycopersicon esculentum]
                  120315
Seq. No.
                  4706_2.R1010
Contig ID
5'-most EST
                  g239\overline{3}391
Method
                  BLASTX
                  q629688
NCBI GI
BLAST score
                  80
                  9.0e-13
E value
Match length
                  85
% identity
                  53
NCBI Description
                  dehydroquinase shikimate dehydrogenase - Common tobacco
                  >gi_535771 (L32794) dehydroquinate dehydratase/shikimate
                  dehydrogenase [Nicotiana tabacum]
Seq. No.
                  120316
Contig ID
                  4706_3.R1010
5'-most EST
                  LIB22-007-Q1-E1-F5
Method
                  BLASTX
                  a3169883
NCBI GI
                                                   . . ....
BLAST score
                  543
                  2.0e-55
E value
                  146
Match length
% identity
                  (AF033194) dehydroquinate dehydratase/shikimate:NADP
NCBI Description
                  oxidoreductase [Lycopersicon esculentum] >gi_3169888
                  (AF034411) dehydroquinate dehydratase/shikimate:NADP
                  oxidoreductase [Lycopersicon esculentum]
Seq. No.
                  120317
                  4707 1.R1010
Contig ID
5'-most EST
                  jC-alXLIB327434P4f02b1
                  BLASTX
Method
                  a2541876
NCBI GI
BLAST score
                  315
E value
                  2.0e-28
Match length
                  200
% identity
                  36
NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein
```

Method

5'-most EST

```
[Nicotiana tabacum]
                    120318
Seq. No.
                     4707 2.R1010
  Contig ID
  5'-most EST
                    jC-atXL118Q1B1D09b1
                    120319
  Seq. No.
                     4711 1.R1010
  Contig ID
  5'-most EST
                    jC-atXLIB327415P4a06b1
  Method
                    BLASTN
  NCBI GI
                    q4753195
  BLAST score
                     35
                     5.0e-10
  E value
  Match length
                     67
                    88
  % identity
                    Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5
  NCBI Description
                    cM, complete sequence
                     120320
  Seq. No.
                     4712 1.R1010
  Contig ID
                     jC-atXLIB327439P1h04b2
  5'-most EST
  Method
                    BLASTN
  NCBI GI
                    q3985931
  BLAST score
                     272
                     1.0e-151
  E value
  Match length
                     426
                     100
  % identity
                    Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
  NCBI Description
                     K21H1, complete sequence [Arabidopsis thaliana]
                     120321
  Seq. No.
                     4713 1.R1010
  Contig ID
  5'-most EST
                     jC-atXLIB327439P1h05b1
                     BLASTX
  Method
                     q4455250
  NCBI GI
  BLAST score
                     348
                     2.0e-32
  E value
  Match length
                     141
  % identity .
                     51
  NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
                     120322
  Seq. No.
                     4715 1.R1010
  Contig ID
                     LIB24-046-Q1-E1-F6
  5'-most EST
  Method
                    BLASTN
  NCBI GI
                     g3176693
  BLAST score
                     436
                     0.0e + 00
  E value
  Match length
                     510
  % identity
                     96
                    Arabidopsis thaliana chromosome I BAC T27I1 genomic
  NCBI Description
                     sequence, complete sequence [Arabidopsis thaliana]
  Seq. No.
                     120323
                     4716 1.R1010
```

jC-atXLIB327406P3c10b2

BLASTX

```
g3947735
NCBI GI
BLAST score
                  347
                  1.0e-32
E value
Match length
                  135
% identity
                  55
NCBI Description
                  (AJ009720) NL27 [Solanum tuberosum]
                  120324
Seq. No.
                  4718 2.R1010
Contig ID
5'-most EST
                  LIB3234-072-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2829893
                  1049
BLAST score
                  1.0e-115
E value
                  206
Match length
% identity
                  100
NCBI Description
                  (AC002311) phosphoglucomutase [Arabidopsis thaliana]
                  120325
Seq. No.
                  4719 1.R1010
Contig ID
                  LIB3176-020-P1-K1-C4
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4455351
BLAST score
                  419
E value
                  1.0e-40
Match length
                  167
% identity
                  61
NCBI Description
                  (AL035524) putative protein [Arabidopsis thaliana]
                  120326
Seq. No.
                  4722 1.R1010
Contig ID
5'-most EST
                  LIB3176-035-P1-K1-H6
Method
                  BLASTX
                  q4587598
NCBI GI
BLAST score
                  483
E value
                  1.0e-48
Match length
                  124
% identity
                  81
NCBI Description
                  (AC006951) putative 3-oxoacyl carrier protein synthase II
                  [Arabidopsis thaliana]
                  120327
Seq. No.
Contig ID
                  4723 1.R1010
5'-most EST
                  LIB25-019-Q1-E1-F3
                  120328
Seq. No.
Contig ID
                  4725 1.R1010
5'-most EST
                  LIB3175-082-P1-K1-G10
Seq. No.
                  120329
Contig ID
                  4728 1.R1010
5'-most EST
                  LIB23-010-Q1-E2-H11
                  120330
Seq. No.
Contig ID
                  4731 1.R1010
5'-most EST
                  jC-atXP102CE4C11T7b1
Method
                  BLASTX
```

```
NCBI GI
                   q464621
BLAST score
                   850
                   3.0e-91
E value
                   233
Match length
                   73
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >qi 280374 pir $28586
                   ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
Seq. No.
                   120331
                   4732 1.R1010
Contig ID
                   LIB22-008-Q1-E1-B7
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3482932
BLAST score
                   410
E value
                   7.0e-40
                   87
Match length
                   90
% identity
                   (AC003970) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120332
Contig ID
                   4734 1.R1010
5'-most EST
                   iC-atXLIB327414P3d03a1
                                                                       dette .
                   BLASTN
Method
                   q3927822
NCBI GI
                   256
BLAST score
E value
                   1.0e-142
                   416
Match length
                   99
% identity
                   Arabidopsis thaliana chromosome II BAC F8N16 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   120333
Seq. No.
Contig ID
                   4734 2.R1010
5'-most EST
                   jC-atXLIB327437P2h05a2
                   BLASTX
Method
NCBI GI
                   q3927831
BLAST score
                   1642
E value
                   0.0e + 00
Match length
                   315
                   99
% identity
NCBI Description
                   (AC005727) similar to mouse ankyrin 3 [Arabidopsis
                   thaliana]
                   120334
Seq. No.
Contig ID
                   4736 1.R1010
5'-most EST
                   jC-atXLIB327416P4e06b1
Method
                   BLASTX
NCBI GI
                   q2507229
BLAST score
                   299
E value
                   6.0e-36
Match length
                   127
% identity
                   61
                   40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)
NCBI Description
                   (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED
```

PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN)

```
cyclophilin - bovine >gi_393300_dbj_BAA03159_ (D14074)
                  cyclophilin [Bos taurus]
                  120335
Seq. No.
                  4737 1.R1010
Contig ID ·
                  g2759275 ·
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4589962
BLAST score
                  67
E value
                  3.0e-81
Match length
                  159
% identity
                  100
                  (AC007169) putative fructokinase [Arabidopsis thaliana]
NCBI Description
                  120336
Seq. No.
                  4739 1.R1010
Contig ID
5'-most EST
                  jC-alXLIB327435P3b05b1
Method
                  BLASTX
NCBI GI
                  q2654208
BLAST score
                  1249
E value
                  1.0e-138
Match length
                  314
                  82 ~
% identity
                  (AF035456) heat shock 70 protein [Spinacia oleracea]
NCBI Description
                  >gi 2773050 (AF039083) heat shock 70 protein [Spinacia
                  oleraceal
                  120337
Seq. No.
                  4740 1.R1010
Contig ID
                  jC-aIX35049Q1E1C05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3599415
BLAST score
                  269
E value
                  4.0e-23
Match length
                  219
                  34
% identity
                  (AF083190) SPF31 [Homo sapiens]
NCBI Description
                  120338
Seq. No.
Contig ID
                  4743 1.R1010
5'-most EST
                  jC-a1X25053Q1E1A03b1
Method
                  BLASTN
NCBI GI
                  q2351066
BLAST score
                  170
E value
                  1.0e-90
Match length
                  494
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MOP9, complete sequence [Arabidopsis thaliana]
                  120339
Seq. No.
                  4745 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327413P4e10b1
Method
                  BLASTN
                  g2924653
NCBI GI
```

>gi_423247_pir__A46579 estrogen receptor-binding

354

BLAST score

```
E value
                    0.0e + 00
 Match length
                    887
 % identity
                    96
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                    MDA7, complete sequence [Arabidopsis thaliana]
                    120340
 Seq. No.
 Contig ID
                    4750 1.R1010
                    jC-a\overline{t}XLIB327428P4f05b2
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q4678386
 BLAST score
                    199
                    8.0e-15
 E value
                    98
 Match length
 % identity
                    45
                    (AL049656) putative protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    120341
                    4753 1.R1010
 Contig ID
 5'-most EST
                    LIB3176-033-P1-K1-B5
                    BLASTX
 Method
 NCBI GI
                    q1483222
 BLAST score
                    563
                    1.0e-57
 E value
Match length
                    250
 % identity
                    41
                    (X99097) peroxidase [Arabidopsis thaliana]
 NCBI Description
                    120342
 Seq. No.
... Contig ID
                    4754 1.R1010
                    LIB3177-021-P1-K2-D2
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g4589962
 BLAST score
                    835
 E value
                    9.0e-90
 Match length
                    165
 % identity
                    100
                    (AC007169) putative fructokinase [Arabidopsis thaliana]
 NCBI Description
                    120343
 Seq. No.
 Contig ID
                    4755_1.R1010
 5'-most EST
                    LIB3176-025-P1-K1-C12
 Seq. No.
                    120344
 Contig ID
                    4756_1.R1010
 5'-most EST
                    LIB22-008-Q1-E1-D9
 Method
                    BLASTN
 NCBI GI
                    g2618601
 BLAST score
                    205
 E value
                    1.0e-111
 Match length
                    406
                    99
 % identity
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                    MHJ24, complete sequence [Arabidopsis thaliana]
 Seq. No.
                    120345
                    4757 1.R1010
 Contig ID
```

```
5'-most EST
                   jC-atXLIB327439P1g07b2
Method
                   BLASTX
                   q4200165
NCBI GI
BLAST score
                   1094
                   1.0e-120
E value
Match length
                   283
                   77
% identity
                   (Y16262) neutral invertase [Daucus carota]
NCBI Description
                   120346
Seq. No.
Contig ID
                   4758 1.R1010
5'-most EST
                   LIB25-092-Q1-E1-D7
                   BLASTN
Method
                   q2924733
NCBI GI
BLAST score
                   525
                   0.0e + 00
E value
Match length
                   915
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUF9, complete sequence [Arabidopsis thaliana]
                   120347
Seq. No.
Contig ID
                   4761_1.R1010
                   jC-atXLIB327439P1g05b2
5'-most EST
Method
                   BLASTX
                   a121368
NCBI GI
                   700
BLAST score
E value
                   1.0e-73
                   314
Match length
% identity
                   GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE)
NCBI Description
                   >gi 68586 pir AJAAQ glutamate--ammonia ligase (EC 6.3.1.2)
                   beta - alfalfa >gi_19605_emb_CAA27570_ (X03931) glutamine synthetase [Medicago sativa] >gi_225302_prf__1211328A
                   synthetase, Gln [Medicago sativa]
                   120348
Seq. No.
                   4763 1.R1010
Contig ID
5'-most EST
                   iC-atXP34C153D23T7a1
Method
                   BLASTX
NCBI GI
                   g4415907
BLAST score
                   366
E value
                   1.0e-34
Match length
                   130
% identity
                   66
                   (AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana]
NCBI Description
                   >gi_4581159_gb_AAD24643.1_AC006919_21 (AC006919) putative
                   60S ribosomal protein L24 [Arabidopsis thaliana]
Seq. No.
                   120349
                   4763 2.R1010
Contig ID
                   jC-atXLIB327410P3h02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4415907
BLAST score
                   620
E value
                   1.0e-64
Match length
                   152
```

BLAST score

990

```
80
% identity
                   (AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana]
NCBI Description
                   >gi_4581159_gb_AAD24643.1_AC006919_21 (AC006919) putative
                   60S ribosomal protein L24 [Arabidopsis thaliana]
                   120350
Seq. No.
                   4764 1.R1010
Contig ID
                   jC-atXLIB327432P3f12b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2827528
BLAST score
                   806
E value
                   4.0e-86
Match length
                   227
% identity
                   70
                   (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                   120351
Seq. No.
Contig ID
                   4766 1.R1010
5'-most EST
                   jC-atXLIB327439P1g06b2
Method
                   BLASTX
NCBI GI
                   g2244797
BLAST score
                   232
E value
                   4.0e-19
Match length
                   71
% identity
                   63
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   120352
Seq. No.
Contig ID
                   4767 1.R1010
5'-most EST
                   jC-atXP100CE1C7T7b1
Method
                   BLASTX
                   g4753651
NCBI GI
BLAST score
                   78
                   4.0e-52
E value
Match length
                   156
% identity
                   71
                   (ALO49751) ribosomal protein L13a like protein [Arabidopsis
NCBI Description
                   thaliana]
                   120353
Seq. No.
                   4767 2.R1010
Contig ID
                   jC-a\(\bar{1}\)XLIB327434P4b06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4753651
BLAST score
                   1005
                   1.0e-109
E value
                   206
Match length
% identity
                   92
                   (ALO49751) ribosomal protein L13a like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   120354
                   4767 3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327410P3a09b1
Method
                   BLASTX
NCBI GI
                   q4753651
```

5'-most EST

```
1.0e-107
E value
Match length
                  206
                  91
% identity
                  (ALO49751) ribosomal protein L13a like protein [Arabidopsis
NCBI Description
                  thaliana]
                  120355
Seq. No.
                  4771 1.R1010
Contig ID
                  LIB22-008-Q1-E1-F12
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2765667
BLAST score
                  408
E value
                  1.0e-39
Match length
                  126
                  64
% identity
                  (Z83312) 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis
NCBI Description
                  thaliana]
                  120356
Seq. No.
Contig ID
                  4774_1.R1010
                  LIB23-029-Q1-E1-G7
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1922964
BLAST score
                  597
E value
                  1.0e-61
Match length
                  188
                  66
% identity
                  (AC000106) Similar to Schizosaccharomyces CCAAT-binding
NCBI Description
                  factor (gb U88525). EST gb_T04310 comes from this gene.
                  [Arabidopsis thaliana]
                  120357
Seq. No.
                  4776_1.R1010
Contig ID
                  jC-atXLIB327439P3g06b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2627181
BLAST score
                  425
                  9.0e-42
E value
Match length
                  143
% identity
                  61
                  (D89619) cycloartenol synthase [Pisum sativum]
NCBI Description
                  120358
Seq. No.
Contig ID
                  4778 1.R1010
                  LIB22-008-Q1-E1-G11
5'-most EST
                  BLASTN
Method
NCBI GI
                  q3668073
BLAST score
                  205
                  1.0e-111
E value
Match length
                  390
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T4C15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120359
Contig ID
                  4785 1.R1010
```

jC-atXLIB327418P3e07b1

```
BLASTX
Method
NCBI GI
                   g4589961
                   911
BLAST score
                   1.0e-98
E value
                   196
Match length
                   24
% identity
                  (AC007169) unknown protein [Arabidopsis thaliana]
NCBI Description
                   120360
Seq. No.
                   4785_2.R1010
Contig ID
                  LIB3177-067-P1-K1-A2
5'-most EST
Method
                   BLASTN
                  g4589950
NCBI GI
BLAST score
                   219
                   1.0e-119
E value
                   586
Match length
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC T28P16 genomic
NCBI Description
                  sequence, complete sequence
                   120361
Seq. No.
                   4785_3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327425P3d12b1
Method
                   BLASTX
NCBI GI
                   q4539460
BLAST score
                   187
                   7.0e-14
E value
                   115
Match length
% identity
                   3
                  (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
                   120362
Seq. No.
                   4787_1.R1010
Contig ID
                   jC-a\overline{1}XLIB327436P4c11b1
5'-most EST
                   BLASTX
Method
                  g4490705
NCBI GI
BLAST score
                   669
                   4.0e-70
E value
Match length
                   134
% identity
                   100
                   (AL035680) ribosomal protein L14-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   120363
Seq. No.
Contig ID
                   4787 2.R1010
                   jC-atXP24C122L21T7006a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2983910
BLAST score
                   205
E value
                   8.0e-16
Match length
                   125
% identity
                   36
                   (AE000745) polysialic acid capsule expression protein
NCBI Description
                   [Aquifex aeolicus]
                   120364
Seq. No.
```

÷2.5

4787_4.R1010

Contig ID

5'-most EST

```
5'-most EST
                   LIB35-042-Q1-E1-D3
                   BLASTX
Method
NCBI GI
                   g4490705
BLAST score
                   392
                   2.0e-57
E value
Match length
                   133
                   82
% identity
                   (AL035680) ribosomal protein L14-like protein [Arabidopsis
NCBI Description
Seq. No.
                   120365
                   4799 1.R1010
Contig ID
                   jC-atXLIB327407P2f06b1
5'-most EST
                   BLASTX
Method
                   q2894598
NCBI GI
BLAST score
                   510
E value
                   2.0e-53
                   117
Match length
                   91
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   120366
Seq. No.
                   4800 1.R1010
Contig ID
5'-most EST
                   LIB23-005-Q1-E1-B1
                   BLASTX
Method
                   q4138137
NCBI GI
                   700
BLAST score
E value
                   1.0e-73
                   154
Match length
% identity
                   (AJ012796) ss-galactosidase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   120367
                   4800 2.R1010
Contig ID
                   jC-a\(\bar{1}\)XLIB327436P4f11b1
5'-most EST
Method
                   BLASTX
                   q3204134
NCBI GI
BLAST score
                   378
E value
                   6.0e-36
                   82
Match length
                   77
% identity
                   (AJ006771) beta-galactosidase [Cicer arietinum]
NCBI Description
Seq. No.
                   120368
                   4800 4.R1010
Contig ID
5'-most EST
                   q152\overline{0}393
                   BLASTN
Method
NCBI GI
                   q2462264
BLAST score
                   47
E value
                   4.0e-17
                   55
Match length
                   96
% identity
                   Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                   120369
Seq. No.
                   4800 6.R1010
Contig ID
```

jC-atXLIB327414P3d08a1

Method

BLASTN

```
Method
                  BLASTX
NCBI GI
                  q3204134
BLAST score
                  1335
                  1.0e-148
E value
                  339
Match length
% identity
                  69
                  (AJ006771) beta-galactosidase [Cicer arietinum]
NCBI Description
                  120370
Seq. No.
                  4800 7.R1010
Contig ID
5'-most EST
                  jC-atXLIB327416P3c06b1
Method
                  BLASTX
NCBI GI
                  q4138137
BLAST score
                  2216
E value
                  0.0e + 00
Match length
                  499
% identity
                  79
                  (AJ012796) ss-galactosidase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  120371
                  4800 8.R1010
Contig ID
                  jC-aTXmonuni25Bb04b1
5'-most EST
Method
                  BLASTX
                  q4138137
NCBI GI
BLAST score
                  332
                  6.0e - 31
E value
Match length
                  63
% identity
                  90
                  (AJ012796) ss-galactosidase [Lycopersicon esculentum]
NCBI Description
                  120372
Seq. No.
                  4800 10.R1010
Contig ID
5'-most EST
                  jC-a\(\bar{1}\)X25048Q1E1F04b1
                  BLASTX
Method
NCBI GI
                  q4138137
BLAST score
                  540
E value
                  2.0e-55
Match length
                  139
% identity
                  70
NCBI Description (AJ012796) ss-galactosidase [Lycopersicon esculentum]
                  120373
Seq. No.
Contig ID
                  4802 1.R1010
5'-most EST
                  q1158702
Method
                  BLASTX
NCBI GI
                  q3687237
BLAST score
                  432
E value
                  1.0e-42
Match length
                  115
% identity
                  75
                   (AC005169) putative Cys3His zinc-finger protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  120374
                  4803 1.R1010
Contig ID
                  jC-atXLIB327426P1d01b1
5'-most EST
```

```
NCBI GI
                   q3059018
                   179
BLAST score
                   8.0e-96
E value
Match length
                   568
% identity
                   100
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12
                   (ESSAII project)
                   120375
Seq. No.
Contig ID
                   4805 1.R1010
5'-most EST
                   LIB22-009-Q1-E1-A8
                   120376
Seq. No.
                   4807 1.R1010
Contig ID
                   jC-atXP82CG1H9T7d3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2213619
                   214
BLAST score
                   8.0e-17
E value
                   87
Match length
% identity
                   46
NCBI Description
                   (AC000103) F21J9.14 [Arabidopsis thaliana]
Seq. No.
                   120377
Contig ID
                   4807 2.R1010
5'-most EST
                   jC-atXP95CG11F11T7070d1
Method
                   BLASTN
NCBI GI
                   q1070003
BLAST score
                   42
                   4.0e-14
E value
Match length
                   42
% identity
                   100
NCBI Description
                   B.napus mRNA for biotin carboxyl carrier protein (pBP3)
                   >gi 3715065 emb A59874.1 A59874 Sequence 3 from Patent
                   WO9707222
                   120378
Seq. No.
                   4807 4.R1010
Contig ID
5'-most EST
                   jC-atXLIB327439P3e08b2
                   120379
Seq. No.
                   4808 1.R1010
Contig ID
                   jC-a\overline{t}XLIB327408P3c11b1
5'-most EST
Method
                   BLASTX
                   g3834312
NCBI GI
BLAST score
                   1562
                   1.0e-174
E value
Match length
                   365
% identity
                   83
NCBI Description
                   (AC005679) Strong similarity to glycoprotein EP1 gb_L16983
                   Daucus carota and a member of S locus glycoprotein family
                   PF_00954. ESTs gb_AA067487, gb_Z35737, gb_Z30815, gb_Z35350, gb_AA713171, gb_AI100553, gb_Z34248,
                   gb AA728536, gb Z30816 an
                   120380
Seq. No.
```

4811_1.R1010

```
5'-most EST
                   jC-atXP9C94B5T7d1
                   BLASTX
Method
NCBI GI
                  q4490737
                   285
BLAST score
                   2.0e-25
E value
Match length
                   130
                   51
% identity
                  (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                   120381
Seq. No.
Contig ID
                   4812 1.R1010
5'-most EST
                   jC-alXLIB327436P4f06b1
                   BLASTX
Method
                   q3763916
NCBI GI
                   711
BLAST score
                   7.0e-75
E value
Match length
                   261
                   52
% identity
                   (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                   120382
                   4812 2.R1010
Contig ID
                  jC-a XLIB327436P4f06a1
5'-most EST '
Method
                   BLASTN
                  q531828
NCBI GI
BLAST score
                   56
                   1.0e-22
E value
                   64
Match length
                   97
% identity
NCBI Description Cloning vector pSport1, complete cds
                  120383
Seq. No.
Contig ID
                   4813 1.R1010
5'-most EST
                   LIB35-047-Q1-E1-D2
                   BLASTX
Method
                   q3201612
NCBI GI
BLAST score
                   1167
                   1.0e-128
E value
                   361
Match length
% identity
                   60
                   (AC004669) putative 2A6 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120384
                   4813 2.R1010
Contig ID
                   LIB3234-059-P1-K1-A9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3201632
BLAST score
                   102
E value
                   8.0e-12
Match length
                   80
                   53
% identity
NCBI Description
                  (AC004669) putative 2A6 protein [Arabidopsis thaliana].
                   120385
Seq. No.
```

4813 3.R1010

```
jC-atXLIB327406P3h11b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1903360
BLAST score
                   571
E value
                   2.0e-58
                   256
Match length
% identity
                   48
                   (AC000104) Similar to Arabidopsis 2A6 (gb X83096). EST
NCBI Description
                   gb T76913 comes from this gene. [Arabidopsis thaliana]
                   120386
Seq. No.
                   4813 4.R1010
Contig ID
                  LIB22-084-Q1-E1-E9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4432856
BLAST score
                   172
                   2.0e-12
E value
Match length
                   66
% identity
                   55
                   (AC006300) putative 2A6 protein [Arabidopsis thaliana]
NCBI Description
Seq. No:
                   120387
                   4816 1.R1010
Contig ID
                  LIB35-038-Q1-E1-B9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3258413
BLAST score
                   171
E value
                   6.0e-12
Match length
                   121
% identity
                   31
                   (AP000007) 404aa long hypothetical alanyl-tRNA synthetase
NCBI Description ·
                   [Pyrococcus horikoshii]
Seq. No.
                   120388
                   4817 1.R1010
Contig ID
                   jC-atXLIB327439P1f09b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4008551
BLAST score
                   210
                   2.0e-16
E value
Match length
                   90
% identity
                   47
NCBI Description
                   (AL034490) pseudouridylate synthase [Schizosaccharomyces
                  pombe]
Seq. No.
                   120389
                   4819 1.R1010
Contig ID
5'-most EST
                   jC-atX24106Q1E1B06b1
Method
                   BLASTN
NCBI GI
                   q4589410
                   78
BLAST score
                   1.0e-35
E value
Match length
                   194
                   89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

F2015, complete sequence

```
120390
Seq. No.
                  4821 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327411P2f02b1
Method
                  BLASTX
NCBI GI
                  g4587989
BLAST score
                  1371
                  1.0e-152
E value
                  366
Match length
% identity
                  72
                   (AF085279) hypothetical Cys-3-His zinc finger protein
NCBI Description
                   [Arabidopsis thaliana]
                  120391
Seq. No.
                  4824 1.R1010
Contig ID
                  LIB25-014-Q1-E1-D9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4455307
BLAST score
                  673
                  8.0e-71
E value
Match length
                  132
% identity
                  93
NCBI Description
                   (AL035528) methionyl-tRNA synthetase-like protein
                   [Arabidopsis thaliana]
                  120392
Seq. No.
                  4825 1.R1010
Contig ID
5'-most EST
                  q394896
Method
                  BLASTX
NCBI GI
                  g1362067
BLAST score
                  310
                  6.0e-28
E value
Match length
                  99
                  67
% identity
NCBI Description
                  small GTP-binding protein - garden pea
                  >qi 871508 emb CAA90082 (Z49902) small GTP-binding protein
                  [Pisum sativum]
Seq. No.
                  120393
                  4825 2.R1010
Contig ID
                  jC-atXLIB327419P4e03b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2289961
BLAST score
                  566
E value
                  4.0e-58
                  143
Match length
% identity
                  78
NCBI Description
                  (U82434) AtRAB8 [Arabidopsis thaliana]
Seq. No.
                  120394
                  4830 1.R1010
Contig ID
                  LIB22-009-Q1-E1-D11
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4633131
BLAST score
                  629
                  1.0e-68
E value
                  140
Match length
% identity
                  99
```

13251

.

5'-most EST

```
(AF110407) ATP sulfurylase precursor [Arabidopsis thaliana]
NCBI Description
                  >gi_4803653_emb_CAB42640.1_ (AJ012586) sulfate
                  adenylyltransferase [Arabidopsis thaliana]
                  120395
Seq. No.
                  4830 2.R1010
Contig ID
5'-most EST
                  g2596643
                  BLASTX
Method
NCBI GI
                  q4633131
BLAST score
                  1069
                  1.0e-117
E value
Match length
                  222
                  95
% identity
NCBI Description
                  (AF110407) ATP sulfurylase precursor [Arabidopsis thaliana]
                  >gi 4803653 emb CAB42640.1 (AJ012586) sulfate
                  adenylyltransferase [Arabidopsis thaliana]
                  120396
Seq. No.
                  4832_1.R1010
Contig ID
                  LIB2\overline{2}-009-Q1-E1-D2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1708420
BLAST score
                  455
E value
                  2.0e-45
Match length
                  128
% identity
                  76
                  ISOFLAVONE REDUCTASE HOMOLOG P3 >gi_1361992_pir__S57613
NCBI Description
                  isoflavonoid reductase homolog - Arabidopsis thaliana
                  >gi 886432 emb CAA89859 (Z49777) isoflavonoid reductase
                  homologue [Arabidopsis thaliana]
                  120397
Seq. No.
                  4837 1.R1010
Contig ID
                  LIB23-052-Q1-E1-F6
5'-most EST
                  BLASTN
Method
NCBI GI
                  q3869071
BLAST score
                  642
                 0.0e+00
E value
                  848
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MIL23, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120398
Contig ID
                  4838 1.R1010
5'-most EST
                  LIB25-038-01-E1-G5
Method
                  BLASTX
NCBI GI
                  q2347199
BLAST score
                  706
                  1.0e-74
E value
Match length
                  141
% identity
NCBI Description
                  (AC002338) protein kinase isolog [Arabidopsis thaliana]
Seq. No.
                  120399
Contig ID
                  4841 1.R1010
```

LIB22-061-Q1-E2-F4

```
120400
Seq. No.
                  4842 1.R1010
Contig ID
                  LIB22-009-Q1-E1-E2
5'-most EST
Method
                  BLASTX
                  g3377813
NCBI GI
BLAST score
                  1091
                  1.0e-119
E value
Match length
                  241
% identity
                  85
NCBI Description
                  (AF076275) No definition line found [Arabidopsis thaliana]
                  120401
Seq. No.
                  4843 1.R1010
Contig ID
                  jC-atXLIB327425P3f11b1
5'-most EST
Method
                  BLASTX
                  g4507873
NCBI GI
BLAST score
                  213
                  6.0e-17
E value
Match length
                  110
% identity
                  38
NCBI Description
                  von Hippel-Lindau binding protein 1
                  >gi_3212112_emb_CAA76761_ (Y17394) prefoldin subunit 3
                  [Homo sapiens]
Seq. No.
                  120402
                  4843_3.R1010
LIB25-050-Q1-E1-C4
Contig ID
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4220632
BLAST score
                  204
E value
                  1.0e-111
Match length
                  370
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K6M13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120403
                  4850 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327417P1d01b1
Method
                  BLASTX
                  g1723480
NCBI GI
BLAST score
                  186
                  2.0e-13
E value
                  93
Match length
% identity
                  44
                  HYPOTHETICAL 31.3 KD PROTEIN C17G8.08C IN CHROMOSOME I
NCBI Description
                  >gi 1213257 emb CAA93691 (Z69795) unknown
                  [Schizosaccharomyces pombe]
                  120404
Seq. No.
                  4850 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327417P2g10b1
Method
                  BLASTN
NCBI GI
                  g4757417
BLAST score
                  139
                  7.0e-72
E value
```

```
Match length
                   675
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   T30G6, complete sequence
                   120405
Seq. No.
                   4851 1.R1010
Contig ID
                   jC-atXP112C127N18T7d2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3451068
BLAST score
                   316
E value
                   9.0e-29
                   147
Match length
% identity
                   39
                   (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120406
                   4852 1.R1010
Contig ID
                   ARABL1-045-Q1-B1-C8
5'-most EST
Method
                   BLASTN
                  g4519192
NCBI GI
BLAST score
                   231
E value
                  1.0e-127
Match length
                   460
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MBK21, complete sequence
                   120407
Seq. No.
                   4855 1.R1010
Contig ID
                   jC-atXLIB327408P3f07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2829893
BLAST score
                   212
                  2.0e-16
E value
Match length
                  74
% identity
                   54
NCBI Description
                  (AC002311) phosphoglucomutase [Arabidopsis thaliana]
                  120408
Seq. No.
                   4856 1.R1010
Contig ID
5'-most EST
                  LIB3168-001-P1-K1-B1
                  BLASTX
Method
NCBI GI
                  q1171577
BLAST score
                   195
                   8.0e-15
E value
                  .108
Match length
% identity
                   40
                  (X95343) hypersensitivity-related gene [Nicotiana tabacum]
NCBI Description
                  120409
Seq. No.
                   4858 1.R1010
Contig ID
5'-most EST
                  LIB23-028-Q1-E1-B8
                  BLASTX
Method
NCBI GI
                  g1653767
BLAST score
                  875
                   4.0e-94
E value
```

```
Match length
                  346
% identity
                  53
                  (D90916) oligopeptidase A [Synechocystis sp.]
NCBI Description
                  120410
Seq. No.
                  4867 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P3g03b2
Seq. No.
                  120411
                  4869 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327413P3c05b1
                  BLASTX
Method
                  g1532169
NCBI GI
BLAST score
                  850
                  2.0e-91
E value
Match length
                  172
                  93
% identity
                   (U63815) similar to a E. coli hypothetical protein F402
NCBI Description
                  encoded by GenBank Accession Number S47768 [Arabidopsis
                  thaliana]
Seq. No.
                  120412
Contig ID
                  4869 2.R1010
5'-most EST
                  ARABL1-037-Q1-E1-A12
Method
                  BLASTX
NCBI GI
                  q1532169
BLAST score
                  196
E value
                  5.0e-15
Match length
                  42
% identity
                  88
                  (U63815) similar to a E. coli hypothetical protein F402
NCBI Description
                  encoded by GenBank Accession Number S47768 [Arabidopsis
                  thaliana]
Seq. No.
                  120413
                  4871 1.R1010
Contig ID
                  LIB22-009-Q1-E1-G9
5'-most EST
Method
                  BLASTN
NCBI GI
                  q3184270
BLAST score
                  237
E value
                  1.0e-130
Match length
                  480
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC T8K22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120414
                  4872 1.R1010
Contig ID
5'-most EST
                  jC-atXP115C249G23T7d1
Seq. No.
                  120415
                  4873 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P1h02b2
Method
                  BLASTN
                  g3046853
NCBI GI
BLAST score
                  431
```

0.0e + 00

E value

```
Match length
                   431
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRA19, complete sequence [Arabidopsis thaliana]
                   120416
Seq. No.
                   4875 1.R1010
Contig ID
                   jC-atXLIB327439P1h03b2
5'-most EST
                   120417
Seq. No.
                   4878 1.R1010
Contig ID
                   jC-atXLIB327439P3g11b2
5'-most EST
                   BLASTN
Method
                   g1245938
NCBI GI
BLAST score
                   23
                   8.0e-03
E value
Match length
                   35
% identity
                   61
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
NCBI Description
                   heart atrium, mRNA, 2998 nt]
Seq. No.
                   120418
                   4881 1.R1010
Contig ID
                   jC-atXP87CG8G8T7b1
5'-most EST
                   BLASTN
Method
                  g2980757
NCBI GI
BLAST score
                   417
                  0.0e + 00
E value
Match length
                   462
% identity
                   97
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18
NCBI Description
                   (ESSAII project)
Seq. No.
                   120419
                   4885 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327407P1c10b2
                   BLASTX
Method
NCBI GI
                   q2388710
BLAST score
                   1591
                  0.0e + 00
E value
                   500
Match length
                   77
% identity
                   (AF017150) betaine aldehyde dehydrogenase [Amaranthus
NCBI Description
                   hypochondriacus]
Seq. No.
                   120420
                   4896 1.R1010
Contig ID
                  LIB3176-115-P2-K1-E1
5'-most EST
Method
                   BLASTX
                  q3122038
NCBI GI
BLAST score
                   273
                   5.0e-24
E value
Match length
                   112
% identity
                   50
                  DIHYDROPYRIMIDINASE RELATED PROTEIN-3 (DRP-3) (COLLAPSIN
NCBI Description
                  RESPONSE MEDIATOR PROTEIN 4) (CRMP-4) >gi 1399542 (U52104)
```

rCRMP-4 [Rattus norvegicus]

```
120421
Seq. No.
                   4898 1.R1010
Contig ID
                   jC-aTXLIB327414P4a02a2
5'-most EST
Method
                   BLASTX
                   g4314378
NCBI GI
                   485
BLAST score
                   8.0e-49
E value
Match length
                   141
% identity
                   67
NCBI Description
                   (AC006232) putative lipase [Arabidopsis thaliana]
                   120422
Seq. No.
                   4904 1.R1010
Contig ID
                   LIB3234-050-P1-K1-F4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4512673
BLAST score
                   601
E value
                   2.0e-62
Match length
                   118
                   99
% identity
NCBI Description
                   (AC006931) putative phosphoprotein phosphatase [Arabidopsis
                   thaliana]
                   120423
Seq. No.
                   4905 1.R1010
Contig ID
                   LIB3176-070-P1-K1-G2
5'-most EST ·
Method
                   BLASTX
NCBI GI
                   q4581856
BLAST score
                   104
E value
                   7.0e-54
Match length
                   135
% identity
                   84
                   (AF116825) 1-deoxy-D-xylulose-5-phosphate reductoisomerase
NCBI Description
                   [Mentha x piperita]
                   120424
Seq. No.
                   4906 1.R1010
Contig ID
5'-most EST
                   jC-atXP100CE3G1T7b1
Method
                   BLASTX
NCBI GI
                   q3169180
BLAST score
                   721
E value
                   3.0e-76
Match length
                   181
                   81
% identity
                   (AC004401) putative casein kinase II catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   120425
Seq. No.
Contig ID
                   4906 2.R1010
                   q121\overline{7}148
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3169180
BLAST score
                   801
E value
                   1.0e-141
Match length
                   256
% identity
                   97
```

```
(AC004401) putative casein kinase II catalytic subunit
NCBI Description
                    [Arabidopsis thaliana]
                    120426
Seq. No.
                    4906 3.R1010
Contig ID
                    \mathtt{LIB2}\overline{2}\mathtt{-010}\mathtt{-Q1}\mathtt{-E1}\mathtt{-C11}
5'-most EST
                    BLASTX
Method
                    g3169180
NCBI GI
BLAST score
                    366
                    9.0e-35
E value
Match length
                    166
% identity
                    57
                    (AC004401) putative casein kinase II catalytic subunit
NCBI Description
                    [Arabidopsis thaliana]
                    120427
Seq. No.
                    4906 4.R1010
Contig ID
5'-most EST
                    g935170
                    BLASTX
Method
NCBI GI
                    q585349
BLAST score
                    391
E value
                    1.0e-43
Match length
                    101
% identity
                   CASEIN KINASE II, ALPHA CHAIN 1 (CK II)
NCBI Description
                    >gi_419752_pir__S31098 casein kinase II (EC 2.7.1.-)
                    alpha-type chain (clone ATCKA1) - Arabidopsis thaliana
                    >gi 391603 dbj BAA01090 (D10246) casein kinase II
                    catalytic subunit [Arabidopsis thaliana]
                    120428
Seq. No.
                    4908 1.R1010
Contig ID
5'-most EST
                    jC-atXLIB327415P3c02b1
                    BLASTX
Method
NCBI GI
                    q3176685
BLAST score
                    1059
                    1.0e-122
E value
Match length
                    237
% identity
                    (AC003671) Strong similarity to spermidine synthase 1,
NCBI Description
                    qb Y08252 and possibly closer similarity to spermidine
                    synthase 2 gb_Y08253 from Datura stramonium. ESTs
                    gb N38155, gb T41738, gb AA597626, gb AA712967 and
                    gb AA712346 come from this ge
                    120429
Seq. No.
                    4908 2.R1010
Contig ID
                    jC-atXLIB327408P3h11b1
5'-most EST
                    BLASTX
Method
NCBI GI
                    q4056467
BLAST score
                    654
E value
                    2.0e-68
Match length
                    123
% identity
NCBI Description
                    (AC005990) Strong similarity to gb AB006693 spermidine
                    synthase from Arabidopsis thaliana. ESTs gb AA389822,
                    gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256
```

Match length

148

come from this gene. [Arabidopsis thaliana]

```
120430
Seq. No.
                  4908 3.R1010
Contig ID
                  LIB3234-053-P1-K1-C9
5'-most EST
                  BLASTX
Method
                  g3176685
NCBI GI
BLAST score
                  555
E value
                  2.0e-60
                  121
Match length
% identity
                  100
                  (AC003671) Strong similarity to spermidine synthase 1,
NCBI Description
                  gb Y08252 and possibly closer similarity to spermidine
                  synthase 2 gb_Y08253 from Datura stramonium. ESTs
                  gb N38155, gb T41738, gb AA597626, gb AA712967 and
                  gb AA712346 come from this ge
                  120431
Seq. No.
                  4910 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P1f06b2
Seq. No.
                  120432
                  4911 1.R1010
Contig ID
                  g3449723
5'-most EST
Method
                  BLASTN
                  g2290120
NCBI GI
BLAST score
                  54
                  3.0e-21
E value
Match length
                  66
% identity
                  95
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
Seq. No.
                  120433
                  4911 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P4d09b1
Method
                  BLASTX
NCBI GI
                  q1749676
BLAST score
                  391
                  3.0e-37
E value
Match length
                  210
% identity
                  41
NCBI Description
                  (D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
                  EMBL Accession Number Z72990 [Schizosaccharomyces pombe]
Seq. No.
                  120434
Contig ID
                  4911 3.R1010
5'-most EST
                  jC-atXP31C145A11T7d2
                  120435
Seq. No.
                  4912 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P2f07b2
Method
                  BLASTX
NCBI GI
                  g2335096
BLAST score
                  340
                  8.0e-32
E value
```

```
% identity
                  47
NCBI Description (AC002339) hypothetical protein [Arabidopsis thaliana]
                  120436
Seq. No.
                  4913 1.R1010
Contig ID
                  jC-atXLIB327439P1f08b2 ...
5'-most EST
                  BLASTX
Method
                  q3522943
NCBI GI
                  144
BLAST score
E value
                  8.0e-09
Match length
                  84
% identity
                  39
NCBI Description
                  (AC004411) putative p-qlycoprotein [Arabidopsis thaliana]
Seq. No.
                  120437
                  4918 1.R1010
Contig ID
                  LIB22-010-Q1-E1-D12
5'-most EST
                  BLASTX
Method
                  q3367516
NCBI GI
                  730
BLAST score
                  1.0e-77
E value
Match length
                  142
% identity
                  99
                  (AC004392) Similar to beta-glucosidase BGQ60 precursor
NCBI Description
                  gb L41869 from Hordeum vulgare. [Arabidopsis thaliana]
                  120438
Seq. No.
                  4921 1.R1010
Contig ID
                  LIB22-010-Q1-E1-D5
5'-most EST
                  BLASTX
Method
                  q3582329
NCBI GI
BLAST score
                  694
E value
                  4.0e-73
                  136
Match length
% identity
                  99
                  (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  120439
                  4922 1.R1010
Contig ID
5'-most EST
                  q2759346
                  BLASTX
Method
NCBI GI
                  q3033395
BLAST score
                  295
E value
                  2.0e-26
                  128
Match length
% identity
NCBI Description
                  (AC004238) putative zinc-finger protein [Arabidopsis
                  thaliana]
Seq. No.
                  120440
                  4925 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P1q02b2
                  BLASTX
Method
NCBI GI
                  q4455323
BLAST score
                  733
E value
                  7.0e~78
Match length
                  147
```

```
% identity
                   100
                   (AL035525) aminopeptidase-like protein [Arabidopsis
 NCBI Description
                   thaliana]
                   120441
 Seq. No.
                   4929 1.R1010
 Contig ID
                   ARABL1-04-Q1-B1-G8
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   q4678332
 BLAST score
                   432
 E value
                   1.0e-42
Match length
                   119
                   75
 % identity
                   (AL049658) putative peptide transporter [Arabidopsis
 NCBI Description
Seq. No.
                   120442
                   4940 1.R1010
 Contig ID
                   jC-atXP74C225F23T7078d1
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   q2129471
 BLAST score
                   1015
                   1.0e-110
 E value
                   293
 Match length
                   68
 % identity
                   glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
 NCBI Description
                   precursor - Scotch pine >gi 1100223 (L32560)
                   glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
                   120443
 Seq. No.
                   4940_2.R1010
 Contig ID
 5'-most EST
                   LIB23-059-Q1-E1-F2
 Method
                   BLASTX
                   g2129471
 NCBI GI
 BLAST score
                   250
 E value
                   3.0e-21
 Match length
                   125
 % identity
                   51
 NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
                   precursor - Scotch pine >gi 1100223 (L32560)
                   glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
                   120444
 Seq. No.
 Contig ID
                   4940_3.R1010
                   jC-a\overline{t}XLIB327438P4c11a2
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   q2129471
 BLAST score
                   327
                   4.0e-31
 E value
Match length
                   102
                   67
 % identity
                   glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
 NCBI Description
                   precursor - Scotch pine >gi 1100223 (L32560)
                   glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
                   120445
 Seq. No.
```

4941_1.R1010

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```
5'-most EST
                   LIB3176-044-P1-K1-B4
                   BLASTX
Method
NCBI GI
                   g2760322
BLAST score
                   1259
                   1.0e-157
E value
Match length
                   291
                   95
% identity
                   (AC002130) F1N21.7 [Arabidopsis thaliana]
NCBI Description
                   120446
Seq. No.
                   4942 1.R1010
Contig ID
                   LIB35-041-Q1-E1-D9
5'-most EST
Method
                   BLASTN
NCBI GI
                  q4199934
                   298
BLAST score
                   1.0e-166
E value
Match length
                   693 .
% identity
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC T3P18,
                   complete sequence [Arabidopsis thaliana]
                   120447
Seq. No.
                   4942 2.R1010
Contig ID
5'-most EST
                  q1158914
                  BLASTN
Method
NCBI GI
                   g4199934
BLAST score
                   297
                   1.0e-166
E value
                   406
Match length
% identity
                   95
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   120448
Seq. No.
Contig ID
                   4942 3.R1010
                   g1520530
5'-most EST
Method ..
                   BLASTN
                   q4199934
NCBI GI
                   133
BLAST score
E value
                   2.0e-68
Match length
                   338
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                   120449
Seq. No.
                   4942 4.R1010
Contig ID
                   q151\overline{7}389
5'-most EST
                   BLASTN
Method
                   g4199934
NCBI GI
BLAST score
                   328
                   0.0e + 00
E value
                   409
Match length
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
```

```
120450
Seq. No.
                   4942 6.R1010
Contig ID
5'-most EST
                   g2763014
Method
                   BLASTN
NCBI GI
                   g4199934
BLAST score
                   194
                   1.0e-105
E value
                   244
Match length
% identity
                   99
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   120451
Seq. No.
                   4944 1.R1010
Contig ID
                   LIB25-027-Q1-E1-F7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1923256
BLAST score
                   4.69
                   7.0e-47
E value
Match length
                   120
% identity
                   80
NCBI Description
                   (U86782) 26S proteasome-associated pad1 homolog [Homo
                   sapiens]
                   120452
Seq. No.
                   4945 1.R1010
Contig ID
                   LIB22-010-Q1-E1-F7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1914685
BLAST score
                   330
                   1.0e-30
E value
Match length
                   74
% identity
                   82
                  (Y12014) RAD23 protein, isoform II [Daucus carota]
NCBI Description
                   120453
Seq. No.
                   4946 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327439P1g10b2
Method
                   BLASTN
NCBI GI
                   g2264316
BLAST score
                   101
E value
                   4.0e-49
Match length
                   795
                   38
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRO11, complete sequence [Arabidopsis thaliana]
                   120454
Seq. No.
                   4947 1.R1010
Contig ID
                  LIB2\overline{2}-085-Q1-E2-F6
5'-most EST
                  BLASTN
Method
                   g4691223
NCBI GI
                   345
BLAST score
                  0.0e+00
E value
Match length
                   416
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
NCBI Description
```

40.

(ESSA project)

```
Seq. No.
                  120455
Contig ID
                  4948 1.R1010
5'-most EST
                  LIB22-027-Q1-E1-B12
Method
                  BLASTX
NCBI GI
                  g4582787
BLAST score
                  1259
E value
                  1.0e-157
Match length
                  331
% identity
                  81
NCBI Description (AJ012281) adenosine kinase [Zea mays]
Seq. No.
                  120456
                  4948 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327409P4f12b1
Method
                  BLASTX
NCBI GI
                  g4582787
BLAST score
                  532
E value
                  3.0e-54
Match length
                  116
% identity
                  86
NCBI Description (AJ012281) adenosine kinase [Zea mays]
                  120457
Seq. No.
                  4948 3.R1010
Contig ID
5'-most EST
                  jC-atXP41C166E22T7s1
Method
                  BLASTX
NCBI GI
                  g4582787
BLAST score
                  167
E value
                  3.0e-30
Match length
                  77
% identity
                  90
NCBI Description (AJ012281) adenosine kinase [Zea mays]
Seq. No.
                  120458
                  4951 1.R1010
Contig ID
                  LIB22-010-Q1-E1-G12
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2245139
BLAST score
                  647
                  8.0e-68
E value
Match length
                  164
% identity
                  78
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  120459
                  4953 1.R1010
Contig ID
5'-most EST
                  LIB3176-058-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  g1022798
BLAST score
                  168
                  2.0e-89
E value
Match length
                  176
                  99
% identity
NCBI Description Arabidopsis thaliana OBP32pep mRNA, partial cds
```

```
120460
Seq. No.
Contig ID
                   4955 1.R1010
                  LIB2\overline{2}-010-Q1-E1-G5
5'-most EST
                   120461
Seq. No.
                   4956_1.R1010
Contig ID
                   jC-a\overline{t}XLIB327412P4f05b1
5'-most EST
                   BLASTN
Method
                   q3775988
NCBI GI
BLAST score
                   40
E value
                   5.0e-13
Match length
                   40
                   100
% identity
                  Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH5
NCBI Description
                   1204.62
Seq. No.
                   4960 1.R1010
Contig ID
                   jC-atXLIB327409P1f02b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2160296
BLAST score
                   1469
E value
                   1.0e-163
Match length
                   291
% identity
                   96
                  (D61395) gamma-VPE [Arabidopsis thaliana]
NCBI Description
                   120463
Seq. No.
                   4960 2.R1010
Contig ID
                   LIB23-006-Q1-E1-E8
5'-most EST
Method
                   BLASTX
                   g3688175
NCBI GI
                   584
BLAST score
E value
                   2.0e-60
Match length
                   131
% identity
NCBI Description
                   (AL031804) gamma-VPE (vacuolar processing enzyme)
                   [Arabidopsis thaliana]
Seq. No.
                   120464
                   4960 3.R1010
Contig ID
5'-most EST
                   jC-atXLIB327427P1f11b1
Method
                   BLASTX
NCBI GI
                   g3688175
BLAST score
                   707
E value
                   9.0e-75
Match length
                   158
                   86
% identity
                   (AL031804) gamma-VPE (vacuolar processing enzyme)
NCBI Description
                   [Arabidopsis thaliana]
                   120465
Seq. No.
                   4960 5.R1010
Contig ID
5'-most EST
                   g3450445
Method
                   BLASTN
NCBI GI
                   g3688169
BLAST score
                   335
                   0.0e + 00
E value
```

5'-most EST

```
Match length
                   369
                   98
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21
                   (ESSAII project)
Seq. No.
                   120466
Contig ID
                   4962_1.R1010
5'-most EST
                   LIB22-049-Q1-E1-H4
                   BLASTN
Method
NCBI GI
                   q4056476
BLAST score
                   60
E value
                   6.0e-25
Match length
                   96
                   91
% identity
                  Arabidopsis thaliana chromosome II BAC F3G5 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   120467
Seq. No.
Contig ID
                   4963_1.R1010
5'-most EST
                   jC-atXLIB327439P2h02b2
Method
                   BLASTN
NCBI GI
                   g2582640
BLAST score
                   51
                   1.0e-19 🚉
E value
Match length
                   55
% identity
                   98
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                  120468
Seq. No.
Contig ID
                   4969_1.R1010
5'-most EST
                  LIB22-035-Q1-E1-E6
Method
                  BLASTN
NCBI GI
                  g2244788
BLAST score
                  282
E value
                   1.0e-157
Match length
                  384
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  120469
Contig ID
                  4969 2.R1010
                  LIB3177-089-P1-K1-A6
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2244788
BLAST score
                  300
E value
                  1.0e-168
Match length
                  427
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  120470
                  4971 1.R1010
Contig ID
```

10

jC-atXLIB327439P2h09b2

```
120471
Seq. No.
Contig ID
                   4972 1.R1010
                   jC-alX22040Q1E1E01b1
5'-most EST
                   BLASTN
Method
                   g3449329
NCBI GI
BLAST score
                   197
E value
                   1.0e-106
Match length
                   773
% identity
                   99
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MDH9, complete sequence [Arabidopsis thaliana]
                   120472
Seq. No.
                   4973_1.R1010
Contig ID
5'-most EST
                   LIB2\overline{2}-011-Q1-K1-A11
Method
                   BLASTX
                   g3033391
NCBI GI
BLAST score
                   634
                   6.0e-68
E value
Match length
                   268
% identity
                   49
                   (AC004238) putative amino acid transporter [Arabidopsis
NCBI Description
                   thaliana]
                   120473
Seq. No.
                   4976_1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327409P1f12b1
Method
                   BLASTX
                   q2924781
NCBI GI
BLAST score
                   752
E value
                   1.0e-135
Match length
                   364
% identity
                   68
                   (AC002334) putative cellulose synthase [Arabidopsis
NCBI Description
                   thaliana]
                   120474
Seq. No.
Contig ID
                   4977 1.R1010
                   jC-a\overline{1}XLIB327435P4e01b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2911072
BLAST score
                   1090
                   1.0e-119
E value
Match length
                   232
                   98
% identity
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120475
                   4977 2.R1010
Contig ID
5'-most EST
                   LIB3234-093-P1-K1-E11
                   BLASTN
Method
NCBI GI
                   q4584387
BLAST score
                   192
E value
                   1.0e-103
Match length
                   736
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7
NCBI Description
```

(ESSA project)

```
Seq. No.
                   120476
                   4978 1.R1010
Contig ID
                   LIB22-011-Q1-K1-B10
5'-most EST
                   120477
Seq. No.
                   4979 1.R1010
Contig ID
                   jC-atX22011Q1K1B04b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2887500
BLAST score
                   822
                   0.0e + 00
E value
                   423
Match length
                   78
% identity
NCBI Description
                   (AC002339) putative AP2 domain-containing protein
                   [Arabidopsis thaliana]
                   120478
Seq. No.
Contig ID
                   4980 1.R1010
5'-most EST
                   jC-atXLIB327420P1d06b1
                   BLASTX
Method
                   q3157947
NCBI GI
BLAST score
                   1466
                   1.0e-163
E value
Match length
                   280
% identity
                   100
                   (AC002131) Similar to protein gb_Z74962 from Brassica
NCBI Description
                   oleracea which is similar to bacterial YRN1 and HEAHIO
                   proteins. ESTs gb T21954, gb T04283, gb Z37609, gb N37366,
                   gb R90704, gb F155\overline{0}0 and gb F\overline{1}4353 come from this gene.
                   [Arabidopsis tha
                   120479
Seq. No.
                   4984 1.R1010
Contig ID
5'-most EST
                   q930812
Method
                   BLASTX
NCBI GI
                   q992706
BLAST score
                   264
                   5.0e-26
E value
Match length
                   88
% identity
                   75
NCBI Description
                  (U33758) UBC13 [Arabidopsis thaliana]
Seq. No.
                   120480
                   4985 1.R1010
Contig ID
5'-most EST
                   LIB22-011-Q1-K1-B9.
Method
                   BLASTX
NCBI GI
                   g4417278
BLAST score
                   1091
E value
                   1.0e-120
Match length
                   195
% identity
                   23
NCBI Description
                  (AC007019) hypothetical protein [Arabidopsis thaliana]
                   120481
Seq. No.
```

4986 1.R1010

```
5'-most EST
                   jC-atX22011Q1K1C01b1
                   BLASTN
Method
                   g3236479
NCBI GI
BLAST score
                   366
                                                                        Va. 1
                   0.0e + 00
E value
                   398
Match length
                   98
% identity
                  Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8
NCBI Description
                   cM, complete sequence
                   120482
Seq. No.
Contig ID
                   4987_1.R1010
                   jC-atXLIB327440P4a03b2
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4589438
BLAST score
                   547
                   0.0e + 00
E value
Match length
                   547
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQJ2, complete sequence
                   120483
Seq. No.
Contig ID
                   4989 1.R1010
5'-most EST
                   g936409
Method
                   BLASTX
NCBI GI
                   g4582436
BLAST score
                   1294
E value
                   1.0e-143
Match length
                   247
% identity
                   100
                  (AC007196) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120484
Contig ID
                   4996_1.R1010
                   jC-atXLIB327440P1b01b1
5'-most EST
Method
                   BLASTX
                   q2809264
NCBI GI
BLAST score
                   402
                   7.0e-40
E value
                   158
Match length
% identity
                   55
                   (AC002560) F21B7.33 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120485
                   4998 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327413P3a12b1
Method
                   BLASTX
NCBI GI
                   q3157928
BLAST score
                   705
E value
                   2.0e-74
Match length
                   142
                  . 99
% identity
                  (AC002131) Similar to fumarylacetoacetate hydrolase,
NCBI Description
                   gb_L41670 from Emericella nidulans. [Arabidopsis thaliana]
```

120486

Seq. No.

```
4999 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327411P1a08b1
Method
                  BLASTN
                  g2088638
NCBI GI
BLAST score
                  468
                  0.0e + 00
E value
Match length
                  480
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T28M21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120487
                  5000 1.R1010
Contiq ID
                  jC-alXLIB327434P1d12b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4559334
BLAST score
                  780
E value
                  4.0e-83
Match length
                  222
% identity
NCBI Description
                  (AC007087) unknown protein [Arabidopsis thaliana]
Seq. No.
                  120488
Contig ID
                  5003 -1.R1010
                  jC-atXLIB327429P4e05b2
5'-most EST
                  BLASTN
Method
NCBI GI
                  q2245073
BLAST score
                  729
E value
                  0.0e + 00
Match length
                  833
% identity
                  99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  120489
Contig ID
                  5005 1.R1010
5'-most EST
                  LIB3177-095-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q3885330
BLAST score
                  1155
E value
                  1.0e-176
Match length
                  509
% identity
                  65
NCBI Description
                  (AC005623) putative cytochrome p450 protein [Arabidopsis
                  thaliana]
Seq. No.
                  120490
Contig ID
                  5005 2.R1010
5'-most EST
                  jC-atXP87C244D12T7b1
Method
                  BLASTX
NCBI GI
                  q3885331
BLAST score
                  270
E value
                  1.0e-23
Match length
                  84
% identity
                  63
NCBI Description
                  (AC005623) putative cytochrome p450 protein [Arabidopsis
```

% identity

65

```
120491
Seq. No.
Contig ID
                   5007 1.R1010
5'-most EST
                   LIB2\overline{2}-011-Q1-K1-F12
Method
                   BLASTN
NCBI GI
                   g4415928
BLAST score
                   529
E value
                   0.0e + 00
Match length
                   553
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F13A10 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   120492
Seq. No.
                   5008 1.R1010
Contig ID
5'-most EST
                   LIB3234-085-Q1-K1-A1
Method
                   BLASTN
NCBI GI
                   q4220644
BLAST score
                   71
E value
                   2.0e-31
Match length
                   137
% identity
                   89
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MXL8, complete sequence [Arabidopsis thaliana]
                   120493
Seq. No.
                   5008_2.R1010
Contig ID
                   LIB2\overline{2}-011-Q1-E1-F2
5'-most EST
Method ·
                   BLASTN
NCBI GI
                   q4220644
BLAST score
                   150
E value
                   1.0e-78
Match length
                   472
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MXL8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   120494
                   5009 1.R1010
Contig ID
                   jC-atX22012Q1E1F07b2
5'-most EST
Method
                   BLASTX
                   g3080374
NCBI GI
BLAST score
                   210
E value
                   1.0e-16
Match length
                   146
% identity
NCBI Description
                   (AL022580) putative protein [Arabidopsis thaliana]
Seq. No.
                   120495
                   5012 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327440P1c09b1
Method
                   BLASTX
NCBI GI
                   g2960364
BLAST score
                   507
E value
                   3.0e-51
Match length
                   141
```

```
NCBI Description (AJ224986) cinnamoyl CoA reductase [Populus balsamifera
                  subsp. trichocarpa]
                  120496
Seq. No.
Contig ID
                  5013 1.R1010
5'-most EST
                  jC-atXP118C155H6T7087d2
Method
                  BLASTX
                  g4572674
NCBI GI
                  564
BLAST score
E value
                  1.0e-118
Match length
                  318
% identity
                  71
NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]
                  120497
Seq. No.
                  5014 1.R1010
Contig ID
5'-most EST
                  LIB22-081-Q1-E2-E12
Method
                  BLASTN
                  q4063737
NCBI GI
                  470
BLAST score
                  0.0e + 00
E value
Match length
                  470
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F24D13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  120498
Seq. No.
Contig ID
                  5015_1.R1010
                  LIB22-011-Q1-K1-G3
5'-most EST
                  BLASTN
Method
                  q2656026
NCBI GI
BLAST score
                  424
E value
                  0.0e + 00
Match length
                  444
% identity
                 . 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
Seq. No.
                  120499
                  5017 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P2b03b2
                  BLASTX
Method
NCBI GI
                  q1335862
BLAST score
                  606
E value
                  7.0e-64
Match length
                  145
                  85
% identity
NCBI Description (U42608) clathrin heavy chain [Glycine max]
Seq. No.
                  120500
Contig ID
                  5018 1.R1010
5'-most EST
                  jC-atXLIB327423P3h01b1
                  120501
Seq. No.
                  5018 2.R1010
Contig ID
                  LIB25-094-Q1-E1-G6
5'-most EST
```

Match length

```
Seq. No.
                   120502
                   5019 1.R1010
Contig ID
                   jC-atXLIB327432P4a11b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3668097
BLAST score
                   807
E value
                   3.0e-86
Match length
                   156
                   100
% identity
NCBI Description
                   (AC004667) putative glycine cleavage system protein H
                   precursor [Arabidopsis thaliana]
Seq. No.
                   120503
                   5020 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P4a12b1
                   BLASTX
Method
NCBI GI
                   q2129516
BLAST score
                   532
E value
                   3.0e-54
                   154
Match length
                   67
% identity
NCBI Description
                   1-aminocyclopropane-1-carboxylate oxidase homolog (clone
                   2A6) - Arabidopsis thaliana >gi_599622_emb_CAA58151
                   (X83096) 2A6 [Arabidopsis thaliana] >g\overline{1}_28\overline{0}9261 (AC\overline{0}02560)
                   F21B7.30 [Arabidopsis thaliana]
Seq. No.
                   120504
                   5021_1.R1010
Contig ID
                   LIB25-025-Q1-E1-C4
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1914683
BLAST score
                   249
E value
                   6.0e-21
Match length
                   204
% identity
                   40
NCBI Description (Y12013) RAD23, isoform I [Daucus carota]
                   120505
Seq. No.
                   5022 1.R1010
Contig ID
                   LIB3175-021-P1-K1-G6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4538943
BLAST score
                   855
E value
                   4.0e-92
Match length
                   198
                   81
% identity
NCBI Description
                   (AL049483) putative beta-galactosidase [Arabidopsis
                   thaliana]
Seq. No.
                   120506
                   5023 1.R1010
Contig ID
                   LIB22-011-Q1-E1-H12
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4490701
BLAST score
                   448
E value
                   0.0e + 00
```

Method

BLASTX

```
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18
NCBI Description
                   (ESSA project)
Seq. No.
                  120507
                  5025 2.R1010
Contig ID
                  LIB22-011-Q1-K1-H3
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3367529
BLAST score
                  361
                  2.0e-34
E value
Match length
                  77
% identity
                  97
                  (AC004392) Strong similarity to gi 2160138 F19K23.6 gene
NCBI Description
                  product from A. thaliana BAC gb AC000375. [Arabidopsis
                  thaliana]
Seq. No.
                  120508
                  5026 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P4b01b1
Method
                  BLASTX
NCBI GI
                  q1658193
BLAST score
                  844
E value
                  2.0e-90
Match length
                  255
% identity
NCBI Description
                  (U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum
                  bicolor
Seq. No.
                  120509
                  5027 1.R1010
Contig ID
5'-most EST
                  jC-a1X25079Q1E1G03b1
Method
                  BLASTN
NCBI GI
                  q2979540
BLAST score
                  369
E value
                  0.0e + 00
Match length
                  652
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC F17K2 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120510
                  5028 1.R1010
Contig ID
                  jC-aTXP91C246J4T7b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3738313
BLAST score
                  499
                  0.0e + 00
E value
Match length
                  520
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC T29E15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120511
                  5028 2.R1010
Contig ID
5'-most EST
                  ARABL1-031-Q1-B1-A6
```

5'-most EST

```
NCBI GI
                   a3738339
BLAST score
                   1050
                   1.0e-119
E value
                   218
Match length
                   100
% identity
NCBI Description
                  (AC005170) putative kinase [Arabidopsis thaliana]
                   120512
Seq. No.
                   5029 1.R1010
Contig ID
5'-most EST
                   jC-alXLIB327435P2d09a1
Method
                  BLASTN
NCBI GI
                  q3985931
BLAST score
                   192
                   1.0e-103
E value
                   374
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21H1, complete sequence [Arabidopsis thaliana]
                  120513
Seq. No.
                  5036_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P1h10b2
Method
                  BLASTN
NCBI GI
                  q4589438
BLAST score
                  166
                  4.0e-88
E value
Match length
                  539
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQJ2, complete sequence
                  120514
Seq. No.
Contig ID
                  5057 1.R1010
5'-most EST
                  g2749317
Method
                  BLASTX
                  g1483177
NCBI GI
BLAST score
                  167
                  2.0e-11
E value
Match length
                  86
% identity
                  40
                  (D86598) antifreeze-like protein (af70) [Picea abies]
NCBI Description
                  120515
Seq. No.
Contig ID
                  5058 1.R1010
                  LIB22-011-Q1-K1-C2
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2477521
BLAST score
                  365
E value
                  0.0e + 00
Match length
                  453
% identity
                  Arabidopsis thaliana chromosome I BAC F22K20 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120516
                  5069 1.R1010
Contig ID
```

jC-atXLIB327411P1g08b1

```
120517
Seq. No.
                  5070 1.R1010
Contig ID
5'-most EST
                  LIB22-011-Q1-K1-D2
Seq. No.
                  120518
                  5078 · 1.R1010
Contig ID
                  jC-aTXLIB327440P1b12b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2673905
BLAST score
                  343
E value
                  8.0e-32
Match length
                  146
% identity
                  56
NCBI Description
                  (AC002561) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  120519
                  5082 1.R1010
Contig ID
                  jC-atXLIB327422P3f04b2
5'-most EST
Method
                  BLASTX
                  g4580464
NCBI GI
BLAST score
                  274
E value
                  8.0e-24
                  207
Match length
% identity
                  40
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                  120520
Seq. No.
                  5101 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327417P1c09a1
Method
                  BLASTN
                  g2290120
NCBI GI
BLAST score
                  46
                  2.0e-16
E value
Match length
                  62
% identity
                  94
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
NCBI Description
                  gene, partial cds
Seq. No.
                  120521
                  5120_1.R1010
Contig ID
5'-most EST
                  LIB22-012-Q1-E1-D9
                  BLASTX
Method
NCBI GI
                  g2655098
BLAST score
                  393
                  3.0e-38
E value
                  92
Match length
% identity
                  74
NCBI Description
                  (AF023472) peptide transporter [Hordeum vulgare]
                  120522
Seq. No.
                  5130 1.R1010
Contig ID
5'-most EST
                  LIB3176-010-P1-K1-H6
                  BLASTX
Method
                  g4263711
NCBI GI
BLAST score
                  628
                  3.0e-65
E value
```

```
Match length
                   241
% identity
                   54
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   120523
                   5130 2.R1010 ...
Contig ID
                   jC-atXP31C146H10T7d2
5'-most EST
Method
                   BLASTX
                   g2088654
NCBI GI
BLAST score
                   1249
                   1.0e-138
E value
                   273
Match length
% identity
                   89
                   (AF002109) 60S acidic ribosomal protein PO isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   120524
                   5130 3.R1010
Contig ID
                   g3450553
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2290120
BLAST score
                   61
E value
                   2.0e-25
Match length
                   65
% identity
                   98
NCBI Description
                  HIV-1 strain MO2 from USA, envelope glycoprotein (env)
                   gene, partial cds
Seq. No.
                   120525
                   5136 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327433P1f04b1
Method
                   BLASTX
NCBI GI
                   g4262250
BLAST score
                   1266
                   1.0e-140
E value
                   276
Match length
% identity
                   90
                   (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                   120526
Seq. No.
                   5138 1.R1010
Contig ID
5'-most EST
                   jC-a1X24092Q1E1A05b1
Method
                   BLASTX
NCBI GI
                   g2811028
BLAST score
                   757
E value
                   1.0e-80
Match length
                   179
% identity
                   84
                  HYPOTHETICAL 47.9 KD PROTEIN M021B04.12 >qi 2191188
NCBI Description
                   (AF007271) similar to S. cerevisiae SIK1P (PID: 9984964)
                   [Arabidopsis thaliana]
Seq. No.
                   120527
                   5140 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327440P1b04b1
Method
                   BLASTX
```

5'-most EST

```
q2980795
NCBI GI
BLAST score
                  707
E value
                  9.0e-75
Match length
                  135
% identity
                  100
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]
                  120528
Seq. No.
                  5142 1.R1010
Contig ID
                  g936074
5'-most EST
Seq. No.
                  120529
                  5142 2.R1010
Contig ID
                  q2597259
5'-most EST
Seq. No.
                  120530
                  5143 1.R1010
Contig ID
                  LIB24-070-Q1-E1-D4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2924777
BLAST score
                  665
E value
                  4.0e-70
Match length
                  130
                  97
% identity
                  (AC002334) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  120531
Contig ID
                  5145 1.R1010
5'-most EST
                  LIB22-012-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  q4314370
BLAST score
                  311
E value
                  1.0e-28
Match length
                  108
% identity
                  58
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]
                  120532
Seq. No.
                  5147 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327440P4a02b2
Method
                  BLASTN
NCBI GI
                  g3133272
BLAST score
                  110
E value
                  1.0e-54
Match length
                  562
% identity
                  97
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T17H7,
                  complete sequence [Arabidopsis thaliana]
                  120533
Seq. No.
                  5148 1.R1010
Contig ID
5'-most EST
                  LIB22-012-Q1-E1-C9
                  120534
Seq. No.
                  5150 1.R1010
Contig ID
```

13278

jC-atXLIB327403P1h04b1

```
Method
                  BLASTX
NCBI GI
                  q3688173
BLAST score
                  471
E value
                  3.0e-47
Match length
                  137
% identity
                  65
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
                120535
Seq. No.
                  5154 1.R1010
Contig ID
5'-most EST
                  jC-atXP82CG2E11T7d3
                  120536
Seq. No.
                  5154 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327402P1g07b1
Seq. No.
                  120537
                  5160 1.R1010
Contig ID
                  LIB24-092-Q1-E1-A4
5'-most EST
                  BLASTX
Method
                  q3080427
NCBI GI
BLAST score
                  823
E value
                  2.0e-88
Match length
                  180
% identity
                  8.6
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                  120538
                  5161_1.R1010
Contig ID
                  jC-atX22012Q1E1E05b1
5'-most EST
Method
                  BLASTX
                  q4580575
NCBI GI
BLAST score
                  903
                  8.0e-98
E value
Match length
                  172
% identity
                  98
NCBI Description (AF082176) auxin response factor 9 [Arabidopsis thaliana]
Seq. No.
                  120539
                  5169 1.R1010
Contig ID
                  jC-atXLIB327440P1c03b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4589410
BLAST score
                  339
                  0.0e+00
E value
                  480
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F2015, complete sequence
                  120540
Seq. No.
                  5171 1.R1010
Contig ID
5'-most EST
                  LIB3176-069-P1-K1-C9
                  BLASTX
Method
NCBI GI
                  g2894561
BLAST score
                  610
E value
                  3.0e-63
```

Contig ID

```
Match length
                  136
                  79
% identity
                  (AL021890) putative protein [Arabidopsis thaliana]
NCBI Description
                  120541
Seq. No.
                  5173 1.R1010
Contig ID
                  LIB2\overline{2}-012-Q1-E1-F5
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4755189
BLAST score
                  396
E value
                  1.0e-38
Match length
                  102
                  75
% identity
NCBI Description (AC007018) putative cytochrome P450 [Arabidopsis thaliana]
                  120542
Seq. No.
                  5175 1.R1010
Contig ID
                  jC-atXLIB327440P4b12b2
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3335331
BLAST score
                   450
E value
                   0.0e + 00
Match length
                   457
                   100
% identity
                  Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   120543
                   5176 1.R1010
Contig ID
                   jC-atXLIB327422P1h10b1
5'-most EST
                   120544
Seq. No.
                   5179 1.R1010
Contig ID
                   LIB25-106-Q1-E1-H3
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4580732
BLAST score
                   292
E value
                   1.0e-163
Match length
                   362
% identity
                   100
                  Genomic sequence for Arabidopsis thaliana BAC F5J5,
NCBI Description
                   complete sequence
                   120545
Seq. No.
                   5180 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P2b01b2
Method
                   BLASTX
                   g2642433
NCBI GI
BLAST score
                   751
                   5.0e-80
E value
                   144
Match length
% identity
                   100
                   (AC002391) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   120546
Seq. No.
```

5182 1.R1010

```
5'-most EST
                    jC-atXLIB327419P2e02b2
  Seq. No.
                    120547
                    5183 1.R1010.
  Contig ID
. 5'-most EST
                    LIB3234-008-P1-K1-A11
 Seq. No.
                    120548
                    5185 1.R1010
  Contig ID
  5'-most EST
                    jC-atXLIB327440P1c12b1
  Method
                    BLASTX
  NCBI GI
                    g1903034
  BLAST score
                    394
  E value
                    4.0e-38
  Match length
                    128
  % identity
                    59
  NCBI Description
                    (X94625) amp-binding protein [Brassica napus]
                    120549
  Seq. No.
  Contig ID
                    5186_1.R1010
                    jC-atXLIB327406P2c12b1
  5'-most EST
  Method
                    BLASTN
  NCBI GI
                    q4589439
  BLAST score
                    187
  E value
                    1.0e-100
  Match length
                    245
  % identity
                    94
  NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MQM1, complete sequence
                    120550
  Seq. No.
  Contig ID
                    5187 1.R1010
  5'-most EST
                    LIB23-063-Q1-E1-E5
 Method
                    BLASTX
 NCBI GI
                    g3451072
 BLAST score
                    447
  E value
                    2.0e-44
 Match length
                    122
  % identity
                    67
 NCBI Description
                    (AL031326) putative protein [Arabidopsis thaliana]
  Seq. No.
                    120551
  Contig ID
                    5188 1.R1010
  5'-most EST
                    jC-atXLIB327419P4e01b1
 Method
                    BLASTN
 NCBI GI
                    q2582640
 BLAST score
                    66
 E value
                    3.0e-28
 Match length
                    78
                    97
  % identity
 NCBI Description
                    Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                    factor, RSp40
 Seq. No.
                    120552
 Contig ID
                    5188 2.R1010
 5'-most EST
                    g957637
 Seq. No.
                    120553
```

```
5189 1.R1010
 Contig ID
 5'-most EST
                   jC-atXP73C223E13T7d2
                   120554
 Seq. No.
                   5189 2.R1010
 Contig ID
                   jC-atXP12C102B8T7040a1
 5'-most EST
                   BLASTX
Method
                   g4432835
NCBI GI
BLAST score
                   267
                   4.0e-23
E value
Match length
                   90
 % identity
                   54
                   (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   120555
Seq. No.
Contig ID
                   5189 3.R1010
                   LIB2\overline{5}-070-Q1-E1-B9
 5'-most EST
Method
                   BLASTX
NCBI GI
                   q4432835
BLAST score
                   422
E value
                   4.0e-41
Match length
                   153
 % identity
                   52
NCBI Description
                   (AC006283) unknown protein [Arabidopsis thaliana]
                   120556
Seq. No.
Contig ID
                   5189 4.R1010
                   jC-atXLIB327432P2b10b2
 5'-most EST
Method
                   BLASTX
NCBI GI
                   q4432835
BLAST score
                   214
E value
                   5.0e-17
Match length
                   72
% identity
                   56
NCBI Description
                   (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                   120557
Contig ID
                   5192 1.R1010
 5'-most EST
                   iC-atXLIB327432P2b12b2
Method
                   BLASTN
NCBI GI
                   g2351069
BLAST score
                   183
E value
                   3.0e-98
Match length
                   503
% identity
                   99
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   120558
Contig ID
                   5192 2.R1010
5'-most EST
                   jC-atXLIB327418P1h09b1
Method
                   BLASTN
NCBI GI
                   g2351069
BLAST score
                   104
E value
                   4.0e-51
Match length
                   522
% identity
                   98
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                   MSH12, complete sequence [Arabidopsis thaliana]
                   120559
Seq. No.
                   5194 1.R1010
Contig ID
                   jC-atXLIB327428P4g07b2
5'-most EST
                   120560
Seq. No.
                   5195 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327423P2h03b1
Method
                   BLASTX
NCBI GI
                   g2244993
BLAST score
                   1259
E value
                   1.0e-139
Match length
                   248
% identity
                   96
                   (Z97341) similarity to AMP-activated protein kinase beta
NCBI Description
                   [Arabidopsis thaliana]
                   120561
Seq. No.
                   5196 1.R1010
Contig ID
5'-most EST
                   q930821
Method
                   BLASTX
                   q3157944
NCBI GI
                   753
BLAST score
E value
                   4.0e-80
                   159
Match length
                   92
% identity
                   (AC002131) Very strong similarity to aminomethyltransferase
NCBI Description
                   precursor gb_U79769 from Mesembryanthemum crystallinum.
                   ESTs gb T431\overline{6}7, gb T21076, gb H36999, gb T22773,
                   gb N380\overline{3}8, gb T137\overline{4}2, gb Z265\overline{4}5, gb T2075\overline{3} and gb W43123
                   come from this ge
                   120562
Seq. No.
                   5199 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327439P2h08b2
                   BLASTN
Method
                   g2351064
NCBI GI
BLAST score
                   192
E value
                   1.0e-103
                   560
Match length
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MDJ22, complete sequence [Arabidopsis thaliana]
                   120563
Seq. No.
                   5199 2.R1010
Contig ID
                   LIB24-071-Q1-E1-C10
5'-most EST
                   BLASTX
Method
NCBI GI
                   g113337
BLAST score
                   245
                   1.0e-20
E value
Match length
                   193
                   31
% identity
NCBI Description
                   ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2
                   ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C)
```

```
>gi 111367 pir S11276 alpha-adaptin c - rat
                    >gi 55729 emb CAA37791 (X53773) alpha-c large chain (AA
                    1-938) [Rattus norvegicus]
                    120564
Seq. No.
                    5199 3.R1010
 Contig ID
                    jC-atXLIB327413P4a07a1
 5'-most EST
 Method
                    BLASTN
 NCBI GI
                    q4519189
 BLAST score
                    267
 E value
                    1.0e-148
 Match length
                    311
 % identity
                    Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 NCBI Description
                    K5A21, complete sequence
 Seq. No.
                    120565
 Contig ID
                    5200 1.R1010
 5'-most EST
                    jC-atXP101CE1H8T7052d1
 Method
                    BLASTX
 NCBI GI
                    q1709006
 BLAST score
                    902
 E value
                    3.0e-97
 Match length
                    230
 % identity
                    80
                    S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
 NCBI Description
                    ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi 726032
                    (U17241) S-adenosylmethionine synthetase [Actinidia
                    chinensis]
                    120566
 Seq. No.
 Contig ID
                    5200 2.R1010
                    jC-atXLIB327431P1c05a1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    a3024127
                    1360
 BLAST score
 E value
                    1.0e-158
 Match length
                    313
                    87
 % identity
                    S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
 NCBI Description
                    ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                    >gi 1655578 emb CAA95857 (Z71272) S-adenosyl-L-methionine
                    synthetase 2 [Catharanthus roseus]
  Seq. No.
                    120567
                    5203 1.R1010
  Contig ID
  5'-most EST
                    jC-atXLIB327439P2h07b2
                    BLASTX
 Method
 NCBI GI
                    q2244952
 BLAST score
                    566
                    2.0e-64
 E value
 Match length
                    139
                    94
 % identity
                    (Z97340) strong similarity to ZK688.3 protein -
 NCBI Description
```

(PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT)

Caenorhabditis elegans [Arabidopsis thaliana]

```
120568
Seq. No.
                   5206 1.R1010
Contig ID
                   jC-a\(\bar{1}\)XLIB327436P4q01b1
5'-most EST
Method
                   BLASTX
                   g4220481
NCBI GI
BLAST score
                   370
                   6.0e-35
E value
                   142
Match length
                   54
% identity
NCBI Description
                  (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                   120569
                   5206 4.R1010
Contig ID
                   jC-a\overline{t}XP60C198A2T7051d1
5'-most EST
Method
                   BLASTX
                   q4220481
NCBI GI
BLAST score
                   212
                   1.0e-16
E value
Match length
                   82
% identity
                   51
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                  120570
                   5209 1.R1010
Contig ID
                  LIB22-013-Q1-E1-B1
5'-most EST
                   120571
Seq. No.
Contig ID
                   5210 1.R1010
                   jC-alXLIB327434P4g06b1
5'-most EST
Method
                   BLASTX
                   g4678349
NCBI GI
BLAST score
                   1245
E value
                   1.0e-137
                   290
Match length
% identity
                   35
NCBI Description (AL049659) putative protein [Arabidopsis thaliana]
                120572
Seq. No.
Contig ID
                   5210_2.R1010
5'-most EST
                  LIB22-013-Q1-E1-B10
                  BLASTX
Method
NCBI GI
                   q4678349
BLAST score
                   1015
E value
                   1.0e-110
Match length
                   256
% identity
                   21
NCBI Description
                  (AL049659) putative protein [Arabidopsis thaliana]
                   120573
Seq. No.
Contig ID
                   5214 1.R1010
5'-most EST
                  LIB22-013-01-E1-B4
Method
                  BLASTN
NCBI GI
                  q3985957
BLAST score
                   445
E value
                  0.0e + 00
Match length
                   453
% identity
                  100
```

BLAST score

```
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYN8, complete sequence [Arabidopsis thaliana]
                  120574
Seq. No.
                  5215 1.R1010
Contig ID
                  jC-atXLIB327440P4g07a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1531758
                  344
BLAST score
                  2.0e-32
E value
Match length
                  65
                  95
% identity
                  (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
NCBI Description
                  unknown protein [Arabidopsis thaliana]
Seq. No.
                  120575
                  5216 1.R1010
Contig ID
5'-most EST
                  jC-atXP8C92E2T7s1
                  BLASTN
Method
                  q3928074
NCBI GI
BLAST score
                  109
E value
                  4.0e-54
Match length
                  528
% identity
                  96
                  Arabidopsis thaliana chromosome II BAC T7F6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  120576
Seq. No.
                  5216 2.R1010
Contig ID
                  jC-atXLIB327413P4e09a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4006890
BLAST score
                  510
E value
                  2.0e-51
Match length
                  113
% identity
                  88
                  (Z99708) ubiquitin--protein ligase-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  120577
Seq. No.
                  5216 3.R1010
Contig ID
5'-most EST
                  LIB3175-059-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q4217999
BLAST score
                  381
E value
                  1.0e-46
Match length
                  167
                  73
% identity
                  (AC006135) putative ubiquitin--protein ligase
NCBI Description
                  (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
                  120578
Seq. No.
                  5216 4.R1010
Contig ID
                  g1053358
5'-most EST
                  BLASTX
Method
                  q4006890
NCBI GI
```

```
5.0e-15
E value
                   85
Match length
% identity
                    65
                    (Z99708) ubiquitin--protein ligase-like protein
NCBI Description
                    [Arabidopsis thaliana]
                    120579
Seq. No.
                    5220_1.R1010
Contig ID
                    jC-atXLIB327440P1a03b1
5'-most EST
                   BLASTX
Method
                    g2462825
NCBI GI
BLAST score
                    586
E value
                    9.0e-61
                    112
Match length
                    99
% identity
                   (AF000657) contains Procite 'RNP1' putative RNA-binding
NCBI Description
                   region [Arabidopsis thaliana]
                    120580
Seq. No.
                    5221_1.R1010
Contig ID
                    jC-atXLIB327440P1a08b1
5'-most EST
Method
                    BLASTX
                    g3785989
NCBI GI
BLAST score
                    721
E value
                    2.0e-76
Match length
                    163
                    87
% identity
                   (AC005560) unknown protein [Arabidopsis thaliana]
NCBI Description
                    120581
Seq. No.
                    5222 1.R1010
Contig ID
5'-most EST
                    jC-atXLIB327440Pla09b1
Method
                    BLASTX
NCBI GI
                    g1346422
BLAST score
                    153
                    8.0e-10
E value
Match length
                    91
% identity
                    37
                   SERINE PALMITOYLTRANSFERASE 2 (LONG CHAIN BASE BIOSYNTHESIS
NCBI Description
                   PROTEIN 2) (SPT 2) >gi_2130481_pir__JC5183 serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission
                    yeast (Schizosaccharomyces pombe) >gi_1001947 (U15645)
                    serine palmitoyltransferase [Schizosaccharomyces pombe]
                    >gi 2414613_emb_CAB16362_ (Z99259) serine
                    palmitoyltransferase 2 [Schizosaccharomyces pombe]
                    120582
Seq. No.
                    5223 1.R1010
Contig ID
                    jC-atX22014Q1E1C06b1
5'-most EST
                    120583
Seq. No.
                    5225 1.R1010
Contig ID
                    jC-atX22013Q1E1C01b1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q4567091
                    260
BLAST score
                    4.0e-41
E value
```

NCBI GI.

q549060

```
Match length
                  182
% identity
                  47
                  (AF128443) SNF-1-like serine/threonine protein kinase
NCBI Description
                  [Glycine max]
Seq. No.
                  120584
                  5227 1.R1010
Contig ID
                  LIB22-073-Q1-E1-H8
5'-most EST
Method
                  BLASTX
                  q4006918
NCBI GI
BLAST score
                  342
                  3.0e-32
E value
Match length
                  105
% identity
                  66
                  (Z99708) peroxidase like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  120585
                  5229 1.R1010
Contig ID
                  LIB3175-059-P1-K1-A6
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2618602
BLAST score:
                  216
E value
                  1.0e-118
Match length
                  459
% identity
                  99 .
                  Arabidopsis thaliana genomic DNA, chromosome 5, Placelone:
NCBI Description
                  MSJ1, complete sequence [Arabidopsis thaliana]
                  120586
Seq. No.
                  5230 1.R1010
Contig ID
                  LIB3175-033-P1-K1-E10
5'-most EST
Method
                  BLASTX
                  g1750376
NCBI GI
BLAST score
                  969
E value
                  1.0e-105
Match length
                  192
% identity
                  95
NCBI Description (U80808) ubiquitin activating enzyme [Arabidopsis thaliana]
                  >qi 3150409 (AC004165) ubiquitin activating enzyme (UBA1)
                   [Arabidopsis thaliana]
                  120587
Seq. No.
                  5241 1.R1010
Contig ID
                  LIB22-013-Q1-E1-E10
5'-most EST
Method
                  BLASTX
                  g3252806
NCBI GI
BLAST score
                  193
                  1.0e-14
E value
Match length
                  114
% identity
                  (AC004705) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  120588
Seq. No.
                  5244 1.R1010
Contig ID
                  LIB2\overline{3}-007-Q1-E1-B8
5'-most EST
                  BLASTX
Method
```

```
BLAST score
                  545
E value
                  1.0e-55
Match length
                  179
% identity
                  60
NCBI Description
                  T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
                  >gi_631656_pir__S43058 CCTeta protein eta chain - mouse
                  >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta_subunit of
                  the chaperonin containing TCP-1 (CCT) [Mus musculus]
Seq. No.
                  120589
                  5245 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327440P1b06b1
Method
                  BLASTX
NCBI GI
                  q3513727
BLAST score
                  708
E value
                  8.0e-75
Match length
                  183
% identity
                  79
NCBI Description
                  (AF080118) contains similarity to TPR domains (Pfam:
                  TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
                  kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis
                  thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative
                  protein [Arabidopsis thaliana]
                  120590
Seq. No.
                  5246 1.R1010
Contig ID
5'-most EST
                  LIB22-013-01-E1-E4
Method
                  BLASTX
NCBI GI
                  g2191150
BLAST score
                  484
E value
                  2.0e-48
Match length
                  117
% identity
                  88
NCBI Description
                   (AF007269) similar to mitochondrial carrier family
                   [Arabidopsis thaliana]
Seq. No.
                  120591
Contig ID
                  5247 1.R1010
5'-most EST
                  LIB3234-075-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g4510342
BLAST score
                  273
E value
                  7.0e-24
Match length
                  180
% identity
                  44
NCBI Description
                  (AC006921) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  120592
Contig ID
                  5249 1.R1010
5'-most EST
                  iC-atXP125C134D23T7d1
Method
                  BLASTX
NCBI GI
                  g629692
BLAST score
                  513
E value
                  4.0e-52
Match length
                  120
% identity
                  82
```

NCBI GI

```
NCBI Description hypothetical protein - common tobacco
                   >qi 506471 emb CAA56189 (X79794) unnamed protein product
                   [Nicotiana tabacum]
Seq. No.
                   120593
                   5251 1.R1010
 Contig ID
                   jC-atX22014Q1E1E11b1
 5'-most EST
Method
                   BLASTN
 NCBI GI
                   g3928074
 BLAST score
                   137
 E value
                   1.0e-70
                   777
Match length
 % identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T7F6 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   120594
                   5252 1.R1010
 Contig ID
                   jC-atXLIB327432P2a04b2
 5'-most EST
                   BLASTX
Method
 NCBI GI
                   q2388582
BLAST score
                   713
 E value
                   1.0e-75
· Match length
                   139
 % identity
                   (AC000098) Contains similarity to Rattus O-GlcNAc
NCBI Description
                   transferase (gb U76557). [Arabidopsis thaliana]
                   120595
Seq. No.
                   5254_1.R1010
 Contig ID
 5'-most EST
                   LIB22-013-Q1-E1-F12
Method
                   BLASTN
NCBI GI
                   q4757395
BLAST score
                   193
                   1.0e-104
E value
Match length
                   390
                   98
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K21L13, complete sequence
Seq. No.
                   120596
 Contig ID
                   5255 1.R1010
 5'-most EST
                   jC-atX22072Q1E1B04b1
Method
                   BLASTX
NCBI GI
                   q2281649
BLAST score
                   732
E value
                   2.0e-77
Match length
                   140
                   97
 % identity
NCBI Description
                   (AF003105) AP2 domain containing protein RAP2.12
                   [Arabidopsis thaliana]
                   120597
Seq. No.
Contig ID
                   5256 1.R1010
 5'-most EST
                   q1217489
Method
                   BLASTN
```

q4589437

```
BLAST score
                  151
                  3.0e-79
E value
Match length
                  325
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MPN9, complete sequence
                  120598
Seq. No.
Contig ID
                  5263 1.R1010
5'-most EST
                  jC-atX22013Q1E1G06b2
Method
                  BLASTN
NCBI GI
                  q3869069
BLAST score
                  271
E value
                  1.0e-151
Match length
                  456
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120599
                  5264 1.R1010
Contig ID
5'-most EST
                  q244\overline{5}978
Method
                  BLASTX
NCBI GI 🐣
                  q2108252
                  59
BLAST score
                  2.0e-33
E value
Match length
                  113
% identity
                  32
                  (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
                  >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
                   [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
                   (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
                  120600
Seq. No.
Contig ID
                  5264_3.R1010
                  jC-atXP125C136F23T7d1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2108252
BLAST score
                  716
E value
                  8.0e-78
Match length
                  246
% identity
                  32
                  (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
                  >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
                   [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
                   (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
Seq. No.
                  120601
Contig ID
                  5271 1.R1010
5'-most EST
                  jC-atXLIB327432P3a03b1
Method
                  BLASTN
NCBI GI
                  q2582640
BLAST score
                  68
E value
                  1.0e-29
Match length
                  76
% identity
                  97
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
```

factor, RSp40 120602 Seq. No. 5272 1.R1010 Contig ID jC-a\(\bar{1}\)XLIB327435P2f11a1 5'-most EST Method BLASTX q4406775 NCBI GI 264 BLAST score 2.0e-22 E value Match length 128 % identity 41 (AC006836) unknown protein [Arabidopsis thaliana] NCBI Description 120603 Seq. No. 5273_1.R1010 Contig ID LIB22-086-Q1-E1-F12 5'-most EST Method BLASTX g2088651 NCBI GI BLAST score 413 4.0e-40 E value Match length 168 53 % identity NCBI Description (AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana] 120604 Seq. No. 5275_1.R1010 Contig ID $LIB2\overline{3}-055-Q1-E1-G5$ 5'-most EST 120605 Seq. No. Contig ID 5278_1.R1010 5'-most EST jC-atXLIB327432P2b09b1 Method BLASTN g2618677 NCBI GI BLAST score 334 E value 0.0e + 00334 Match length % identity 100 NCBI Description Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana] 120606 Seq. No.

Contig ID 5279 1.R1010 5'-most EST jC-a1X22044Q1E1D01b1

Method BLASTN NCBI GI q2191157 BLAST score 490 E value 0.0e + 00Match length 490 % identity 100

NCBI Description Arabidopsis thaliana BAC IG002P16

120607 Seq. No. Contig ID 5282 1.R1010 5'-most EST ARABL1-041-Q1-B1-C7 Method BLASTX

NCBI GI q4758520

Contig ID

```
BLAST score
                   168
E value
                   2.0e-11
Match length
                   174
% identity
NCBI Description
                  hect domain and RLD 2 > gi 4079809 gb AAD08657.1 (AF071172)
                   HERC2 [Homo sapiens]
Seq. No.
                   120608
                   5283 1.R1010
.Contig ID
                   jC-atXLIB327406P1g01b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3377820
                   501
BLAST score
E value
                   1.0e-50
Match length
                   102
% identity
                   99
                   (AF076275) contains similarity to coatomer zeta chains
NCBI Description
                   [Arabidopsis thaliana]
                   120609
Seq. No.
Contig ID
                   5286_1.R1010
5'-most EST
                  LIB22-014-Q1-E1-A3
Method
                  BLASTN
NCBI GI
                   q2351062
BLAST score
                   421
E value
                   0.0e + 00
Match length
                   425
% identity
                   100 '
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAH20, complete sequence [Arabidopsis thaliana]
                   120610
Seq. No.
                   5287 1.R1010
Contig ID
5'-most EST
                   jC-atX22013Q1E1A11b1
Method
                   BLASTN
NCBI GI
                   q2853071
BLAST score
                   304
E value
                   1.0e-171
Match length
                   328
% identity
                   98
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7
NCBI Description
                   (ESSA project)
Seq. No.
                   120611
                   5288 1.R1010
Contig ID
5'-most EST
                   jC-atXP118C153P17T7086d2
Method
                   BLASTN
NCBI GI
                   g4521999
BLAST score
                   309
E value
                  1.0e-173
Match length
                   958
                   99
% identity
                  Arabidopsis thaliana chromosome II BAC F2G1 genomic
NCBI Description
                  sequence, complete sequence
                   120612
Seq. No.
```

5288 2.R1010

Seq. No.

```
5'-most EST
                  jC-atXLIB327412P3c01b1
Method
                  BLASTN
NCBI GI
                  g4521999
BLAST score
                  221
E value
                  1.0e-121
                  509
Match length
% identity
                  97
                  Arabidopsis thaliana chromosome II BAC F2G1 genomic
NCBI Description
                  sequence, complete sequence
                  120613
Seq. No.
                  5291 1.R1010
Contig ID
                  LIB22-014-Q1-E1-B1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4678301
BLAST score
                  381
                  1.0e-36
E value
Match length
                  128
                  56
% identity
                   (AL049655) pectate lyase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  120614
Seq. No.
                  5293 1.R1010
Contig ID
                  LIB3175-068-P1-K1-F5
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4115377
BLAST score
                  917
                  4.0e-99
E value
Match length
                  246
% identity
                  73
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  120615
                  5295 1.R1010
Contig ID
                  LIB22-014-Q1-E1-B2
5'-most EST
Seq. No.
                  120616
                  5298 1.R1010
Contig ID
                  g241\overline{4}023
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3335340
BLAST score
                  554
E value
                  1.0e-56
Match length
                  135
% identity
                  76
NCBI Description
                  (AC004512) Strong similarity to xylglucan
                  endo-transglycolsylase (TCH4) gene gb U27609, first exon
                  contains strong similarity to meri 5 gene gb Z17989 from A.
                  thaliana. EST gb N37583 comes from this gene. [Arabidopsis
                  thaliana]
                  120617
Seq. No.
                  5298 2.R1010
Contig ID
5'-most EST
                  LIB25-098-Q1-E1-C6
```

```
5299 1.R1010
Contig ID
5'-most EST
                   jC-atXP73C224D1T7b1
                   BLASTX
Method
                   g3193285
NCBI GI
BLAST score
                   782
                   3.0e-83
E value
Match length
                   167
% identity
                   92
                   (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120619
                   5299 2.R1010
Contig ID
                   jC-atXLIB327430P4b04b1
5'-most EST
Method
                   BLASTX
                   g3193285
NCBI GI
BLAST score
                   491
E value
                   2.0e-49
Match length
                   109
% identity
                   91
                   (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120620
                   5299 3.R1010
Contig ID
                   jC-atXLIB327421P1g06a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3193282
BLAST score
                   300
E value
                   1.0e-168
Match length
                   412
% identity
                   89
NCBI Description
                   Arabidopsis thaliana BAC T14P8
Seq. No.
                   120621
Contig ID
                   5303 1.R1010
5'-most EST
                   LIB22-014-Q1-E1-C1
Method
                   BLASTX
NCBI GI
                   q113742
BLAST score
                   381
E value
                   9.0e-37
Match length
                   131
% identity
                   53
                   AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE)
NCBI Description
                   >gi_147142 (M15273) peptidase N [Escherichia coli]
>gi_147144 (M15676) aminopeptidase N [Escherichia coli]
                   >gi_1787163 (AE000195) aminopeptidase N [Escherichia coli]
                   >gi_4062498_dbj_BAA35684_ (D90731) Aminopeptidase n (EC
                   3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia
                   coli]
Seq. No.
                   120622
                   5304 1.R1010
Contig ID
                   jC-atXLIB327421P2b07b1
5'-most EST
Method
                   BLASTN
                   g2760164
NCBI GI
BLAST score
                   308
                   1.0e-172
E value
Match length
                   681
```

Method

BLASTX

```
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18P6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120623
                  5305 1.R1010
Contig ID
                  jC-atXLIB327406P3g10b2
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4580745
BLAST score
                  399
E value
                  0.0e + 00
Match length
                  415
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
                  complete sequence
Seq. No.
                  120624
Contig ID
                  5306 1.R1010
5'-most EST
                  LIB22-051-Q1-E1-G5
Method
                  BLASTX
NCBI GI
                  q2499115
BLAST score
                  267
E value
                  2.0e-23
Match length
                  67
                  79
% identity
                  VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >qi 1835788
NCBI Description
                  (U86662) VPS41 [Lycopersicon esculentum]
Seq. No.
                  120625
                  5307 1.R1010
Contig ID
5'-most EST
                  LIB3175-003-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  q3335356
BLAST score
                  334
E value
                  0.0e + 00
Match length
                  441
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120626
Contig ID
                  5308_1.R1010
5'-most EST
                  LIB25-001-Q1-E2-F2
Method
                  BLASTX
NCBI GI
                  q4415907
BLAST score
                  571
E value
                  1.0e-58
Match length
                  139
% identity
NCBI Description
                  (AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana]
                  >gi_4581159_gb_AAD24643.1_AC006919 21 (AC006919) putative
                  60S ribosomal protein L24 [Arabidopsis thaliana]
                  120627
Seq. No.
                  5308 2.R1010
Contig ID
                  jC-atXLIB327440P1a04b1
5'-most EST
```

% identity

```
NCBI GI
                   q3413706
BLAST score
                   177
E value
                   9.0e-13
Match length
                   68
                   44
% identity
NCBI Description
                   (AC004747) hypothetical protein [Arabidopsis thaliana]
                   120628
Seq. No.
Contig ID
                   5311 1.R1010
5'-most EST
                   jC-atXLIB327440P1a06b1
Seq. No.
                   120629
                   5312 1.R1010
Contig ID
                   LIB22-014-Q1-E1-C8
5'-most EST
                   BLASTX
Method
NCBI GI
                   g283004
BLAST score
                   323
                   6.0e-30
E value
                   131
Match length
% identity
                   30
                  DNA-binding protein Gt-2 - rice >gi_20249_emb_CAA48328
NCBI Description
                   (X68261) gt-2 [Oryza sativa]
Seq. No.
                   120630
Contig ID
                   5314_1.R1010
                   LIB22-014-Q1-E1-D1
5'-most EST
Method
                   BLASTX
                  q1076414
NCBI GI
                   375
BLAST score
                   9.0e-36
E value
                   148
Match length
% identity
                   48
NCBI Description
                   subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis
                   thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974)
                   subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                   120631
Contig ID
                   5317 1.R1010
                   jC-atXLIB327440P4a11b2
5'-most EST
                   BLASTN
Method
                   q4589420
NCBI GI
                   423
BLAST score
                   0.0e + 00
E value
Match length
                   423
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K3G17, complete sequence
Seq. No.
                   120632
Contig ID
                   5318_1.R1010
5'-most EST
                  jC-atXLIB327412P3b06b1
Method
                  BLASTX
NCBI GI
                 · q82263
BLAST score
                  1087
E value
                  1.0e-119
                  284
Match length
```

```
NCBI Description ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
                  c1 precursor (clone pC(1)3II) - potato
                  120633
Seq. No.
                  5318 2.R1010
Contig ID
                  g934704
5'-most EST
                  BLASTX
Method
                  g82263
NCBI GI
                   556
BLAST score
                  8.0e-57
E value
                  164
Match length
                   68
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                  cl precursor (clone pC(1)3II) - potato
                  120634
Seq. No.
                  5318 3.R1010
Contig ID
                  jC-atXLIB327422P3e03b2
5'-most EST
                  BLASTX
Method
                  q231924
NCBI GI
BLAST score
                  250
                   4.0e-21
E value
                   49
Match length
                  92
% identity
NCBI Description CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC181)
                  120635
Seq. No.
                  5318 4.R1010
Contig ID
                  q2062830
5'-most EST
                  BLASTN
Method
NCBI GI
                  q2462264
BLAST score
                  39
E value
                  3.0e-12
                   43
Match length
% identity
                  98
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  120636
Seq. No.
                  5318 5.R1010
Contig ID
                   jC-atXLIB327440P4a05b2
5'-most EST
                  BLASTX
Method
                  g82263
NCBI GI
BLAST score
                   761
                   8.0e-81
E value
                  173
Match length
% identity
                   80
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                  c1 precursor (clone pC(1)3II) - potato
                  120637
Seq. No.
                   5318 6.R1010
Contig ID
5'-most EST
                   jC-a\overline{1}XLIB327435P2f08a1
Method
                  BLASTX
                  q82263
NCBI GI
BLAST score
                  586
E value
                  2.0e-60
                  131
Match length
```

Method

BLASTX

```
85
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                  cl precursor (clone pC(1)3II) - potato
Seq. No.
                  120638
                  5319 1.R1010
Contig ID
                  jC-atXLIB327440P4a06b2
5'-most EST
                  BLASTN
Method
NCBI GI
                  q4220633
BLAST score
                  35
E value
                  5.0e-10
Match length
                  131
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K7J8, complete sequence [Arabidopsis thaliana]
                  120639
Seq. No.
                  5321 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327440P4a07b2
Method
                  BLASTX
NCBI GI
                  q1360088
BLAST score
                  316
E value
                  6.0e-29
Match length
                  62
% identity
                  89
NCBI Description
                  (X97947) Zn finger protein [Nicotiana tabacum]
Seq. No.
                  120640
                  5322 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327440P4a08b2
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  25
E value
                  7.0e-04
Match length
                  36
% identity
                  60
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  120641
Contig ID
                  5322 2.R1010
5'-most EST
                  LIB3176-074-P1-K1-E4
                  120642
Seq. No.
Contig ID
                  5324 1.R1010
5'-most EST
                  LIB23-040-Q1-E1-F8
                  BLASTX
Method
NCBI GI
                  q1806628
BLAST score
                  201
                  2.0e-15
E value
Match length
                  73
% identity
                  63
                  (U79250) glycerol-3-phosphate dehydrogenase [Homo sapiens]
NCBI Description
                  120643
Seq. No.
Contig ID
                  5326_1.R1010
                  LIB22-014-Q1-E1-E10
5'-most EST
```

```
NCBI GI
                   q2827524
BLAST score
                   249
E value
                   6.0e-23
Match length
                   137
% identity
                   44
                   (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                   120644
Seq. No.
                   5327 1.R1010
Contig ID
                   LIB2\overline{2}-014-Q1-E1-E11
5'-most EST
                   120645
Seq. No.
                   5328 1.R1010
Contig ID
5'-most EST
                   LIB3168-032-P1-K1-G2
                   BLASTX
Method
NCBI GI
                   g2499535
BLAST score
                   205
                   7.0e-16
E value
Match length
                   62
% identity
                   66
NCBI Description
                   2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >qi 595681
                   (U13238) 2-oxoglutarate/malate translocator [Spinacia
                   oleracea]
                   120646
Seq. No.
                   5330 1.R1010
Contig ID
5'-most EST
                   LIB35-025-Q1-E1-B2
Method
                   BLASTN
NCBI GI
                   g3985952
BLAST score
                   281
E value
                   1.0e-157
Match length
                   418
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MRC8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   120647
                   5331 1.R1010
Contig ID
                   LIB2\overline{2}-014-Q1-E1-E4
5'-most EST
                   BLASTN
Method
                   g4589434
NCBI GI
BLAST score
                   311
E value
                   1.0e-175
Match length
                   331
                   98
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MNJ7, complete sequence
Seq. No.
                   120648
                   5332 1.R1010
Contig ID
5'-most EST
                   jC-alXLIB327436P1d11b1
Method
                   BLASTX
NCBI GI
                   g4539457
BLAST score
                   449
                   1.0e-44
E value
Match length
                   105
                   78
% identity
```

```
NCBI Description (ALO49500) heat shock transcription factor-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  120649
                  5335 1.R1010
Contig ID
                  jC-atXP85C241M19T7b1
5'-most EST
                  BLASTX
Method
                  g1718097
NCBI GI
                  798
BLAST score
                  4.0e-85
E value
                  249
Match length
% identity
                  59
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                  (41 KD ACCESSORY PROTEIN) (DVA41) >qi 626048 pir A55016
                  lysosomal membrane protein DVA41 - slime mold
                  (Dictyostelium discoideum) >gi 532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]
                  120650
Seq. No.
                  5335 2.R1010
Contig ID
5'-most EST
                  q2747439
Method
                  BLASTX
NCBI GI
                  q1718097
BLAST score
                  219
E value
                  2.0e-17
Match length
                  115
% identity
                  41
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                  (41 KD ACCESSORY PROTEIN) (DVA41) >gi 626048 pir A55016
                  lysosomal membrane protein DVA41 - slime mold
                  (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]
                  120651
Seq. No.
                  5335_3.R1010
Contig ID
                  g2733743
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1718097
BLAST score
                  640
E value
                  9.0e-67
Match length
                  187
% identity
NCBI Description
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
                  (41 KD ACCESSORY PROTEIN) (DVA41) >gi 626048 pir A55016
                  lysosomal membrane protein DVA41 - slime mold
                  (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]
Seq. No.
                  120652
                  5335 5.R1010
Contig ID
                  LIB22-014-01-E1-E8
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1718097
BLAST score
                  363
                  1.0e-34
E value
Match length
                  104
% identity
                  62
```

```
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
                   (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016
                   lysosomal membrane protein DVA41 - slime mold
                   (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar
                   ATPase subunit DVA41 [Dictyostelium discoideum]
                   120653
Seq. No.
                   5337 1.R1010
Contig ID
                  jC-a\overline{t}XP61C199N1T7d1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q531832
BLAST score
                   41
                   2.0e-13
E value
Match length
                   56
                   95
% identity
NCBI Description Cloning vector pSport2, complete sequence
                  120654
Seq. No.
Contig ID
                   5338 1.R1010
5'-most EST
                  g510789
Method
                  BLASTX
NCBI GI
                  g2865623
BLAST score
                   519
E value
                  1.0e-52
Match length
                  132
% identity
                  83
NCBI Description
                   (AF045286)
                  GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                   [Arabidopsis thaliana]
                  120655
Seq. No.
                   5339_1.R1010
Contig ID
5'-most EST
                  LIB22-014-Q1-E1-F11
                  BLASTX
Method
NCBI GI
                  g2252828
BLAST score
                   377
                  3.0e-36
E value
Match length
                  123
% identity
                   67
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
                  120656
Seq. No.
Contig ID
                  5342_1.R1010
5'-most EST
                  LIB22-014-Q1-E1-F4
                  120657
Seq. No.
Contig ID
                  5343 1.R1010
5'-most EST
                  LIB22-014-Q1-E1-F5
Method
                  BLASTN
                  g3402695
NCBI GI
BLAST score
                  56
E value
                  2.0e-22
Match length
                  151
% identity
                  89
NCBI Description Arabidopsis thaliana chromosome II BAC T3K9 genomic
```

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No:
                   120658
                   5344 1.R1010
Contig ID
5'-most EST
                   jC-alXLIB327436P3g09b1
Method
                   BLASTX
NCBI GI
                   g2388585
BLAST score
                   551
                   2.0e-56
E value
Match length
                   126
% identity
                   88
                   (AC000098) Similar to Caenorhabditis unknown protein
NCBI Description
                   T03F1.1 (gb U88169). [Arabidopsis thaliana]
                   120659
Seq. No.
                   5345 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P2a02b2
Method
                   BLASTX
NCBI GI
                   g3540184
BLAST score
                   747
E value
                   1.0e-79
Match length
                   142
% identity
                   100
NCBI Description
                  (AC004122) Similar to endoxylanases [Arabidopsis thaliana]
                   120660
Seq. No.
                   5346 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327409P1e09b1
Method
                   BLASTX
NCBI GI
                   g2911042
BLAST score
                   1307
E value
                   1.0e-145
Match length
                   262
% identity
                   100
NCBI Description
                   (AL021961) Phosphoglycerate dehydrogenase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   120661
                  5347_1.R1010
LIB22-018-Q1-E1-A7
Contig ID
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4586098
BLAST score
                   272
                   1.0e-151
E value
Match length
                   288
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
                   (ESSA project)
Seq. No.
                   120662
Contig ID
                   5349 1.R1010
                   LIB22-014-Q1-E1-G11
5'-most EST
Method
                  BLASTN
NCBI GI
                   q2462264
BLAST score
                   50
E value
                   1.0e-18
                   54
Match length
                   98
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
```

5'-most EST

```
120663
 Seq. No.
                    5349 2.R1010
 Contig ID
                    jC-atXLIB327440P1c08b1
 5'-most EST
                    BLASTN
 Method
 NCBI GI
                    q2582640
 BLAST score
                    68
 E value
                    1.0e-29
 Match length
                    76
 % identity
                    97
 NCBI Description
                    Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                    factor, RSp40
                    120664
Seq. No.
                    5350 1.R1010
 Contig ID
 5'-most EST
                    jC-aIXLIB327436P1e07b1
 Method
                    BLASTX
 NCBI GI
                    q2500347
 BLAST score
                    434
                    1.0e-42
 E value
 Match length
                    128
 % identity
                    70
 NCBI Description
                    NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG
                    >gi_3878691_emb_CAA90127_ (Z49911) similar to ribosomal
                    protein (L7AE family); cDNA EST EMBL:D73957 comes from this
                    gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST
                    EMBL:D74077 comes from this gene; cDNA EST EMBL:D71393
                    comes from this gene; cD
                    120665
 Seq. No.
                    5352_1.R1010
 Contig ID
                    jC-aTX22014Q1E1G09b1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q3600059
 BLAST score
                    761
 E value
                    3.0e-81
 Match length
                    142
                    100
 % identity
                    (AF080120) contains similarity to WB domains, G-beta
 NCBI Description
                    repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03)
                    [Arabidopsis thaliana]
 Seq. No.
                    120666
                    5355 1.R1010
 Contig ID
 5'-most EST
                    LIB3168-011-P1-K1-E1
 Method
                    BLASTX
 NCBI GI
                    q2341032
 BLAST score
                    295
 E value
                    2.0e-26
 Match length
                    92
                    74
 % identity
                    (AC000104) EST qb ATTS0956 comes from this gene.
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    120667
                    5357 1.R1010
 Contig ID
```

 $LIB2\overline{2}-054-Q1-E2-A12$

Seq. No.

Contig ID

120672

5365 1.R1010

```
Method
                   BLASTN
NCBI GI
                   q4580454
BLAST score
                   653
                   0.0e+00
E value
Match length
                   661
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC T2G17 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   120668
                   5361 1.R1010
Contig ID
                   jC-atX22014Q1E1H12b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3395938
BLAST score
                   638
E value
                   2.0e-66
Match length
                   166
% identity
                   40
NCBI Description
                   (AF076924) polypyrimidine tract-binding protein homolog
                   [Arabidopsis thaliana]
Seq. No.
                   120669
Contig ID
                   5362 1.R1010
                  jC-atXLIB327440P4d04b2
5'-most EST
Method
                  BLASTN
NCBI GI
                   q2244991
BLAST score
                   194
E value
                   1.0e-105
Match length
                   456
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                   120670
                   5363 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327431P3e12a1
Method
                  BLASTX
NCBI GI
                   q4580461
BLAST score
                   1136
E value
                   1.0e-125
Match length
                  262
% identity
NCBI Description
                  (AC006081) unknown protein [Arabidopsis thaliana]
Seq. No.
                   120671
Contig ID
                   5364 1.R1010
5'-most EST
                  jC-atX22014Q1E1H04b1
Method
                  BLASTX
NCBI GI
                  q4467156
BLAST score
                  954
E value
                  1.0e-103
Match length
                  247
% identity
                  70
NCBI Description
                  (AL035540) putative protein [Arabidopsis thaliana]
```

NCBI Description

```
jC-alXLIB327436P3f03b1
 5'-most EST
 Method
                    BLASTX
                    g832876
· NCBI GI
 BLAST score
                    739
 E value
                    3.0e-78
 Match length
                    251
 % identity
                    63
                    (L41345) ascorbate free radical reductase [Solanum
 NCBI Description
                    lycopersicum] >gi 1097368 prf 2113407A ascorbate free
                    radical reductase [Lycopersicon esculentum]
                    120673
 Seq. No.
                    5368 1.R1010
 Contig ID
                    LIB22-026-Q1-E1-E11
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g2464913
 BLAST score
                    591
 E value
                    3.0e-61
 Match length
                    120
 % identity
                    99
 NCBI Description
                    (299708) sugar transporter like protein [Arabidopsis
                    thaliana]
 Seq. No.
                    120674
                    5370 1.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327432P3b08b1
 Method
                    BLASTX
 NCBI GI
                    g2894607
 BLAST score
                    368
 E value
                    4.0e-35
 Match length
                    82
 % identity
                    82
                    (ALO21889) NAM (no apical meristem) - like protein
 NCBI Description
                    [Arabidopsis thaliana]
                    120675
 Seq. No.
                    5374 1.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327421P3c05b1
 Method
                    BLASTN
                    q4406805
 NCBI GI
                    375
 BLAST score
                    0.0e+00
 E value
 Match length
                    525
 % identity
                    100
                    Arabidopsis thaliana chromosome II BAC T27K22 genomic
 NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
                    120676
 Seq. No.
                    5377 1.R1010
 Contig ID
                    LIB22-015-Q1-E1-C10
 5'-most EST
                    BLASTX
 Method
                    g4185141
 NCBI GI
 BLAST score
                    489
                    5.0e-49
 E value
 Match length
                    154
                    73
 % identity
```

(AC005724) putative calmodulin-binding protein [Arabidopsis

thaliana] 120677 Seq. No. 5377_3.R1010 Contig ID LIB25-043-Q1-E1-C2 5'-most EST Method BLASTN NCBI GI q4539290 BLAST score 76 E value 1.0e-34 Match length 267 % identity 94 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project) Seq. No. 120678 Contig ID 5380 1.R1010 jC-atXLIB327416P3f11b1 5'-most EST BLASTX Method NCBI GI q4581146 BLAST score 1375 E value 0.0e + 00Match length 358 % identity 91 (AC006919) putative fructose-bisphosphate aldolase, NCBI Description cytoplasmic [Arabidopsis thaliana] 120679 Seq. No. 5380 2.R1010 Contig ID 5'-most EST jC-alXLIB327436P3a12b1 Seq. No. 120680 Contig ID 5380_3.R1010 5'-most EST q935024 Method **BLASTX** NCBI GI q4581146 BLAST score 308 E value 4.0e-28 Match length 125 % identity 62 NCBI Description (AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana] Seq. No. 120681 5380 4.R1010 Contig ID $g272\overline{2}544$ 5'-most EST Method BLASTX NCBI GI q1168410 BLAST score 423 E value 2.0e-41 Match length 105 % identity 83 FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2 NCBI Description >gi_2118267_pir__S58167 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi 927505 emb CAA61947 (X89829) fructose-1,6-bisphosphate aldolase [Pisum sativum]

120682

Seq. No.

```
5380 5.R1010
Contig ID
                  LIB3176-109-P1-K1-C2
5'-most EST
                  BLASTX
Method
                  q4581146
NCBI GI
                  354
BLAST score
E value
                  2.0e-33
                  88 -
Match length
                  81
% identity
                  (AC006919) putative fructose-bisphosphate aldolase,
NCBI Description
                  cytoplasmic [Arabidopsis thaliana]
Seq. No.
                  120683
Contig ID
                  5381 1.R1010
5'-most EST
                  jC-a1X24077Q1E1G07b1
                  BLASTX
Method
NCBI GI
                  q4204268
BLAST score
                  815
                  2.0e-87
E value
                  148
Match length
% identity
                  100
                  (AC005223) 62134 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  120684
                  5382_1.R1010
Contig ID
                  jC-aTXLIB327422P1b11b1
5'-most EST
Method
                  BLASTX
                  g4582459
NCBI GI
BLAST score
                  453
                  6.0e-45
E value
                  143
Match length
% identity
                  66
                  (AC007071) putative RanBP7/importin protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  120685
Contig ID
                  5385 1.R1010
5'-most EST
                  jC-atXLIB327420P4a07b1
Seq. No.
                  120686
                  5387 1.R1010
Contig ID
5'-most EST
                  jC-atXP112C132G21T7d2
Method
                  BLASTN
NCBI GI
                  q3212846
BLAST score
                  271
                  1.0e-150
E value
                  700
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  120687
Seq. No.
Contig ID
                  5388 1.R1010
5'-most EST
                  jC-atXP87CG8H8T7b1
                                                                           , g = 1
Seq. No.
                  120688
Contig ID
                  5389 1.R1010
                  LIB25-104-Q1-E1-B9
5'-most EST
```

```
Method
                  BLASTN
NCBI GI
                  q4519193
BLAST score
                  324
E value
                  0.0e+00
Match length
                  360
% identity
                  62
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MDC11, complete sequence
Seq. No.
                  120689
Contig ID
                  5390 1.R1010
5'-most EST
                  jC-atX22015Q1E1F09b1
Method
                  BLASTN
NCBI GI
                  q4589410
BLAST score
                  183
E value
                  2.0e-98
Match length
                  321
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F2015, complete sequence
Seq. No.
                  120690
Contig ID
                  5391_1.R1010
5'-most EST
                  jC-atXP65C206L14T7057d1
                  BLASTN
Method
NCBI GI
                  q4220638
BLAST score
                  69
E value
                  3.0e - 30
Match length
                  407
% identity
                  81
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIF21, complete sequence [Arabidopsis thaliana]
                  120691
Seq. No.
Contig ID
                  5391 2.R1010
5'-most EST
                  jC-atXLIB327432P4d08b1
                  BLASTN
Method
NCBI GI
                  q4220638
BLAST score
                  49
E value
                  3.0e-18
Match length
                  206
                  84
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIF21, complete sequence [Arabidopsis thaliana]
                  120692
Seq. No.
Contig ID
                  5393_1.R1010
                  LIB22-015-Q1-E1-G9
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4572675
BLAST score
                  162
E value
                  4.0e-11
Match length
                  97
% identity
                  53
NCBI Description
                  (AC006954) unknown protein [Arabidopsis thaliana]
Seq. No.
                  120693
```

5'-most EST

```
5394 2.R1010
Contig ID
5'-most EST
                  LIB22-015-Q1-E1-H10
                  120694
Seq. No.
                  5396 1.R1010
Contig ID
                  LIB3175-022-P1-K1-A1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2982434
BLAST score
                  1784
E value
                  0.0e+00
Match length
                  374
% identity
                  91
NCBI Description
                  (AL022224) putative protein [Arabidopsis thaliana]
                  120695
Seq. No.
                  5397 1.R1010
Contig ID
5'-most EST
                  jC-alXLIB327435P2e10b1
Method
                  BLASTN
NCBI GI
                  q3335331
BLAST score
                  338
E value
                  0.0e + 00
Match length
                  590
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  120696
Contig ID
                  5399 1.R1010
5'-most EST
                  jC-atXLIB327432P4b09b1
Method
                  BLASTN
NCBI GI
                  q2351068
BLAST score
                  377
E value
                  0.0e + 00
Match length
                  425
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRH10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120697.
                  5401 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327422P1e09b1
Seq. No.
                  120698
                  5405 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P4b08b1
Method
                  BLASTN
NCBI GI
                  q2351069
BLAST score
                  152
E value
                  8.0e-80
Match length
                  412
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSH12, complete sequence [Arabidopsis thaliana]
                  120699
Seq. No.
                  5410 1.R1010
Contig ID
                  LIB22-016-Q1-E1-B2
```

```
Method
                    BLASTN
 NCBI GI
                   g2815404
 BLAST score
                    509
                    0.0e + 00
 E value
 Match length
                    662
 % identity
                    100
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                    MMG4, complete sequence [Arabidopsis thaliana]
                    120700
 Seq. No.
 Contig ID
                    5411_1.R1010
                    jC-atXLIB327409P4g04b1
 5'-most EST
 Method
                    BLASTX
                    g4106690
 NCBI GI
                    285
 BLAST score
                    2.0e-25
 E value
 Match length
                    100
 % identity
                    52
                    (AL035065) putative urea active transporter
 NCBI Description
                    [Schizosaccharomyces pombe]
                    120701
 Seq. No.
 Contig ID
                    5415_1.R1010
                    LIB22-016-Q1-E1-B7
 5'-most EST
 Method
                    BLASTN
                    g3193282
 NCBI GI
                    380
 BLAST score
 E value
                    0.0e + 00
                    380
 Match length
 % identity
                    92
 NCBI Description Arabidopsis thaliana BAC T14P8
                    120702
 Seq. No.
                    5416_1.R1010
 Contig ID
 5'-most EST
                    g502\overline{1}11
 Method
                    BLASTX
                    q4758946
 NCBI GI
                    217
 BLAST score
 E value
                    3.0e-17
                    88
 Match length
 % identity
                    50 '
 NCBI Description
                    POP2 (yeast homolog) >gi_4106061_gb_AAD02685_ (AF053318)
                    CCR4-associated factor 1 [Homo sapiens]
                    120703
 Seq. No.
                    5416 2.R1010
 Contig ID
                    LIB3176-024-P1-K1-G4
 5'-most EST
 Method
                    BLASTX
                    a4263711
 NCBI GI
 BLAST score
                    948
                    1.0e-102
 E value
                    246
 Match length
 % identity
                    72
                    (AC006223) putative CCR4-associated transcription factor
NCBI Description
                    [Arabidopsis thaliana]
```

```
Contig ID
                   5416 3.R1010
5'-most EST
                   jC-atXLIB327414P3b04a1
Method
                   BLASTX
                  g4263711
NCBI GI
                   239
BLAST score
E value
                   8.0e-20
                   66
Match length
% identity
                   71
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   120705
                   5417 1.R1010
Contig ID
                  jC-atX22016Q1E1B09b1
5'-most EST
                   BLASTX
Method
                  g4510401
NCBI GI
BLAST score
                   449
                   1.0e-44
E value
Match length
                   126
% identity
                   64
                   (AC006587) putative general negative regulator of
NCBI Description
                   transcription [Arabidopsis thaliana]
Seq. No.
                   120706
                   5418 1.R1010
Contig ID
                   jC-atXLIB327432P2c11b2
5'-most EST
Method
                   BLASTX
NCBI GI
                  q100226
BLAST score
                   416
                   2.0e-40
E value
                   140
Match length
% identity
                   56
NCBI Description
                  hypothetical protein - tomato >gi_19275_emb_CAA78112_
                   (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi_445619_prf__1909366A Leu zipper protein
                   [Lycopersicon esculentum]
                   120707
Seq. No.
Contig ID
                  5419 1.R1010
5'-most EST
                  LIB2\overline{3}-039-Q1-E1-G2
                  BLASTX
Method
NCBI GI
                   q4512625
BLAST score
                   771
E value
                   3.0e-82
Match length
                   155
% identity
                   100
                   (AC004793) ESTs gb T20423, gb AA712864, gb H76323 and
NCBI Description
                   gb Z25560 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   120708
Contig ID
                  5421_1.R1010
                  LIB22-055-Q1-E1-D11
5'-most EST
                  BLASTN
Method
NCBI GI
                   q4512656
BLAST score
                   319
E value
                  1.0e-179
Match length
                   741
```

```
98
% identity
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  120709
                  5423 1.R1010
Contig ID
                  jC-atXLIB327432P4c01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3850070
BLAST score
                  359
E value
                  5.0e-34
Match length
                  107
% identity
                  60
NCBI Description (AL033385) transketolase [Schizosaccharomyces pombe]
                  120710
Seq. No.
                  5424 1.R1010
Contig ID
                  LIB24-104-Q1-E2-E8
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2160166
BLAST score
                  661
E value
                  5.0e-69
Match length
                  289
                  53
% identity
NCBI Description (AG000132) No definition line found [Arabidopsis thaliana]
                  120711
Seq. No.
                  5425 1.R1010
Contig ID
5'-most EST
                  LIB3176-091-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q4585966
BLAST score
                  635
E value
                  4.0e-66
Match length
                  239
% identity
                  58
                  (AC005287) Putative dihyrdolipoamide acetyltransferase
NCBI Description
                  [Arabidopsis thaliana]
                  120712
Seq. No.
                  5427_1.R1010
Contig ID
                  LIB23-056-Q1-E1-E5
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3510347
BLAST score
                  37
                  4.0e-11
E value
Match length
                  137
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
                  120713
Seq. No.
                  5428 1.R1010
Contiq ID
5'-most EST
                  jC-atXLIB327432P2c10b2
Method
                  BLASTX
                  g4160518
NCBI GI
BLAST score
                  94
```

. .

7.0e-33

E value

BLAST score

433

Match length 107 % identity 64 (AJ131346) beta-glucosidase [Caldicellulosiruptor sp. 14B] NCBI Description 120714 Seq. No. Contig ID 5429_1.R1010 jC-atXLIB327432P4c09b1 5'-most EST Method BLASTX q2827710 NCBI GI BLAST score 668 E value 4.0e-74Match length 165 % identity 81 NCBI Description (AL021684) lysosomal Pro-X carboxypeptidase - like protein [Arabidopsis thaliana] 120715 Seq. No. Contig ID 5431 1.R1010 jC-atXLIB327432P3c09b1 5'-most EST Method BLASTX g3646320 NCBI GI BLAST score 330 E value 1.0e-30 Match length 89 % identity 74 (AJ000759) MADS-box protein [Malus domestica] NCBI Description 120716 Seq. No. Contig ID 5435 1.R1010 5'-most EST jC-atXLIB327432P4c08b1 Method BLASTN g3075383 NCBI GI BLAST score 455 E value 0.0e + 00Match length 463 % identity 100 Arabidopsis thaliana chromosome II BAC T1D16 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 120717 Seq. No. 5437 1.R1010 Contig ID jC-atXLIB327432P3c08b1 5'-most EST BLASTX Method NCBI GI q2708745 BLAST score 423 1.0e-41 E value 96 Match length % identity 83 (AC003952) putative calcium-dependent ser/thr protein NCBI Description kinase [Arabidopsis thaliana] 120718 Seq. No. Contig ID 5438 1.R1010 5'-most EST jC-atXLIB327432P2d04b1 Method BLASTX NCBI GI g2088649

```
E value
                  1.0e-75
                  171
Match length
% identity
                  88
NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]
                  120719
Seq. No.
                  5438 2.R1010
Contig ID
                  jC-atXLIB327431P3a07a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2088649
BLAST score
                  159
E value
                  4.0e-35
                  134
Match length
% identity
                  69
NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]
                  120720
Seq. No.
                  5439 1.R1010
Contig ID
                  jC-atXLIB327427P4h12b2
5'-most EST
Method
                  BLASTX
                  q4406780
NCBI GI
BLAST score
                  1592
E value
                  1.0e-178
Match length
                  353
% identity
                  86
NCBI Description (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
                  120721
Seq. No.
                  5439 2.R1010
Contig ID
                  LIB3168-086-P1-K1-D12
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4406780
                  805
BLAST score
                  2.0e-86
E value
Match length
                  154
% identity
                  (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                  120722
Seq. No.
Contig ID
                  5439 3.R1010
                  LIB3175-007-P1-K1-A2
5'-most EST
Method
                  BLASTX
                  q4406780
NCBI GI
                  631
BLAST score
                  5.0e-66
E value
Match length
                  132
% identity
NCBI Description
                  (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
                  120723
Seq. No.
                  5441 1.R1010
Contig ID
5'-most EST
                  LIB2\overline{3}-031-Q1-E1-G12
                  120724
Seq. No.
```

```
Contig ID
                  5442 1.R1010
5'-most EST
                   jC-atXLIB327431P2d08a1
                  BLASTX
Method
                  q4079632
NCBI GI
BLAST score
                   908
E value
                  5.0e-98
Match length
                  201
                  90
% identity
NCBI Description
                  (AJ131722) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  120725
                  5442 2.R1010
Contig ID
                  LIB22-021-Q1-E1-G7
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4508075
BLAST score
                  595
E value
                  1.0e-61
                  159
Match length
                  83
% identity
                  (AC005882) 50259 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  120726
                  5442_3.R1010
Contig ID
5'-most EST
                  .jC-atX22070Q1E1H06b1
                  BLASTX
Method
                  q4508075
NCBI GI
BLAST score
                  924
E value
                  1.0e-107
Match length
                  243
% identity
NCBI Description
                  (AC005882) 50259 [Arabidopsis thaliana]
Seq. No.
                   120727
                   5445 1.R1010
Contig ID
                  jC-atXLIB327432P2d03b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4733973
BLAST score
                   213
E value
                  6.0e-17
Match length
                  136
% identity
                   43
                  (AC007264) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120728
                   5447 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327426P1b03b1
Method
                  BLASTX
NCBI GI ·
                   g542200
BLAST score
                   764
E value
                   4.0e-81
Match length
                  247
% identity
                   60
NCBI Description
                  hypothetical protein - garden asparagus
                  >gi 452714 emb CAA54526 (X77320) unknown [Asparagus
                  officinalis]
```

```
5447 2.R1010
Contig ID
5'-most EST
                   g2047577
Method
                   BLASTX
                   g3158376
NCBI GI
BLAST score
                   548
                   4.0e-56
E value
                   132
Match length
% identity
                   82
                   (AF035385) unknown [Arabidopsis thaliana]
NCBI Description
                   120730
Seq. No.
                   5447 3.R1010
Contig ID
5'-most EST
                   jC-atXP102CE5F4T7032d1
                   BLASTX
Method
                   g542200
NCBI GI
BLAST score
                   386
                   4.0e-37
E value
                   112
Match length
% identity
                   63
                  hypothetical protein - garden asparagus
NCBI Description
                   >gi 452714 emb CAA54526 (X77320) unknown [Asparagus
                   officinalis]
                   120731
Seq. No.
                   5447 4.R1010
Contig ID
                   jC-atXLIB327437P2b04b1
5'-most EST
Method
                   BLASTX
                   g643469
NCBI GI
BLAST score
                   137
                   5.0e-31
E value
Match length
                   105
% identity
                   65
                   (U19886) unknown [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   120732
                   5447 5.R1010
Contig ID
5'-most EST
                   g933<del>6</del>97
Method
                   BLASTX
                   g3158376
NCBI GI
BLAST score
                   503
                   8.0e-51
E value
                   104
Match length
                   91
% identity
                  (AF035385) unknown [Arabidopsis thaliana]
NCBI Description
                   120733
Seq. No.
                   5447 6.R1010
Contig ID
5'-most EST
                   g931<del>3</del>43
Method
                   BLASTX
NCBI GI
                   g3158376
BLAST score
                   599
E value
                   3.0e-64
Match length
                   130
                   89
% identity
NCBI Description
                  (AF035385) unknown [Arabidopsis thaliana]
                   120734
Seq. No.
```

```
5447 8.R1010
Contig ID
                  jC-atXLIB327413P2d12b1
5'-most EST
Method
                  BLASTX
                  g3158376
NCBI GI
BLAST score
                  486
                  6.0e-49
E value
Match length
                  131
                  75
% identity
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
                  120735
Seq. No.
                  5447 10.R1010
Contig ID
                  LIB25-044-Q1-E1-D12
5'-most EST
                  BLASTX
Method
                  g3158376
NCBI GI
BLAST score
                  440
                  3.0e-45
E value
Match length
                  158
% identity
                  81
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                  120736
                  5448 1.R1010 ·
Contig ID
                  jC-atX35040Q1E1C05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4309738
BLAST score
                  556
                  2.0e-60
E value
Match length
                 . 132
% identity
                  87
NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]
                  120737
Seq. No.
                  5448 2.R1010
Contig ID
                  LIB22-016-Q1-E1-E8
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4309738
BLAST score
                  582
                  4.0e-60
E value
Match length
                  120
% identity
                  92
NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]
                  120738
Seq. No.
                  5451 1.R1010
Contig ID
5'-most EST
                  LIB22-016-Q1-E1-F11
                  120739
Seq. No.
                  5452 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P4d01b1
Method
                  BLASTX
NCBI GI
                  g2253579
BLAST score
                  237
E value
                  1.0e-19
Match length
                  142
% identity
                  49
NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.

120746

```
120740
   Seq. No. ·
                     5454 1.R1010
   Contig ID
   5'-most EST
                     LIB22-016-Q1-E1-F3
   Seq. No.
                     120741
                     5459 1.R1010
  Contig ID
                     jC-atXLIB327432P2d10b1
   5'-most EST
                     BLASTX
  Method
  NCBI GI
                     q4314387
  BLAST score
                     535
  E value
                     1.0e-54
  Match length
                     103
                     100
   % identity
                     (AC006232) putative beta-alanine synthetase [Arabidopsis
  NCBI Description
                     thaliana]
                     120742
  Seq. No.
                     5460_1.R1010
  Contig ID
   5'-most EST
                     jC-atXLIB327420P1d12b1
                     120743
  Seq. No.
  Contig ID
                     5460_2.R1010
   5'-most EST
                     jC-atXLIB327420P1d12a1
  Method
                     BLASTN
                     g2462264
  NCBI GI
  BLAST score
                     54
  E value
                     4.0e-21
  Match length
                     54
                     100
  % identity
  NCBI Description
                     Cucumis sativus mRNA for patatin-like protein, partial
  Seq. No.
                     120744
                     5462 1.R1010
  Contig ID
   5'-most EST
                     ARABL1-18-Q1-B1-E8
  Method
                     BLASTN
  NCBI GI
                     q4572664
  BLAST score
                     422
  E value
                     0.0e + 00
  Match length
                     422
                     100
  % identity
                     Arabidopsis thaliana chromosome II BAC F25P17 genomic
  NCBI Description
                     sequence, complete sequence
                     120745
  Seq. No.
                     5465 1.R1010
  Contig ID
  5'-most EST
                     jC-atXLIB327432P3d09b1
  Method
                     BLASTX
  NCBI GI
                     q3033400
  BLAST score
                     490
  E value
                     2.0e-53
  Match length
                     130
identity
                     82
                     (AC004238) putative Ser/Thr protein kinase [Arabidopsis
  NCBI Description
                     thaliana]
```

```
5467 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P4d10b1
Method
                   BLASTN
NCBI GI
                   g2749918
BLAST score
                   248
E value
                   1.0e-137
Match length
                   490
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F3I6 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   120747
                   5469 1.R1010
Contig ID
                   jC-atXLIB327432P3d06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3152587
BLAST score
                   340
E value
                   8.0e-32
Match length
                   86
% identity
NCBI Description
                   (AC002986) Similar to CREB-binding protein homolog
                   gb U88570 from D. melanogaster and contains similarity to
                   callus-associated protein gb_U01961 from Nicotiana tabacum.
                   EST gb W43427 comes from this gene. [Arabidopsis thaliana]
                   120748
Seq. No.
Contig ID
                   5470 1.R1010
                   LIB23-066-Q1-E1-A7
5'-most EST
Seq. No.
                   120749
                   5474 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P2e03b1
Method
                   BLASTX
NCBI GI
                   g2244949
BLAST score
                   576
E value
                   2.0e-59
Match length
                   122
% identity
                   98
                   (Z97339) similarity to ORF - Lilium longiflorum
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   120750
                   5476 1.R1010
Contig ID
                   jC-atXLIB327407P4a11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g549061
BLAST score
                   433
                   1.0e-42
E value
Match length
                   125
% identity
                   66
                   T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA)
NCBI Description
                   (CCT-ZETA-1) >gi_631655_pir__S43063 CCT (chaperonin containing TCP-1) zeta chain - mouse
                   >gi 468554 emb CAA83432 (Z31557) CCT (chaperonin
                   containing TCP-1) zeta subunit [Mus musculus]
```

```
5478 1.R1010
Contig ID
                  LIB25-066-Q1-E1-B1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2829913
BLAST score
                   406
E value
                   1.0e-39
Match length
                   115
                   75
% identity
NCBI Description
                   (AC002291) putative carboxyphosphonoenolpyruvate mutase
                   [Arabidopsis thaliana]
Seq. No.
                   120752
                   5480 1.R1010
Contig ID
                   LIB22-016-Q1-E1-H6
5'-most EST
Method
                   BLASTN
NCBI GI
                  g3600029
BLAST score
                   412
E value
                   0.0e + 00
Match length
                   420
                   100
% identity
NCBI Description Arabidopsis thaliana BAC T12H2O
Seq. No.
                  120753
                   5481 2.R1010
Contig ID
                   LIB23-060-Q1-E1-F9
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4263753
BLAST score
                   222
                   1.0e-122
E value
Match length
                   249
                   96
% identity
                  Arabidopsis thaliana chromosome V map near 60.5 cM,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                   120754
                   5482 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P2e02b2
Method
                  BLASTX
NCBI GI
                   q4572674
BLAST score
                   416
E value
                   2.0e-42
Match length
                   94
% identity
                   100
                  (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
                   120755
Seq. No.
Contig ID
                   5484 1.R1010
                   LIB24-064-Q1-E1-D12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3983665
BLAST score
                   329
E value
                   1.0e-30
Match length
                   87
% identity
                   74
                  (AB011271) importin-beta2 [Oryza sativa]
NCBI Description
                  120756
Seq. No.
```

r.

NCBI GI

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```
Contig ID
                   5485 1.R1010
                   LIB3177-038-P1-K1-F8
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3122572
                   545
BLAST score
E value
                   8.0e-56
                   149
Match length
                   72
% identity
                   NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
                   SUBUNIT) >gi_1084434_pir_S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
                   >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial
                   complex I subunit [Solanum tuberosum]
                   120757
Seq. No.
                   5486 1.R1010
Contig ID
5'-most EST
                   g2048434
                   120758
Seq. No.
                   5486 2.R1010
Contig ID
5'-most EST
                   q2733417
Method
                   BLASTX
                   q2245079 ·
NCBI GI
                   234
BLAST score
                   2.0e-19
E value
                   100
Match length
% identity
                   53
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   120759
Seq. No.
                   5486 3.R1010
Contig ID
5'-most EST
                   jC-atXP61C200M18T7d1
Method
                   BLASTX
NCBI GI
                   q2245079
BLAST score
                   329
                   1.0e-32
E value
                   193
Match length
% identity
                   47
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   120760
Seq. No.
Contig ID
                   5489 1.R1010
5'-most EST
                   LIB3177-064-P1-K1-D10
                   BLASTX
Method
NCBI GI
                   q3688182
BLAST score
                   687
E value
                   2.0e-72
Match length
                   145
% identity
                   90
NCBI Description
                  (AL031804) P-Protein - like protein [Arabidopsis thaliana]
                   120761
Seq. No.
Contig ID
                   5489 2.R1010
5'-most EST
                   q1216044
Method
                   BLASTX
```

q3413705

.....

```
BLAST score
                   65
E value
                   3.0e-81
Match length
                   179
                   84
% identity
                   (AC004747) putative glycine dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   120762
Seq. No.
Contig ID
                   5490 1.R1010
5'-most EST
                   jC-atXLIB327432P3d11b1
Method
                   BLASTN
NCBI GI
                  q4558586
BLAST score
                   351
                   0.0e + 00
E value
Match length
                   435
                  100
% identity
                  Arabidopsis thaliana chromosome 1 BAC T518 sequence,
NCBI Description
                  complete sequence
                  120763
Seq. No.
Contig ID
                  5492_1.R1010
5'-most EST
                  LIB3234-017-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g3024434
BLAST score
                  2042
                  0.0e + 00
E value
Match length
                   424
                  96
% identity
                  26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_
                   (D88663) Tat binding protein 1 [Brassica rapa]
                  120764
Seq. No.
Contig ID
                  5493_1.R1010
5'-most EST
                  jC-atXLIB327408P3d11b1
                  BLASTX
Method
NCBI GI
                  q1171978
BLAST score
                   294
                  3.0e-26
E value
Match length
                   67
                  91
% identity
                  POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                   (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi 2911051 emb CAA17561 (AL021961)
                  poly(A)-binding protein [Arabidopsis thaliana]
                  120765
Seq. No.
                  5493_2.R1010
Contig ID
5'-most EST
                  LIB3168-030-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  a1171978
BLAST score
                  606
                  2.0e-62
E value
Match length
                  266 .
% identity
                  53
                  POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                   (PABP 2) >gi 304109 (L19418) poly(A)-binding protein
```

```
poly(A)-binding protein [Arabidopsis thaliana]
                   120766
Seq. No.
                   5494 1.R1010
Contig ID
                  LIB3175-055-P1-K1-D2
5'-most EST
                   BLASTX
Method
                   q2369766
NCBI GI
                   750
BLAST score
                   1.0e-121
E value
Match length
                   297
% identity
                   71
                  (AJ001304) hypothetical protein [Citrus x paradisi]
NCBI Description
                   120767
Seq. No.
                   5494 2.R1010
Contig ID
                  jC-atX35052Q1E1D01b1
5'-most EST
Method
                   BLASTX
                   q4263522
NCBI GI
BLAST score
                   84
E value
                   5.0e-13
Match length
                   102 .
% identity
                   42
NCBI Description
                   (AC004044) hypothetical protein [Arabidopsis thaliana]
                   120768
Seq. No.
                   5496 1.R1010
Contig ID
5'-most EST
                  jC-alXLIB327435P3h10b1
Method
                   BLASTX
NCBI GI
                   g2583125
BLAST score
                  1334
E value
                   1.0e-149
Match length
                   337
% identity
                   80
NCBI Description
                   (AC002387) putative transketolase precursor [Arabidopsis
                  thaliana]
Seq. No.
                   120769
                   5496 2.R1010
Contig ID
5'-most EST
                  jC-atXL117Q1B1B10a1
Method
                   BLASTX
NCBI GI
                   g2583125
BLAST score
                  2168
E value
                   0.0e+00
Match length
                   469
% identity
NCBI Description
                   (AC002387) putative transketolase precursor [Arabidopsis
                  thaliana]
Seq. No.
                   120770
                   5496 4.R1010
Contig ID
                   g2597577
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2583125
BLAST score
                  267
                   6.0e-23
E value
Match length
                  92
```

[Arabidopsis thaliana] >qi 2911051 emb CAA17561 (AL021961)

```
70
% identity
                   (AC002387) putative transketolase precursor [Arabidopsis
NCBI Description
                   thaliana]
                   120771
Seq. No.
                   5496 5.R1010
Contig ID
                   jC-atXP123C162E13T7073d1
5'-most EST
                   BLASTX
Method
                   g2583125
NCBI GI
BLAST score
                   305
                   2.0e-27
E value
                   87
Match length
                   72
% identity
                   (AC002387) putative transketolase precursor [Arabidopsis
NCBI Description
                   thaliana]
                   120772 -
Seq. No.
                   5496 11.R1010
Contig ID
                  LIB22-089-Q1-E1-G2
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2583125
BLAST score
                   675
                   4.0e-71
E value
Match length
                   131
% identity
                   100
                   (AC002387) putative transketolase precursor [Arabidopsis
NCBI Description
                   thaliana]
                   120773
Seq. No.
                   5497 1.R1010
Contig ID
                  LIB23-047-Q1-E1-A9
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3928150
BLAST score
                   728
E value
                   8.0e-83
Match length
                   186
% identity
                   84
NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]
                   120774
Seq. No.
                  5503 1.R1010
Contig ID
                  LIB2\overline{2}-017-Q1-E1-B7
5'-most EST
Method
                  BLASTN
                   g4580744
NCBI GI
BLAST score
                   338
                  0.0e + 00
E value
Match length
                  390
                   99
% identity
NCBI Description
                  Sequence of BAC F15I1 from Arabidopsis thaliana chromosome
                   1, complete sequence
                   120775
Seq. No.
                   5510 1.R1010
Contig ID
5'-most EST
                   g2723197
                  BLASTX
Method
                  q1709804
NCBI GI
BLAST score
                   304
```

% identity

78

```
E value
                   2.0e-27
Match length
                   70
                   80
% identity
                   26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED
NCBI Description
                   ATPASE DOMAIN PROTEIN 44) >gi_1045497 (U36395) conserved
                   ATPase domain protein 44 [Spermophilus tridecemlineatus]
                   >gi 2213932 (AF006305) 26S proteasome regulatory subunit
                   [Homo sapiens]
Seq. No.
                   120776
Contig ID
                   5510 2.R1010
                   LIB22-017-Q1-E1-C3
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2960216
BLAST score
                   963
E value
                   1.0e-104
Match length
                   207
                   88
% identity
                   (AJ223384) 26S proteasome regulatory ATPase subunit 10b
NCBI Description
                   (S10b) [Manduca sexta]
Seq. No.
                   120777
Contig ID
                   5514_1.R1010
5'-most EST
                   jC-atXLIB327412P1b04b1
Method
                   BLASTX
                   q4115377
NCBI GI
BLAST score
                   275
E value
                   5.0e-51
                   306
Match length
% identity
                   38
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120778
                   5515 1.R1010
Contig ID
5'-most EST
                  LIB3177-091-P1-K1-B4
                   120779
Seq. No.
                   5516_1.R1010
Contig ID
                   jC-atXLIB327402P3e04a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3318617
BLAST score
                   1404
E value
                   1.0e-156
Match length
                   267
                   100
% identity
                   (AB016066) mitochondrial phosphate transporter [Arabidopsis
NCBI Description
                   thaliana]
                   120780
Seq. No.
Contig ID
                   5518 1.R1010
5'-most EST
                  q113\overline{0}577
Method
                  BLASTX
NCBI GI
                  q4519539
BLAST score
                  833
E value
                  2.0e-89
Match length
                  196
```

```
NCBI Description
                  (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
                  domestica]
                  120781
Seq. No.
                  5519 1.R1010
Contig ID
5'-most EST
                  LIB22-017-Q1-E1-D12
                  BLASTX
Method
NCBI GI
                  q116923
BLAST score
                  277
E value
                  1.0e-24
Match length
                  114
% identity
                  42
                  COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                  >gi_111414_pir__S13520 beta-COP protein - rat
                  >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus
                  norvegicus]
                  120782
Seq. No.
                  5520 1.R1010
Contig ID
                  jC-atXP86CG10B8T7d2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q66618
BLAST score
                  860
                  1.0e-92
E value
                  199
Match length
% identity
                  94
                  3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
NCBI Description
                  precursor - Arabidopsis thaliana
                  120783
Seq. No.
                  5520 2.R1010
Contig ID
                  jC-atXLIB327405P3d12b1
5'-most EST
Method
                  BLASTX
                  g3176708
NCBI GI
BLAST score
                  164
E value
                  4.0e-11
Match length
                  130
% identity
                  36
NCBI Description
                  (AC002392) putative proline-rich protein APG [Arabidopsis
                  thaliana]
                  120784
Seq. No.
                  5520 4.R1010
Contig ID
5'-most EST
                  LIB3168-077-P1-K1-B7
                  BLASTX
Method
                  g2492952
NCBI GI
BLAST score
                  281
E value
                  9.0e-25
Match length
                  68
% identity
                  74
                  CHORISMATE SYNTHASE 1 PRECURSOR
NCBI Description
                  (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)
                  >gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1
                  precursor - tomato >gi_410482_emb_CAA79859_ (Z21796)
                  chorismate synthase 1 [Lycopersicon esculentum]
                  120785
```

```
5520 5.R1010
Contig ID
                  jC-a\overline{t}XLIB327405P3h12b1
5'-most EST
Method
                   BLASTX
                  q114171
NCBI GI
                   190
BLAST score
E value
                  3.0e-14
                   70
Match length
% identity
                   61
                  3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE PRECURSOR
NCBI Description
                   (3-ENOLPYRUVYLSHIKIMATE-5-PHOSPHATE SYNTHASE) (EPSP
                  SYNTHASE) >gi_99781_pir__S12744 3-phosphoshikimate
                   1-carboxyvinyltransferase (EC 2.5.1.19) precursor - rape
                  >gi 17815 emb CAA35839 (X51475)
                   5-enolpyruvylshikimate-3-phosphate synthase [Brassica
                  napus]
                   120786
Seq. No.
                   5521 1.R1010
Contiq ID
                  g1520791
5'-most EST
Method
                  BLASTX
                   g2911057
NCBI GI
BLAST score
                   620
E value
                   2.0e-64
Match length
                  118
% identity
                   99
                   (AL021961) caffeoyl-CoA O-methyltransferase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   120787 -
Seq. No.
Contig ID
                  5521 2.R1010
                  jC-atXLIB327432P3c12b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2911057
                   915
BLAST score
E value
                   5.0e-99
Match length
                   176
                   100
% identity
                   (AL021961) caffeoyl-CoA O-methyltransferase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  120788
Seq. No.
                   5521 3.R1010
Contig ID
                  jC-aTXP25C125A10T7d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1679853
BLAST score
                   599
E value
                   6.0e-62
Match length
                   119
                   91
% identity
                   (Z82982) caffeoyl-CoA O-methyltransferase 5 [Nicotiana
NCBI Description
                   tabacum]
                   120789
Seq. No.
Contig ID
                  5523 1.R1010
                   jC-atXLIB327407P4c09b1
5'-most EST
                   BLASTX
Method
```

g629602

NCBI GI

Contig ID

```
BLAST score
                   1403
                   0.0e + 00
E value
                   746
Match length
% identity
                  probable imbibition protein - wild cabbage
NCBI Description
                   >gi 488787 emb CAA55893_ (X79330) putative imbibition
                  protein [Brassica oleracea]
                   120790
Seq. No.
                   5523 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327411P2d08b1
Method
                   BLASTX
                   q282994
NCBI GI
BLAST score
                   276
                   4.0e-24
E value
                   91
Match length
% identity
                   54
                  Sip1 protein - barley >gi 167100 (M77475) seed imbibition
NCBI Description
                  protein [Hordeum vulgare]
                   120791
Seq. No.
Contig ID
                   5525 1.R1010
5'-most EST
                   jC-atXP50C179J1T7029d1
                   120792
Seq. No.
                   5525 2.R1010
Contig ID
                   jC-atXLIB327432P3c10b1
5'-most EST
                   120793
Seq. No.
                   5525 4.R1010
Contig ID
5'-most EST
                   g115\overline{9}022
Seq. No.
                   120794
                   5529 1.R1010
Contig ID
                   jC-atXP4C88L18T7091a1
5'-most EST
Method
                   BLASTX
                   q4544443
NCBI GI
BLAST score
                   572
É value
                   7.0e-59
Match length
                   131
% identity
                   (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
                   120795
Seq. No.
                   5532 1.R1010
Contig ID
                   LIB22-062-Q1-E1-C1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1616787
BLAST score
                   1016
                   1.0e-134
E value
Match length
                   245
                   97
% identity
                  (U71122) pyruvate decarboxylase [Arabidopsis thaliana]
NCBI Description
                   120796
Seq. No.
```

5534 1.R1010

```
jC-atXLIB327416P1h04b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4263704
BLAST score
                  595
                  2.0e-61
E value
Match length
                  151
                  79
% identity
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  120797
Contig ID
                  5534_2.R1010
                  LIB24-050-Q1-E1-G8
5'-most EST
                  BLASTX
Method
NCBI GI
                  a4263704
BLAST score
                  734
E value
                  6.0e-78
                  170
Match length
% identity
                  85
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  120798
Contig ID
                  5536_1.R1010
                  jC-atXLIB327432P2c09b2
5'-most EST
Method
                  BLASTN
                  q4432829
NCBI GI
BLAST score
                  186
                  1.0e-100
E value
                  357
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T1B3 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  120799
Seq. No.
Contig ID
                  5541 1.R1010
                  jC-atXLIB327432P2c06b2
5'-most EST
Method
                  BLASTX
                  q4335737
NCBI GI
BLAST score
                  307
                  3.0e-29
E value
                  136
Match length
% identity
                  50
NCBI Description
                   (AC006248) putative serine/threonine kinase [Arabidopsis
                  thaliana]
                  120800
Seq. No.
Contig ID
                  5542_1.R1010
                  LIB3176-002-Q1-K1-F12
5'-most EST
Method
                  BLASTX
                  q4220527
NCBI GI
BLAST score
                  629
                  2.0e-65
E value
                  205
Match length
% identity
                  54
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
```

5'-most EST

```
Seq. No.
                   120801
                   5544 1.R1010
Contig ID
                  jC-atXLIB327402P1f05b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g337767
BLAST score
                   202
E value
                   3.0e-15
Match length
                   182
                   17
% identity
NCBI Description
                  (M60258) cerebroside sulfate activator protein [Homo
                  sapiens]
Seq. No.
                   120802
Contig ID
                   5544 2.R1010
5'-most EST
                  LIB35-042-Q1-E1-H7
Seq. No.
                   120803
Contig ID
                   5544 3.R1010
5'-most EST
                   g501898
                   120804
Seq. No.
Contig ID
                   5544_4.R1010
                  jC-a\overline{t}XLIB327430P4c12b1
5'-most EST
Method
                  BLASTN
                  g4106527
NCBI GI
BLAST score
                   51
                  3.0e-19
E value
Match length
                  83
                  59.
% identity
NCBI Description Mus musculus Pontin52 mRNA, complete cds
                   120805
Seq. No.
Contig ID
                  5549_1.R1010
5'-most EST
                  LIB3168-072-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q4432860
BLAST score
                   586
                   2.0e-60
E value
Match length
                  117
                   97
% identity
                   (AC006300) putative glucose-induced repressor protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   120806
Contig ID
                   5550 1.R1010
5'-most EST
                  jC-atXLIB327432P3b12b1
Method
                  BLASTX
NCBI GI
                  q4539302
BLAST score
                   437
E value
                  8.0e-49
Match length
                  119
% identity
                  82
NCBI Description
                  (AL049480) putative protein [Arabidopsis thaliana]
Seq. No.
                  120807
Contig ID
                  5552 1.R1010
```

jC-atXP102CE5F5T7b1

5'-most EST

```
Method
                   BLASTX
                   a99772
 NCBI GI
                   267
 BLAST score
                   3.0e-42
 E value
                   137
 Match length
 % identity
                   ubiquitin 81-aa extension protein 2 - Arabidopsis thaliana
 NCBI Description
                   >gi 166936 (J05540) ubiquitin extension protein (UBQ6)
                   [Arabidopsis thaliana] >gi_3522953 (AC004411) ubiquitin
                   extension protein (UBQ6) [Arabidopsis thaliana]
 Seq. No.
                   120808
                   5552_2.R1010
 Contig ID
                   LIB25-028-Q1-E1-H3
 5'-most EST
 Method
                   BLASTX
                   q99772
 NCBI GI
 BLAST score
                   607
                   5.0e-63
 E value
Match length
                   157
 % identity
                   ubiquitin 81-aa extension protein 2 - Arabidopsis thaliana
 NCBI Description
                   >gi 166936 (J05540) ubiquitin extension protein (UBQ6)
                   [Arabidopsis thaliana] >gi_3522953 (AC004411) ubiquitin
                   extension protein (UBQ6) [Arabidopsis thaliana]
                   120809
 Seq. No.
                   5552 3.R1010
 Contig ID
· 5'-most EST
                   jC-atXLIB327405P4f05b1
Method
                   BLASTX
NCBI GI
                   q99771
BLAST score
                   269
E value
                   2.0e-57
Match length
                   117
 % identity
NCBI Description
                   ubiquitin 81-aa extension protein 1 - Arabidopsis thaliana
                   >gi 166934 (J05539) ubiquitin extension protein (UBQ5)
                   [Arabidopsis thaliana]
Seq. No.
                   120810
                   5553 1.R1010
 Contig ID
 5'-most EST
                   jC-atXLIB327432P3b11b1
 Seq. No.
                   120811
 Contig ID
                   5553 2.R1010
                   jC-a\overline{t}XLIB327411P1e03b1
 5'-most EST
Method
                   BLASTN
 NCBI GI
                   q2582640
 BLAST score
                   59
                   3.0e-24
E value
Match length
                   75
                   96
 % identity
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
Seq. No.
                   120812
Contig ID
                   5555 1.R1010
```

jC-atXLIB327409P3h08a1

```
BLASTN
Method
NCBI GI
                  g4678705
                   484
BLAST score
                  0.0e + 00
~E value
                  562
Match length
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                   (ESSA project)
                  120813
Seq. No.
                   5555_2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327403P3a06b2
Method
                  BLASTN
                   g4678705
NCBI GI
BLAST score
                   458
                  0.0e + 00
E value
                  1085
Match length
                  98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                   (ESSA project)
                  120814
Seq. No.
Contig ID
                   5555 3.R1010
5'-most EST
                   g2048849
Method
                  BLASTN
                  g4678705
NCBI GI
BLAST score
                   375
                   0.0e+00
E value
Match length
                   454
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                   (ESSA project)
                  120815
Seq. No.
                   5555 4.R1010
Contig ID
5'-most EST
                  LIB3234-004-P1-K1-H11
Method
                  BLASTN
NCBI GI
                   g4678705
BLAST score
                   422
E value
                   0.0e + 00
Match length
                   853
                   97
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                   (ESSA project)
                   120816
Seq. No.
                   5555 5.R1010
Contig ID
5'-most EST
                   jC-atXLIB327412P3c04b1
Method
                  BLASTX
NCBI GI
                  g2827631
BLAST score
                   629
E value
                   1.0e-101
Match length
                  191
                  100
% identity
                  (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
```

Contig ID

```
5556 1.R1010
Contig ID
                   LIB22-017-Q1-E1-G9
5'-most EST
                   120818
Seq. No.
                   5559 1.R1010
Contig ID
                   jC-a\(\bar{1}\)XLIB327436P3b12b1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4585891
                   526
BLAST score
E value
                   0.0e + 00
                   526
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T103 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   120819
                   5560 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P4b05b1
                   BLASTX
Method
NCBI GI
                   g2829885
BLAST score
                   505
E value
                   4.0e-51
Match length
                   106
% identity
                   97
                   (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120820
                   5561 1.R1010
Contig ID
                   jC-atXLIB327432P4b04b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2828280
BLAST score
                   794
                   6.0e-85
E value
Match length
                   157
% identity
                   92
                   (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 2832633 emb CAA16762 (AL021711) putative protein
                   [Arabidopsis thaliana]
                   120821
Seq. No.
                   5565 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327419P3b07b2
                   120822
Seq. No.
                   5567 2.R1010
Contig ID
5'-most EST
                   LIB3176-026-P1-K1-C5
Method
                   BLASTN
NCBI GI
                   g2760165
BLAST score
                   333
E value
                   0.0e + 00
Match length
                   400
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   120823
```

5568 1.R1010

E value

```
5'-most EST
                    jC-atXLIB327420P3f05b1
                    BLASTX
Method
                    g3212879
NCBI GI
BLAST score
                    1138
                    1.0e-125
E value
                    243
Match length
                    92
% identity
                    (AC004005) putative ribosomal protein L7 [Arabidopsis
NCBI Description
                    thaliana]
                    120824
Seq. No.
                    5568 4.R1010
Contig ID
                    q345\overline{0}244
5'-most EST
                    BLASTX
Method
                    g3212879
NCBI GI
                    430
BLAST score
                    3.0e-42
E value
                    80
Match length
                    100
% identity
                    (AC004005) putative ribosomal protein L7 [Arabidopsis
NCBI Description
                    thaliana]
                    120825
Seq. No.
                    5569 1.R1010
Contig ID
                    jC-atXP73CF2F4T7d2
5'-most EST
                    BLASTX
Method
                    g4587552
NCBI GI
BLAST score
                    1416
                    1.0e-157
E value
                    322
Match length
                    90
% identity
NCBI Description
                    (AC006577) Strong similarity to gb S77096 aldehyde
                    dehydrogenase homolog from Brassica napus and is a member
                    of PF 00171 Aldehyde dehydrogenase family. ESTs gb T46213,
                    gb_T4\(\overline{2}\)164, gb_T43682, gb_N96380, gb_T42973, gb
                    120826
Seq. No.
                    5569 2.R1010
Contig ID
                    jC-alXLIB327435P4b05b1
5'-most EST
                    BLASTX
Method
                    g4587552
NCBI GI
BLAST score
                    855
                    6.0e-92
E value
                    188
Match length
                    89
 % identity
                    (AC006577) Strong similarity to gb S77096 aldehyde
NCBI Description
                    dehydrogenase homolog from Brassica napus and is a member
                    of PF 00171 Aldehyde dehydrogenase family. ESTs gb T46213,
                    gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb
                    120827
Seq. No.
                    5569 3.R1010
Contig ID
                    jC-a\(\bar{1}\)XLIB327435P4b05a1
 5'-most EST
                    BLASTX
Method
NCBI GI
                    g4587552
BLAST score
                    627
                    3.0e-65
```

```
Match length
                   140
 % identity
                   88
                    (AC006577) Strong similarity to gb S77096 aldehyde
 NCBI Description
                   dehydrogenase homolog from Brassica napus and is a member
                   of PF 00171 Aldehyde dehydrogenase family. ESTs gb T46213,
                   gb T42164, gb T43682, gb N96380, gb T42973, gb
                   120828
 Seq. No.
 Contig ID
                   5569 4.R1010
                   jC-atXLIB327407P3b07b1
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   g4587552
 BLAST score
                   581
 E value
                   8.0e-60
 Match length
                   172
                   78
% identity
 NCBI Description
                   (AC006577) Strong similarity to gb S77096 aldehyde
                   dehydrogenase homolog from Brassica napus and is a member
                   of PF 00171 Aldehyde dehydrogenase family. ESTs gb_T46213,
                   gb T42164, gb T43682, gb N96380, gb T42973, gb
 Seq. No.
                   120829
 Contig ID
                   5569 6.R1010
 5'-most EST
                   LIB22-028-Q1-E1-B7
 Method
                   BLASTX
 NCBI GI
                   q4587552
 BLAST score
                   558
                   2.0e-74
 E value
 Match length
                   175
 % identity
                   (AC006577) Strong similarity to gb S77096 aldehyde
 NCBI Description
                   dehydrogenase homolog from Brassica napus and is a member
                   of PF 00171 Aldehyde dehydrogenase family. ESTs gb T46213,
                   gb T4\overline{2}164, gb T43682, gb N96380, gb T42973, gb
 Seq. No.
                   120830
                   5569_7.R1010
 Contig ID
 5'-most EST
                   jC-atXLIB327425P1e05b1
 Method
                   BLASTX
 NCBI GI
                   q4587552
 BLAST score
                   59
 E value
                   4.0e-17
 Match length
                   103
 % identity
 NCBI Description
                   (AC006577) Strong similarity to gb S77096 aldehyde
                   dehydrogenase homolog from Brassica napus and is a member
                   of PF 00171 Aldehyde dehydrogenase family. ESTs gb T46213,
                   gb T42164, gb T43682, gb N96380, gb T42973, gb
 Seq. No.
                   120831
                   5578 1.R1010
 Contig ID
 5'-most EST
                   jC-atXLIB327432P3b02b1
 Method
                   BLASTN
 NCBI GI
                   g3063438
 BLAST score
                   298
 E value
                   1.0e-167
Match length
                   395
```

```
% identity
                  Complete sequence of Arabidopsis F22013, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
                   120832
Seq. No.
                   5579 1.R1010
Contig ID
                   LIB3168-087-P1-K1-F6
5'-most EST
                   BLASTN
Method
                   g2264302
NCBI GI
BLAST score
                   505
E value
                   0.0e+00
Match length
                   646
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAC12, complete sequence [Arabidopsis thaliana]
                   120833
Seq. No.
                   5579 2.R1010
Contig ID
                   LIB2\overline{2}-018-Q1-E1-A9
5'-most EST
Method
                   BLASTN
                   g2264302
NCBI GI
BLAST score
                   210
E value
                   1.0e-114
Match length
                   464
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAC12, complete sequence [Arabidopsis thaliana]
                   120834
Seq. No.
                   5582 1.R1010
Contig ID
                   LIB2\overline{2}-018-Q1-E1-B12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4584548
BLAST score
                   2518
E value
                   0.0e + 00
Match length
                   509
% identity
                   95
                   (AL049608) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120835
Contig ID
                   5584_1.R1010
5'-most EST
                   LIB23-016-Q1-E1-C5
Method
                   BLASTN
NCBI GI
                   q3449330
                   450
BLAST score
                   0.0e + 00
E value
Match length
                   653
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MDJ14, complete sequence [Arabidopsis thaliana]
                   120836
Seq. No.
                   5585 1.R1010
Contig ID
5'-most EST
                   jC-atX22018Q1E1B04b1
Method
                   BLASTN
                   q3128143
NCBI GI
```

BLAST score

E value

6.0e-15

```
E value
                  0.0e + 00
Match length
                   442
                   96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTI20, complete sequence [Arabidopsis thaliana]
                   120837
Seq. No.
                  5587 2.R1010
Contig ID
                  jC-atXLIB327432P3b10b1
5'-most EST
Method
                  BLASTX
                  g2244866
NCBI GI
BLAST score
                  766
                  1.0e-81
E value
Match length
                  144
% identity
                  100
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   120838
Seq. No.
Contig ID
                  5588 1.R1010
5'-most EST
                  jC-atXLIB327420P3b03b1
Method
                  BLASTX
                   q4454032
NCBI GI
BLAST score
                   446
                   3.0e-44
E value
                  137
Match length
% identity
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120839
                   5591 1.R1010
Contig ID
5'-most EST
                  LIB24-024-Q1-E1-C9
Method
                   BLASTX
NCBI GI
                   q3033384
BLAST score
                   1019
                   1.0e-111
E value
Match length
                   286
% identity
                   (AC004238) putative CTP synthase [Arabidopsis thaliana]
NCBI Description
                   120840
Seq. No.
Contig ID
                   5591 2.R1010
5'-most EST
                   jC-atXLIB327415P4d05b1
Method
                   BLASTX
NCBI GI
                   q2104535
BLAST score
                   542
                   3.0e-55
E value
                   158
Match length
% identity
                   (AF001308) T10M13.13 [Arabidopsis thaliana]
NCBI Description
                   120841
Seq. No.
                   5593 1.R1010
Contig ID
5'-most EST
                   jC-atX22018Q1E1C02b1
Method
                   BLASTX
NCBI GI
                   q4455244
BLAST score
                   195
```

```
Match length
                   142
% identity
                   36
                   (AL035523) MtN3-like protein [Arabidopsis thaliana]
NCBI Description
                   120842
Seq. No.
                   5594 1.R1010
Contig ID
                   jC-aTXP11C97P23T7037d1
5'-most EST
                   BLASTX
Method
                   g3935145
NCBI GI
BLAST score
                   240
                   8.0e-20
E value
                   113
Match length
                   45
% identity
NCBI Description
                  (AC005106) T25N20.9 [Arabidopsis thaliana]
                 120843
Seq. No.
                   5594 2.R1010
Contig ID
                  LIB22-037-Q1-E1-D6
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3935145
BLAST score
                   199
E value
                   4.0e-15
Match length
                  73
% identity
                   52
NCBI Description
                  (AC005106) T25N20.9 [Arabidopsis thaliana]
                   120844
Seq. No.
Contig ID
                   5595 1.R1010
5'-most EST
                  LIB22-018-Q1-E1-C4
Method
                   BLASTX
NCBI GI
                   g1707022
BLAST score
                   188
                   4.0e-14
E value
Match length
                   67
% identity
                   52
NCBI Description
                  (U78721) proline-rich protein isolog [Arabidopsis thaliana]
                   120845
Seq. No.
                   5596 1.R1010
Contig ID
5'-most EST
                  LIB3176-061-P1-K1-F7
Method
                  BLASTX
NCBI GI
                   g2980793
BLAST score
                   1067
                   1.0e-116
E value
Match length
                   247
% identity
                  85
NCBI Description
                   (AL022197) putative protein [Arabidopsis thaliana]
                   120846
Seq. No.
                   5597 1.R1010
Contig ID
5'-most EST
                   jC-atX22018Q1E1C07b1
Method
                  BLASTN
NCBI GI
                   q3128141
BLAST score
                  316
                  1.0e-178
E value
                   430
Match length
```

% identity

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQD22, complete sequence [Arabidopsis thaliana]
                  120847
Seq. No.
                  5599 1.R1010
Contig ID
                  jC-atXP94CH4G4T7b1
5'-most EST
                  BLASTX
Method
                  g2191165
NCBI GI
BLAST score
                  327
                  8.0e-30
E value
                  106
Match length
                  57
% identity
NCBI Description
                  (AF007270) A IG002P16.14 gene product [Arabidopsis
                  thaliana]
                  120848
Seq. No.
                  5599 2.R1010
Contig ID
5'-most EST
                  jC-atXP50C180F2T7073d1
                  BLASTN
Method
                  g531828
NCBI GI
                   58
BLAST score
                  2.0e-23
E value
Match length
                   62
                  98
% identity
NCBI Description
                  Cloning vector pSport1, complete cds
                  120849
Seq. No.
                  5599 3.R1010
Contig ID
5'-most EST
                  jC-atXP24C120O13T7025a1
                  120850
Seq. No.
                  5600 1.R1010
Contig ID
                   jC-atXLIB327428P1h04b2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1046225
                   1095
BLAST score
                   1.0e-120
E value
Match length
                   212
                   100
% identity
                  (U21952) ethylene response sensor [Arabidopsis thaliana]
NCBI Description
                  >gi 2623308 (AC002409) ethylene response sensor (ERS)
                   [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene
                   [Arabidopsis thaliana]
                   120851
Seq. No.
                   5600 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P3c04b1
Method
                  BLASTX
                   g1046225
NCBI GI
BLAST score
                   1016
E value
                   1.0e-119
Match length
                   225
                   95
% identity
                  (U21952) ethylene response sensor [Arabidopsis thaliana]
NCBI Description
                   >gi 2623308 (AC002409) ethylene response sensor (ERS)
                   [Arabidopsis thaliana] >gi 1584365 prf 2122405A ERS gene
```

[Arabidopsis thaliana]

```
120852
Seq. No.
Contig ID
                  5601 1.R1010
5'-most EST
                  LIB22-021-Q1-E1-B9
                  BLASTX
                  g3776578
NCBI GI
                  385
BLAST score
                  9.0e-37
E value
Match length
                  143
% identity
                  50
                  (AC005388) ESTs gb F13915 and gb_F13916 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
Seq. No.
                  120853
Contig ID
                  5601 2.R1010
                  jC-atXLIB327432P4c05b1
5'-most EST
Method
                  BLASTN
                  q4586349
NCBI GI
BLAST score
                  65
E value
                  6.0e-28
Match length
                  89
% identity
                  93
                  Arabidopsis thaliana DNA for glucose-1-phosphate
NCBI Description
                  adenylyltransferase, complete cds
Seq. No.
                  120854
Contig ID
                  5603 1.R1010
5'-most EST
                  jC-atXLIB327409P2f03b1
Method
                  BLASTX
                  q4586244
NCBI GI
BLAST score
                  357
                  1.0e-33
E value
Match length
                  162
% identity
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                  120855
Seq. No.
                  5605 1.R1010
Contig ID
5'-most EST
                  LIB3176-068-P1-K1-F12
Method
                  BLASTN
                  g4678258
NCBI GI
BLAST score
                  161
E value
                  3.0e-85
                  479
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F617
                  (ESSA project)
                  120856
Seq. No.
                  5606 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P4c07b1
Method
                  BLASTX
NCBI GI
                  g2088822
BLAST score
                  280
                  3.0e-24
E value
Match length
                  227
                  33
% identity
```

```
(AF003384) K07B1.4 gene product [Caenorhabditis elegans]
NCBI Description
Seq. No.
                  120857
                   5606 4.R1010
Contig ID
                  g2749216
5'-most EST
                   120858
Seq. No.
                   5608 1.R1010
Contig ID
                   jC-a\overline{t}XLIB327432P4c02b1
5'-most EST
                   BLASTN
Method
                   g2262155
NCBI GI
BLAST score
                   461
                   0.0e + 00
E value
Match length
                   499
% identity
                   98
                   DNA sequence of Arabidopsis thaliana BAC F5J6 from
NCBI Description
                   chromosome IV, complete sequence [Arabidopsis thaliana]
                   120859
Seq. No.
                   5609 1.R1010
Contig ID
                   jC-atXLIB327432P4c03b1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2264319
BLAST score
                   54
                   2.0e-21
E value
Match length
                   226
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXA21, complete sequence [Arabidopsis thaliana]
                   120860
Seq. No.
                   5611 1.R1010
Contig ID
                   jC-atXLIB327432P4c12b1
5'-most EST
                   120861
Seq. No.
                   5613 1.R1010
Contig ID
5'-most EST
                   LIB35-048-Q1-E1-H11
Method
                   BLASTN
NCBI GI
                   g3510347
BLAST score
                   269
E value
                   1.0e-149
Match length
                   433
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MSJ11, complete sequence [Arabidopsis thaliana]
                   120862
Seq. No.
Contig ID
                   5614 1.R1010
                   jC-atXLIB327401P3d12b2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2582640
BLAST score
                   63
E value
                   2.0e-26
Match length
                   75
                   96
% identity
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
```

```
120863
Seq. No.
Contig ID
                  5614 2.R1010
5'-most EST
                  jC-atXLIB327432P2d01b2
                  BLASTN
Method
                  q2462264
NCBI GI
BLAST score
                  44
                  3.0e-15
E value
Match length
                  52
                  96
% identity
                  Cucumis sativus mRNA for patatin-like protein, partial
NCBI Description
                  120864
Seq. No.
Contig ID
                  5614 3.R1010
5'-most EST
                  LIB35-016-Q1-E1-F4
Method
                  BLASTX
                  g4538929
NCBI GI
BLAST score
                  163
E value
                  8.0e-11
Match length
                  171
% identity
                  24
                   (ALO49483) putative nucleic acid binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  120865
Seq. No.
Contig ID
                  5615 1.R1010
5'-most EST
                  jC-atX22018Q1E1E04b1
Seq. No.
                  120866
Contig ID
                  5618 1.R1010
5'-most EST
                  LIB23-053-Q1-E1-A8
Method
                  BLASTX
NCBI GI
                   q4581959
BLAST score
                   349
                   1.0e-32
E value
Match length
                   123
                   29
% identity
                   (AJ005807) disulphide isomerase [Caenorhabditis briggsae]
NCBI Description
                  >gi_4581962_emb_CAB40204.1_ (AJ005808) disulphide isomerase
                   [Caenorhabditis briggsae]
Seq. No.
                   120867
                   5620 1.R1010
Contig ID
                   jC-atXLIB327432P2d05b1
5'-most EST
Method
                   BLASTX
                   q1724100
NCBI GI
BLAST score
                   561
                   2.0e-60
E value
                  275
Match length
% identity
                  (U79765) porin [Mesembryanthemum crystallinum]
NCBI Description
Seq. No.
                   120868
                   5625_1.R1010
Contig ID
                  LIB3176-065-P1-K1-G10
5'-most EST
                  BLASTN
Method
```

q3702731

NCBI GI

```
BLAST score
                   490
                  0.0e + 00
E value
Match length
                  548
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFC19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120869
                  5626 1.R1010
Contig ID
5'-most EST
                  jC-aTXLIB327432P2d09b2
Method
                  BLASTX
NCBI GI
                  g3850816
BLAST score
                  519
                  8.0e-53
E value
Match length
                  102
% identity
                  88
                  (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                  sativa]
                  120870
Seq. No.
                  5631 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P4d04b1
Method
                  BLASTX
NCBI GI
                  g3176659
BLAST score
                  112
E value
                  3.0e-09
Match length
                  70
% identity
                  49
NCBI Description
                  (AC004393) Strong similarity to receptor kinase gb M80238
                  from A. thaliana. [Arabidopsis thaliana]
                  120871
Seq. No.
                  5635 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P3d05b1
Method
                  BLASTX
                  g2911078
NCBI GI
BLAST score
                  376
E value
                   4.0e-61
Match length
                  243
% identity
                  57
NCBI Description
                  (AL021960) putative protein [Arabidopsis thaliana]
                  120872
Seq. No.
                  5637 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P4d02b1
Method
                  BLASTX
                  g4646203
NCBI GI
                  309
BLAST score
                  3.0e-28
E value
                  95
Match length
                  59
% identity
                  (AC007230) Belongs to PF 00026 Eukaryotic aspartyl protease
NCBI Description
                  family. [Arabidopsis thaliana]
                  120873
Seq. No.
                  5640 1.R1010
Contig ID
5'-most EST
                  jC-aTXLIB327432P4d03b1
```

```
Method
                  BLASTX
NCBI GI
                  g4678354
BLAST score
                  938
E value
                  1.0e-101
Match length
                  185
% identity
                   (ALO49659) cysteine endopeptidase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  120874
Seq. No.
                  5640 2.R1010
Contig ID
                  LIB3177-096-P1-K1-D11
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4678354
BLAST score
                  1191
E value
                  1.0e-131
Match length
                  227
% identity
                   (ALO49659) cysteine endopeptidase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  120875
Seq. No.
Contig ID
                  5646 1.R1010
5'-most EST
                   jC-atXLIB327409P4c05b1
Method
                  BLASTN
NCBI GI
                  q2582640
BLAST score
                   67
E value
                   4.0e-29
Match length
                  74
                  99
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  120876
Seq. No.
Contig ID
                   5647 1.R1010
5'-most EST
                  LIB3176-101-P1-K1-B6
Seq. No.
                   120877
Contig ID
                   5647 2.R1010
5'-most EST
                  LIB25-002-Q1-E1-C7
Method
                  BLASTX
NCBI GI
                   q4097569
BLAST score
                   374
E value
                   2.0e-35
Match length
                   92
% identity
                  73
NCBI Description
                  (U64915) GMFP4 [Glycine max]
Seq. No.
                   120878
Contig ID
                   5647 3.R1010
                   jC-atXmonuni27Bb12b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4097569
BLAST score
                  86
                   3.9e-02
E value
                   58
Match length
% identity
                   54
```

```
(U64915) GMFP4 [Glycine max]
NCBI Description
Seq. No.
                  120879
Contig ID
                  5648 1.R1010
                  LIB23-031-Q1-E1-G8
5'-most EST
                  BLASTX
Method
                  q3915847
NCBI GI
                  426
BLAST score
                  6.0e-42
E value
                  83
Match length
                  100
% identity
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  120880
                  5652 1.R1010
Contig ID
                  jC-atXLIB327409P4c04b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2129581
BLAST score
                  322
E value
                  1.0e-29
Match length
                  147
% identity
                  47
                  envelope Ca2+-ATPase precursor - Arabidopsis thaliana
NCBI Description
                  >qi 471089 dbj BAA03091 (D13984) chloroplast envelope
                  Ca2+-ATPase precursor [Arabidopsis thaliana]
                  >qi 4165448 emb CAA49558 (X69940) envelope Ca2+-ATPase
                  [Arabidopsis thaliana]
Seq. No.
                  120881
Contig ID
                  5653 1.R1010
                  LIB3234-096-P1-K1-G5
5'-most EST
Method
                  BLASTX
                  g3738309
NCBI GI
BLAST score
                  236
E value
                  2.0e-19
                  58
Match length
                  79
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  120882
Seq. No.
Contig ID
                  5654 1.R1010
                  LIB22-019-Q1-E1-A11
5'-most EST
Method
                  BLASTX
                  g2459445
NCBI GI
BLAST score
                  512
E value
                  1.0e-51
Match length
                  185
% identity
                  54
                  (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  120883
                  5660 1.R1010
Contig ID
                  LIB22-019-Q1-E1-A7
5'-most EST
```

120884

Method

BLASTX

```
5661 1.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327420P1a10b1
 Seq. No.
                    120885
 Contig ID
                    5663 1.R1010
                    jC-atXLIB327432P3e01b1
 5'-most EST
 Method
                    BLASTX
                    g4337206
 NCBI GI
 BLAST score
                    323
                    1.0e-29
 E value
                    147
 Match length
 % identity
                    46
                    (AC006403) putative replication factor-A protein
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    120886
 Contig ID
                    5667 2.R1010
 5'-most EST
                    jC-atXLIB327432P4e06b1
 Method
                    BLASTN
 NCBI GI
                    q3047100
 BLAST score
                    190
 E value
                    1.0e-102
 Match length
                    592
 % identity
                    98
NCBI Description Arabidopsis thaliana BAC F6N23
                    120887
 Seq. No.
 Contig ID
                    5668 1.R1010
 5'-most EST
                    jC-atXP122C117J6T7081a1
 Method
                    BLASTX
 NCBI GI
                    g2244759
 BLAST score
                    335
 E value
                    1.0e-51
 Match length
                    115
 % identity
                    86
 NCBI Description
                   (Z97335) selenium-binding protein [Arabidopsis thaliana]
 Seq. No.
                    120888
 Contig ID
                    5668 2.R1010
 5'-most EST
                    jC-atXP119C206D5T7d1
 Seq. No.
                    120889
 Contig ID
                    5668 3.R1010
 5'-most EST
                    jC-atXP119C196A3T7084a1
 Method
                    BLASTX
                    q4263695
 NCBI GI
 BLAST score
                    75
                    9.0e-30
 E value
 Match length
                    93
 % identity
                    (AC006223) putative myosin II heavy chain [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    120890
 Contig ID
                    5668 4.R1010
 5'-most EST
                    jC-atXLIB327438P1d09a1
```

5'-most EST

```
g2244759
NCBI GI
BLAST score
                  970
                  1.0e-105
E value
                  232
Match length
                  82
% identity
                  (Z97335) selenium-binding protein [Arabidopsis thaliana]
NCBI Description
                  120891
Seq. No.
                  5668_6.R1010
Contig ID
5'-most EST
                  jC-atX23025Q1E1D02a1
Method
                  BLASTX
NCBI GI
                  g2244760
BLAST score
                  413
                  2.0e-40
E value
                  76
Match length
                  99
% identity
                  (Z97335) selenium-binding protein [Arabidopsis thaliana]
NCBI Description
                  120892
Seq. No.
                  5668_8.R1010
Contig ID
5'-most EST
                  LIB24-077-Q1-E1-A4
Method
                  BLASTX
                  g2244759
NCBI GI
BLAST score
                  1415
                  1.0e-178
E value
Match length
                  305
                  99
% identity
                  (Z97335) selenium-binding protein [Arabidopsis thaliana]
NCBI Description
                  120893
Seq. No.
                  5669 1.R1010
Contig ID
5'-most EST
                  LIB23-007-Q1-E1-C11
                  BLASTX
Method
NCBI GI
                  g1706336
BLAST score
                  388
                  2.0e-37
E value
Match length
                  100
% identity
                  70
                  UROPORPHYRINOGEN DECARBOXYLASE >gi_1001337_dbj_BAA10824_
NCBI Description
                  (D64006) uroporphyrinogen decarboxylase [Synechocystis sp.]
                  120894
Seq. No.
                  5671 1.R1010
Contig ID
5'-most EST
                  LIB25-029-Q1-E1-G1
Method
                  BLASTX
NCBI GI
                  g4587615
BLAST score
                  1119
                  1.0e-123
E value
Match length
                  235
% identity
                  97
                  (ACO06951) putative acyl-CoA synthetase [Arabidopsis
NCBI Description
                  thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213)
                  putative acyl-CoA synthetase [Arabidopsis thaliana]
                  120895
Seq. No.
Contig ID
                  5672_1.R1010
```

jC-atXLIB327432P4e04b1

```
BLASTX
Method
NCBI GI
                  q4314355
BLAST score
                  555
E value
                  5.0e-57
                  119
Match length
                  91
% identity
                  (AC006340) unknown protein [Arabidopsis thaliana]
NCBI Description
                  120896
Seq. No.
                  5674 1.R1010
Contig ID
                  jC-atX22019Q1E1C10b1
5'-most EST
                  BLASTN
Method
                  g2098816
NCBI GI
BLAST score
                  350
                  0.0e + 00
E value
Match length
                  426
                  98
% identity
NCBI Description Arabidopsis thaliana BAC F19G10, complete sequence
                  120897
Seq. No.
                  5675 1.R1010
Contig ID
                  jC-atX24061Q1E1D08b1
5'-most EST
                  BLASTN
Method
                  g2828183
NCBI GI
BLAST score
                  397
                  0.0e + 00
E value
Match length
                  455
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPL12, complete sequence [Arabidopsis thaliana]
                  120898
Seq. No.
                  5676 1.R1010
Contig ID
5'-most EST
                  LIB24-120-Q1-E1-F5
Method
                  BLASTX
                  g1346812
NCBI GI
BLAST score
                  600
E value
                  1.0e-62
Match length
                  182
                   67
% identity
                  26S PROTEASE REGULATORY SUBUNIT 8 (PROTEASOME SUBUNIT P45)
NCBI Description
                   (THYROID HORMONE RECEPTOR INTERACTING PROTEIN 1) (TRIP1)
                  >gi 2136007 pir I53510 proteasome subunit p45 - human
                  >gi 976227_dbj_BAA07919_ (D44467) 26S proteasome subunit
                  p45 [Homo sapiens] >gi_1096205_prf__2111282A 26S proteasome
                  [Homo sapiens]
                  120899
Seq. No.
Contig ID
                  5676 2.R1010
5'-most EST
                  g16969
Method
                  BLASTX
NCBI GI
                  g3122626
BLAST score
                  183
E value
                  3.0e-13
Match length
                  86
% identity
                  49
NCBI Description 26S PROTEASE REGULATORY SUBUNIT 8 >gi 2245467 (U97538) DUG
```

[Drosophila melanogaster] 120900 Seq. No. Contig ID 5679 1.R1010 5'-most EST g2748587 120901 . Seq. No. 5681 1.R1010 Contig ID 5'-most EST jC-atXLIB327432P3e12b1 Method BLASTX NCBI GI q4056465 BLAST score 457 E value 2.0e-45 Match length 119 % identity 82 NCBI Description (AC005990) F508.40 [Arabidopsis thaliana] 120902 Seq. No. Contig ID 5683 1.R1010 5'-most EST LIB35-030-01-E1-C12 120903 Seq. No. 5684 1.R1010 Contig ID jC-atXP94CH5F12T7002d1 5'-most EST · BLASTX Method NCBI GI q4539327 BLAST score 2249 0.0e + 00E value Match length 442 % identity 100 NCBI Description (AL035679) putative proton pump [Arabidopsis thaliana] 120904 Seq. No. 5684 2.R1010 Contig ID 5'-most EST jC-atXLIB327411P3a01b1 Method BLASTX NCBI GI q4539327 BLAST score 304 E value 5.0e-46 Match length 148 % identity 79 NCBI Description (AL035679) putative proton pump [Arabidopsis thaliana] Seq. No. 120905 Contia ID 5687 1.R1010 5'-most EST jC-atXLIB327432P4f01b1 Seq. No. 120906 Contig ID 5688 1.R1010 5'-most EST jC-atXLIB327419P4a04b1 Method BLASTN NCBI GI g2582640 BLAST score 57 · · · E value 6.0e-23 Match length 65 % identity 97

NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing

% identity

94

factor, RSp40 120907 Seq. No. 5688 2.R1010 Contig ID LIB23-014-Q1-E1-D1 5'-most EST BLASTX Method g4105798 NCBI GI 712 BLAST score 4.0e-75 E value 202 Match length 54 % identity (AF049930) PGP237-11 [Petunia x hybrida] NCBI Description 120908 Seq. No. 5688 3.R1010 Contig ID 5'-most EST LIB3176-102-P1-K1-A2 BLASTX Method g4105798 NCBI GI BLAST score 162 3.0e-14E value 51 Match length 67 % identity (AF049930) PGP237-11 [Petunia x hybrida] NCBI Description 120909 84 Seq. No. 5688_5.R1010 Contig ID LIB22-019-Q1-E1-D12 5'-most EST BLASTX Method g4105798 NCBI GI 175 BLAST score 2.0e-12 E value 46 Match length 61 % identity (AF049930) PGP237-11 [Petunia x hybrida] NCBI Description 120910 Seq. No. 5691 1.R1010 Contig ID 5'-most EST jC-atXP69C219P22T7040d1 Method BLASTN g4220645 NCBI GI BLAST score 424 0.0e + 00E value Match length 931 85 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MYA6, complete sequence [Arabidopsis thaliana] 120911 Seq. No. 5691 2.R1010 Contig ID 5'-most EST jC-atXLIB327417P2b04b1 Method BLASTN g4220645 NCBI GI BLAST score 282 1.0e-157 E value Match length 1277

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

120912 Seq. No. 5692 1.R1010 Contig ID g2733177 5'-most EST BLASTN Method q3869069 NCBI GI 222 BLAST score 1.0e-121 E value 386 Match length 99 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MEB5, complete sequence [Arabidopsis thaliana] 120913 Seq. No. Contig ID 5693 1.R1010 jC-atXLIB327432P2f10b2 5'-most EST BLASTX Method q4586021 NCBI GI 496 BLAST score 6.0e-50 E value 134 Match length 79 % identity (AC007170) putative cytoplasmic aconitate hydratase NCBI Description [Arabidopsis thaliana] 120914 Seq. No. Contig ID 5695 1.R1010 jC-atXLIB327432P2f11b2 5'-most EST BLASTN Method q2582640 NCBI GI BLAST score 42 5.0e-14 E value 62 Match length 94 % identity Arabidopsis thaliana mRNA for arginine/serine-rich splicing NCBI Description factor, RSp40 120915 Seq. No. 5697 1.R1010 Contig ID jC-atX35005Q1E1F11b1 5'-most EST Method BLASTX g4835226 NCBI GI 285 BLAST score 3.0e-25 E value 96 Match length 57 % identity (AL049862) putative protein [Arabidopsis thaliana] NCBI Description 120916 Seq. No. 5697 2.R1010 Contig ID jC-atXLIB327438Pla10a1 5'-most EST Method BLASTX NCBI GI g4006891 BLAST score 168 E value 9.0e-12 59 Match length

MYA6, complete sequence [Arabidopsis thaliana]

% identity

```
% identity
                   54
NCBI Description
                   (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                   120917
                   5699 1.R1010
Contig ID
                   LIB24-009-Q1-E1-H5
5'-most EST
                   BLASTX
Method
                   q4584346
NCBI GI
BLAST score
                   265
                   4.0e-23
E value
Match length
                   87
% identity
                   57
                  (AC007127) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120918
                   5703 1.R1010
Contig ID
                   jC-atXLIB327410P2a10b1
5'-most EST
Method
                   BLASTX
                   q4558678
NCBI GI
BLAST score
                   63
E value
                   9.0e-70
Match length
                   165
% identity
                   84
                  (AC006586) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   120919
Contig ID
                   5703 3.R1010
5'-most EST
                   jC-atXmonuni26Ch04b1
Method
                   BLASTX
                   g4558678
NCBI GI
BLAST score
                   306
E value
                   7.0e-28
Match length
                   71
% identity
                   79
                   (AC006586) unknown protein [Arabidopsis thaliana]
NCBI Description
                  120920
Seq. No.
                   5703 4.R1010
Contig ID .
5'-most EST
                   LIB3176-018-P1-K1-H6
Method
                   BLASTN -
NCBI GI
                   q4558674
BLAST score
                   60
                  8.0e-25
E value
                   408
Match length
                   89
% identity
                  Arabidopsis thaliana chromosome II BAC F7B19 genomic
NCBI Description
                  sequence, complete sequence
                   120921
Seq. No.
                   5709 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327409P3f03b1
Method
                   BLASTX
NCBI GI
                   q3738257
BLAST score
                   622
E value
                   1.0e-64
Match length
                   145
```

```
NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
                   nigra]
                   120922
 Seq. No.
                   5709 2.R1010
 Contig ID
                   jC-atXLIB327424P1a12b2
.5'-most EST
                   BLASTX
Method
                   g3738257
NCBI GI
 BLAST score
                   128
                   0.0e+00
 E value
                   385
Match length
                   87
 % identity
                   (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
 NCBI Description
                   nigra]
                   120923
 Seq. No.
                  √5709 4.R1010
 Contig ID
 5'-most EST
                   g2413072
 Method
                   BLASTX
                   g2499498
 NCBI GI
 BLAST score
                   417
                   8.0e-41
 E value
                   86
Match length
                   94
 % identity
                   PHOSPHOGLYCERATE KINASE, CYTOSOLIC
 NCBI Description
                   >qi 1161602 emb CAA88840 (Z48976) phosphoglycerate kinase
                    (PGK) [Nicotiana tabacum]
                   120924
 Seq. No.
                   5710 1.R1010
 Contig ID
 5'-most EST
                   LIB22-055-Q1-E1-D5
                   BLASTX
 Method
                   g1628622
 NCBI GI
 BLAST score
                   529
                   5.0e-54
 E value
                   150
 Match length
                    69
 % identity
                   (U72631) flavonol synthase [Arabidopsis thaliana]
 NCBI Description
                   >gi 1805305 (U84258) flavonol synthase [Arabidopsis
                   thaliana] >gi_1805307 (U84259) flavonol synthase
                    [Arabidopsis thaliana] >gi 1805309 (U84260) flavonol
                   synthase [Arabidopsis thaliana]
                   120925
 Seq. No.
 Contig ID
                   5711_1.R1010
                   g430<del>0</del>13
 5'-most EST
 Method
                   BLASTX
                   g3582329
 NCBI GI
 BLAST score
                    241
 E value
                   2.0e-20
 Match length
                   103
 % identity
                    47
                   (AC005496) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   120926
 Seq. No.
 Contig ID
                   5713 1.R1010
                   LIB22-019-Q1-E1-F5
 5'-most EST ·
```

```
Seq. No.
                  120927
                  5714 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P2g05b1
Method
                  BLASTX
                  g2401257
NCBI GI
BLAST score
                  178
                  5.0e-20
E value
                  106
Match length
                  54
% identity
                 (D63951) TBZ17 [Nicotiana tabacum]
NCBI Description
Seq. No.
                  120928
                  5714 2.R1010
Contig ID
                  jC-alXLIB327435P2g04a1
5'-most EST
                  BLASTX
Method
                  g2244744
NCBI GI
BLAST score
                  289
                  1.0e-25
E value
                  101
Match length
                  51
% identity
NCBI Description (Y13676) bZIP DNA-binding protein [Antirrhinum majus]
                  120929
Seq. No.
                  5715 2.R1010
Contig ID
5'-most EST
                  LIB22-082-Q1-E2-C6
                  BLASTX
Method
                  g113334
NCBI GI
BLAST score
                  727
                  8.0e-77
E value
                  327
Match length
                  46
% identity
                  ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2
NCBI Description
                  ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A)
                   (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT)
                  >gi 90291 pir A30111 alpha-adaptin A - mouse
                  >gi_49878_emb_CAA33096_ (X14971) alpha-adaptin (A) (AA
                  1-977) [Mus musculus]
Seq. No.
                  120930
                  5716 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P4g02b1
Method
                  BLASTX
NCBI GI
                  g4204303
BLAST score
                  271
                  2.0e-23
E value
                  182
Match length
                  33
% identity
                  (AC003027) lcl_prt_seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
                  120931
Seq. No.
                  5717 1.R1010
Contig ID
                  LIB2\overline{2}-041-Q1-E1-C6
5'-most EST
Seq. No.
                  120932
                  5718 1.R1010
Contig ID
```

Method

```
5'-most EST
                  LIB25-105-Q1-E1-E1
                  120933
Seq. No.
Contig ID
                  5720 1.R1010
5'-most EST
                  LIB35-017-Q1-E1-C12
                  BLASTX
Method
                  q3482967 ...
NCBI GI
BLAST score
                  503
                  5.0e-51
E value
Match length
                  96
                  100
% identity
                  (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                  thaliana] >qi 4559345 qb AAD23006.1 AC006585 1 (AC006585)
                  protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.
                  120934
Contig ID
                  5721 1.R1010
5'-most EST
                  iC-atXLIB327408P1c08b1
                  BLASTX
Method
                  q1351135
NCBI GI
BLAST score
                  1541
                  1.0e-172
E value
                  295
Match length
% identity
                  SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
NCBI Description
                  >gi_436792_emb_CAA50317_ (X70990) sucrose synthase
                  [Arabidopsis thaliana]
Seq. No.
                  120935
                  5722 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P4g06b1
Method
                  BLASTX
NCBI GI
                  q4559372
BLAST score
                  1179
E value
                  1.0e-130
Match length
                  225
% identity
                  (AC006585) putative CONSTANS protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4646235 gb AAD26898.1 AC007266 6 (AC007266) putative
                  CONSTANS protein [Arabidopsis thaliana]
Seq. No.
                  120936
Contig ID
                  5723 1.R1010
5'-most EST
                  jC-alXLIB327435P2h10a1
Method
                  BLASTN
NCBI GI
                  q4371278
BLAST score
                   476
E value
                  0.0e + 00
Match length
                  1046
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC T2N18 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  120937
Seq. No.
                  5724_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327420P1h06b1
```

BLASTX

Match length

```
NCBI GI
                   g1350783
 BLAST score
                   248
E value
                   1.0e-20
Match length
                   297
 % identity
                   6
                   RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR
 NCBI Description
                   >qi 282883 pir S27756 receptor-like protein kinase
                   precursor - Arabidopsis thaliana >gi 166850 (M84660)
                   receptor-like protein kinase [Arabidopsis thaliana]
                   >gi 2842492 emb CAA16889 (AL021749) receptor-like protein
                   kinase 5 precursor (RLK5) [Arabidopsis thaliana]
                   120938
 Seq. No.
 Contig ID
                   5724 2.R1010
                   jC-aTXP83CG3E5T7030a1
 5'-most EST
 Method
                   BLASTN
                   q57923
 NCBI GI
 BLAST score
                   54
                   2.0e-21
 E value
Match length
                   58
                   98
 % identity
                   M.musculus Flk-1 mRNA
 NCBI Description
                   120939
 Seq. No.
 Contig ID
                   5729 1.R1010
 5'-most EST
                   jC-atXLIB327411P2f09b1
Method
                   BLASTX
 NCBI GI
                   g2244798
 BLAST score
                   339
                   1.0e-31
 E value
Match length
                   101
 % identity
                   69
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                   120940
 Seq. No.
                   5730 1.R1010
 Contig ID
                   LIB2\overline{2}-019-Q1-E1-H11
 5'-most EST
                   120941
 Seq. No.
 Contig ID
                   5733 1.R1010
                   LIB25-029-Q1-E1-D3
 5'-most EST
 Method
                   BLASTX
                   q1041702
 NCBI GI
                   775
 BLAST score
                   1.0e-82
 E value
 Match length
                   167
 % identity
                   8.6
                   (U30476) expansin At-EXP1 [Arabidopsis thaliana]
 NCBI Description
                   120942
 Seq. No.
 Contig ID
                   5734 1.R1010
                   jC-atXLIB327432P2h06b2
 5'-most EST
                   BLASTN
Method
 NCBI GI
                   g2191126
 BLAST score
                   249
 E value
                   1.0e-138
```

```
98
% identity
NCBI Description Arabidopsis thaliana BAC IG002N01
Seq. No.
                  120943
                  5737 1.R1010
Contig ID
                  jC-a\overline{t}XP121C120C24T7079d1
5'-most EST
Method
                  BLASTX
                  g2244896
NCBI GI
BLAST score
                  1064
                  1.0e-116
E value
Match length
                  224
% identity
                  92
                  (Z97338) similar to HSR201 protein N.tabacum [Arabidopsis
NCBI Description
                  thaliana]
                  120944
Seq. No.
                  5737 2.R1010
Contig ID
                  LIB3176-012-P1-K1-E9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2244896
BLAST score
                  413
E value
                  3.0e-40
Match length
                  110
% identity
NCBI Description (Z97338) similar to HSR201 protein N.tabacum [Arabidopsis
                  thaliana]
Seq. No.
                  120945
                  5738 1.R1010
Contig ID
                  LIB25-026-Q1-E1-E8
5'-most EST.
Method
                  BLASTN
                  g4757399
NCBI GI
BLAST score
                  139
                  4.0e-72
E value
                  340
Match length
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MEE13, complete sequence
                  120946
Seq. No.
                  5739_2.R1010
Contig ID
                  LIB22-060-Q1-E1-H9
5'-most EST
                  BLASTX
Method
                  q4467139
NCBI GI
BLAST score
                  500
                  3.0e-50
E value
                  95
Match length
                  99
% identity
                  (AL035540) putative protein phosphatase-2c [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  120947
Contig ID .
                  5740 1.R1010
                  jC-atXLIB327440Pld06b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3319344
BLAST score
                  565
```

```
4.0e-58
 E value
 Match length
                    128
 % identity
                    87
                    (AF077407) contains similarity to UDP-glucoronosyl and
 NCBI Description
                   ·UDP-glucosyl transferases (Pfam: UDPGT.hmm, score: 85.94)
                    [Arabidopsis thaliana]
                    120948
 Seq. No.
                   5741 1.R1010
 Contig ID
                    LIB3176-014-P1-K1-H12
 5'-most EST
                    BLASTX
 Method
                    g4539423
 NCBI GI
 BLAST score
                    88
 E value
                   9.0e-40
 Match length
                    91
 % identity
                    88
                    (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    120949
                   5744 1.R1010
 Contig ID
                   LIB25-040-Q1-E1-C8
 5'-most EST
 Method
                   BLASTX
                   g4678332
NCBI GI
 BLAST score
                    603
                    1.0e-62
 E value
 Match length
                    145
 % identity
                    84
                    (AL049658) putative peptide transporter [Arabidopsis
 NCBI Description
                   thaliana]
                    120950
 Seq. No.
                   5748 1.R1010
 Contig ID
 5'-most EST
                   LIB3175-055-P1-K1-E3
                   BLASTN
 Method
 NCBI GI
                   g2264314
 BLAST score
                    24
 E value
                   2.0e-03
 Match length
                    469
 % identity
                    49
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MQK4, complete sequence [Arabidopsis thaliana]
                    120951
 Seq. No.
                   5749 1.R1010
 Contig ID
 5'-most EST
                    jC-atXLIB327432P4e05b1
                   120952
 Seq. No.
                   5752 1.R1010
 Contig ID
                   LIB24-091-Q1-E1-A6
 5'-most EST
 Method
                   BLASTN
 NCBI GI
                   q3449321
 BLAST score
                   377
                   0.0e + 00
 E value
                   409
 Match length
                   98
 % identity
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MTG10, complete sequence [Arabidopsis thaliana] 120953 Seq. No. 5756 1.R1010 Contig ID 5'-most EST LIB3175-057-P1-K1-F6 120954 Seq. No. 5760_1.R1010 Contig ID 5'-most EST jC-atXLIB327432P2f02b2 BLASTN Method g2281081 NCBI GI BLAST score 437 E value 0.0e + 00437 Match length % identity 68 Arabidopsis thaliana chromosome II BAC F18019 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 120955 Seq. No. 5763 1.R1010 Contig ID 5'-most EST LIB22-020-Q1-E1-C2 BLASTN Method NCBI GI g3132469 BLAST score 174 3.0e-93 E value Match length 293 % identity 96 NCBI Description Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana] 120956 Seq. No. 5767 1.R1010 Contig ID jC-atXmonuni26Ch10b1 5'-most EST Method BLASTX NCBI GI g1706917 BLAST score 234 3.0e-19 E value Match length 114 % identity 44 FLAVONOL SULFOTRANSFERASE-LIKE >gi 2129586 pir S69188 NCBI Description flavonol sulfotransferase - Arabidopsis thaliana >gi 833767 emb CAA86850.1 (Z46823) Flavonol sulfotransferase [Arabidopsis thaliana] 120957 Seq. No. 5768 1.R1010 Contig ID 5'-most EST jC-alXLIB327436P4a03b1 Method BLASTN NCBI GI g3869065 BLAST score 175 E value 1.0e-93 Match length 262 % identity 97 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K24M7, complete sequence [Arabidopsis thaliana]

120958

```
Contig ID
                   5769 1.R1010
                   LIB22-020-Q1-E1-D1
 5'-most EST
 Method
                   BLASTX
                    q4220476
 NCBI GI
                    523
 BLAST score
                    3.0e-53
 E value
                    112
 Match length
                    96
 % identity
                    (AC006069) ribophorin I-like protein [Arabidopsis thaliana]
 NCBI Description
                   120959
 Seq. No.
                   5771 1.R1010
 Contig ID
 5'-most EST
                   LIB3234-080-P1-K1-H3
 Method
                   BLASTX
                   g3242717
 NCBI GI
 BLAST score
                    730
                   2.0e-77
 E value
                   182
 Match length
 % identity
                   81
                   (AC003040) putative APG protein [Arabidopsis thaliana]
 NCBI Description
                   120960
Seq. No.
                   5773 1.R1010
 Contig ID
 5'-most EST
                   LIB24-035-Q1-E1-A11
 Method
                   BLASTX
 NCBI GI
                   g3413705
 BLAST score
                   529
                    6.0e-54
 E value
 Match length
                   120
 % identity
                    (AC004747) putative glycine dehydrogenase [Arabidopsis
 NCBI Description
                   thaliana]
                   120961
 Seq. No.
                   5775 1.R1010
 Contig ID
 5'-most EST
                   jC-atXLIB327415P1f10b1
                   BLASTN
 Method
                   g4388714
 NCBI GI
 BLAST score
                    211
 E value
                    1.0e-115
 Match length
                    386
                   98
 % identity
 NCBI Description
                   Arabidopsis thaliana chromosome II BAC F5K7 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   120962
Seq. No.
                   5775_2.R1010
 Contig ID
 5'-most EST
                   LIB25-012-Q1-E1-G8
 Method
                   BLASTN
 NCBI GI
                   g4388714
 BLAST score
                   328
 E value
                   0.0e + 00
 Match length
                   540
                   99
 % identity
                   Arabidopsis thaliana chromosome II BAC F5K7 genomic
 NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

```
120963
Seq. No.
Contig ID
                  5776 1.R1010
5'-most EST
                  LIB25-013-Q1-E1-F12
Method
                  BLASTX
                  q3004556
NCBI GI
BLAST score
                  518
                  2.0e-52
E value
                  109
Match length
                  97
% identity
                  (AC003673) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  120964
Seq. No.
                  5776 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P2f09b1
Method
                  BLASTX
                  g3004556
NCBI GI
BLAST score
                  228
E value
                  1.0e-18
Match length
                  109
% identity
                  82
                  (AC003673) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  120965
Seq. No.
Contig ID
                  5777 1.R1010
5'-most EST
                  LIB25-056-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                  q2342687
BLAST score
                  329
E value
                  2.0e-30
Match length
                  106
% identity
                  58
                   (AC000106) Similar to Beta integral membrane protein
NCBI Description
                   (qb U43629). EST qb W43122 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  120966
Contig ID
                  5778 1.R1010
5'-most EST
                  jC-atXLIB327422P1c09b1
Method
                  BLASTN
NCBI GI
                  q3510337
BLAST score
                  250
E value
                  1.0e-138
Match length
                  504
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19E20, complete sequence [Arabidopsis thaliana]
                  120967
Seq. No.
Contig ID
                  5779 1.R1010
                  jC-alXLIB327435P2f06a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4678928
BLAST score
                  230
                  6.0e-19
E value
Match length
                  144
% identity
                  45
                  (AL049711) putative serine/threonine protein kinase
NCBI Description
```

```
[Arabidopsis thaliana]
                  120968
Seq. No.
                  5785 1.R1010
Contig ID
                  jC-atXLIB327432P4f12b1
5'-most EST
                  120969
Seq. No.
                  5786 1.R1010
Contig ID
                  jC-atXP82CG2F6T7d3
5'-most EST
                  BLASTX
Method
                  g927577
NCBI GI
BLAST score
                  418
                  3.0e-56
E value
Match length
                  208
% identity
                  58
                  (U12927) alpha-galactosidase [Phaseolus vulgaris]
NCBI Description
                  120970
Seq. No.
                  5786 2.R1010
Contig ID
                  LIB3177-075-P1-K1-D10
5'-most EST
                  BLASTX
Method
                  g927577
NCBI GI
BLAST score
                  301
                  4.0e-32
E value
Match length
                  126
% identity
                  (U12927) alpha-galactosidase [Phaseolus vulgaris]
NCBI Description
                  120971
Seq. No.
                  5790_1.R1010
Contig ID
5'-most EST
                  LIB22-020-Q1-E1-E7
                  BLASTX
Method
                  g113742
NCBI GI
BLAST score
                  624
                  6.0e-65
E value
Match length
                  227
                  55
% identity
                  AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE)
NCBI Description
                  >gi 147142 (M15273) peptidase N [Escherichia coli]
                  >gi 147144 (M15676) aminopeptidase N [Escherichia coli]
                  >gi_1787163 (AE000195) aminopeptidase N [Escherichia coli]
                  >gi 4062498 dbj BAA35684 (D90731) Aminopeptidase n (EC
                  3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia
                  coli]
                  120972
Seq. No.
Contig ID
                  5794 1.R1010
                  LIB25-082-Q1-E1-H1
5'-most EST
Method
                  BLASTX
                  g3861068
NCBI GI
BLAST score
                  345
E value
                  3.0e-32
Match length
                  142
% identity
                   (AJ235272) unknown [Rickettsia prowazekii]
NCBI Description
```

120973

```
Contig ID
                  5795 1.R1010
5'-most EST
                  jC-atXLIB327432P1g07b1
Method
                  BLASTN
NCBI GI
                  g4063737
                  176
BLAST score
E value
                  3.0e-94
Match length
                  380
% identity
                  95
                  Arabidopsis thaliana chromosome II BAC F24D13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  120974
                  5798_1.R1010
Contig ID
5'-most EST
                  g1216780
                  120975
Seq. No.
Contig ID
                  5799 2.R1010
                  LIB22-020-Q1-E1-F5
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3292807
BLAST score
                  819
                  0.0e + 00
E value
Match length
                  823
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19
                  (ESSAII project)
                  120976
Seq. No.
Contig ID
                  5800 1.R1010
                  LIB2<del>2</del>-020-Q1-E1-F6
5'-most EST
Method
                  BLASTX
                  g1200205
NCBI GI
BLAST score
                  461
                  5.0e-46
E value
Match length
                  98
% identity
                  88
NCBI Description
                  (X95753) DAG [Antirrhinum majus]
                  120977
Seq. No.
Contig ID
                  5804 1.R1010
5'-most EST
                  jC-atXLIB327432P3g03b1
Method
                  BLASTX
NCBI GI
                  g2980785
BLAST score
                  500
E value
                  1.0e-50
Match length
                  119
% identity
                  82
NCBI Description (ALO22198) SERINE CARBOXYPEPTIDASE II - like protein
                  [Arabidopsis thaliana]
                  120978
Seq. No.
Contig ID
                  5805_1.R1010
5'-most EST
                  jC-atXLIB327432P4g04a1
Method
                  BLASTN
NCBI.GI
                  g4469002
BLAST score
                  249
                  1.0e-137
E value
```

```
284
Match length
% identity
                   96
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                   (ESSA project)
                  120979
Seq. No.
                  5807 1.R1010
Contig ID
                  jC-atXLIB327411P1a05b1
5'-most EST
                  120980
Seq. No.
                  5808 1.R1010
Contig ID
                  jC-atXLIB327432P4g05b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3212846
BLAST score
                  534
E value
                  0.0e + 00
                  869.
Match length
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  120981
Seq. No.
                  5810 1.R1010
Contig ID
                  LIB35-048-Q1-E1-H3
5'-most EST
                  120982
Seq. No.
Contig ID
                  5818 1.R1010
5'-most EST
                  LIB24-018-Q1-E1-C4
Method
                  BLASTX
                  g3264757
NCBI GI
BLAST score
                  64
                  7.0e-12
E value
Match length
                  117
                  50
% identity
                  (AF071888) zeaxanthin epoxidase [Prunus armeniaca]
NCBI Description
                  120983
Seq. No.
                  5820 1.R1010
Contig ID
5'-most EST
                  jC-a\(\bar{1}\)XLIB327436P3a04b1
Method
                  BLASTX
                   q3170525
NCBI GI
BLAST score
                  1562
                  1.0e-174
E value
                  358
Match length
                  80
% identity
                  (AF054615) cellulase [Fragaria x ananassa]
NCBI Description
                  120984
Seq. No.
                  5820 2.R1010
Contig ID
                  LIB3168-035-P1-K1-E2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3170525
BLAST score
                   469
                  5.0e-47
E value
Match length
                  119
                  75
% identity
                  (AF054615) cellulase [Fragaria x ananassa]
NCBI Description
```

BLAST score

```
Seq. No.
                   120985
                   5821 1.R1010
Contig ID
                  LIB22-020-Q1-E1-H4
5'-most EST
Seq. No.
                   120986
                   5822 1.R1010
Contig ID
                   jC-a\overline{t}XP89C245A21T7028d1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4519194
                   169
BLAST score
                   6.0e-90
E value
Match length
                   466
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHM17, complete sequence
                   120987
Seq. No.
                   5822 2.R1010
Contig ID
5'-most EST
                   jC-a\overline{t}XLIB327426P4e02a1
                   BLASTN
Method
NCBI GI
                   g1785729
BLAST score
                   176
                   4.0e-94
E value
                   187
Match length
                   99
% identity
NCBI Description A.thaliana mitochondrial genome, part B
                   120988
Seq. No.
                   5822 3.R1010
Contig ID
                   g2749497
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4519194
                   224
BLAST score
                   1.0e-122
E value
Match length
                   441
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHM17, complete sequence
                   120989
Seq. No.
                   5824 1.R1010
Contig ID
                   jC-atXLIB327416P2e12b1
5'-most EST
Method
                   BLASTX
                   g4584110
NCBI GI
BLAST score
                   401
                   1.0e-38
E value
Match length
                   163
% identity
                   48
NCBI Description
                   (AJ133639) SAH7 protein [Arabidopsis thaliana]
                   120990
Seq. No.
                   5824 2.R1010
Contig ID
                   jC-atXLIB327413P3d11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4584110
```

```
2.0e-28
E value
                   129
Match length
% identity
                   50
                   (AJ133639) SAH7 protein [Arabidopsis thaliana]
NCBI Description
                   120991
Seq. No.
Contig ID
                   5826 1.R1010
                   jC-a\(\bar{1}\)X24054Q1E1B04b1
5'-most EST
                   BLASTX
Method
                   g4559382
NCBI GI
                   902
BLAST score
                   1.0e-97
E value
Match length
                   172
% identity
                   100
                   (AC006526) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   120992
Seq. No.
                   5829 1.R1010
Contig ID
                   g241\overline{3}548
5'-most EST
                   120993
Seq. No.
Contig ID
                   5829 2.R1010
5'-most EST
                   g550242
Method
                   BLASTX
                   g4539330
NCBI GI
BLAST score
                   436
                   6.0e-43
E value
Match length
                   191
                   53
% identity
                   (AL035679) putative receptor-like protein kinase (fragment)
NCBI Description
                   [Arabidopsis thaliana]
                   120994
Seq. No.
Contig ID
                   5830 1.R1010
                   jC-a\overline{t}XLIB327408P3g06b1
5'-most EST
                   120995
Seq. No.
                   5837 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327413P1f01b1
Method
                   BLASTX
                   q3377797
NCBI GI
                   794
BLAST score
                   1.0e-84
E value
                   181
Match length
                   87
% identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
                   120996
Seq. No.
                   5837 2.R1010
Contig ID
5'-most EST
                   q2047539
Method
                   BLASTX
NCBI GI
                   q3377797
```

NCBI Description

```
BLAST score
                   453
E value
                   6.0e-45
Match length
                   94
                   94
% identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
                   120997
Seq. No.
                   5837 3.R1010
Contig ID
5'-most EST
                   g2580640
Method
                   BLASTN
                   g3298610
NCBI GI
BLAST score
                   50
                  7.0e-19
E value
Match length
                   126
                   87
% identity
NCBI Description
                  Arabidopsis thaliana BAC T2H3
                   120998
Seq. No.
                  5837 4.R1010
Contig ID
5'-most EST
                 _ g258<del>0</del>737
Method
                  BLASTX
                   g3377797
NCBI GI
BLAST score
                   344
                   5.0e-32
E value
Match length
                   68
                   99
% identity
NCBI Description
                   (AF075597) Similar to 60S ribosome protein L19; coded for
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
                   120999
Seq. No.
                  5837 5.R1010
Contig ID
5'-most EST
                   g2580934
Method
                  BLASTN
NCBI GI
                   q3298610
BLAST score
                   54
                   3.0e-21
E value
Match length
                   106
                  89
% identity
NCBI Description
                  Arabidopsis thaliana BAC T2H3
                   121000
Seq. No.
                   5837 6.R1010
Contig ID
5'-most EST
                  g2580681
Method
                  BLASTX
NCBI GI
                  g3377797
BLAST score
                   308
                   9.0e-28
E value
Match length
                  84
                  76
% identity
                  (AF075597) Similar to 60S ribosome protein L19; coded for
```

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

121001 Seq. No. Contig ID 5837 7.R1010 5'-most EST g2580828 Method BLASTX NCBI GI g3377797 BLAST score 101 E value 1.0e-29 Match length 75 90 % identity

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

121002 Seq. No. 5837 8.R1010 Contig ID 5'-most EST g2758868 Method BLASTX g3377797 NCBI GI BLAST score 306 8.0e-62 E value

Match length 197 % identity 73

(AF075597) Similar to 60S ribosome protein L19; coded for NCBI Description by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by

A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

121003 Seq. No.

Contig ID 5837 11.R1010

5'-most EST g2047571 BLASTX Method NCBI GI q3377797 BLAST score 340 E value 9.0e-32 Match length 76 87 % identity

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 121004

Contig ID 5837 12.R1010 5'-most EST LIB22-031-Q1-E1-E5

Method BLASTX NCBI GI g2213595 BLAST score 588 E value 2.0e-61

```
Match length
                    159
 % identity
                    80
                    (ACO00348) T7N9.15 [Arabidopsis thaliana]
 NCBI Description
                    121005
 Seq. No.
                    5837 16.R1010
 Contig ID
                    g1158715
 5'-most EST
                    BLASTX
 Method
                    q3377797
 NCBI GI
 BLAST score
                    356
 E value
                    2.0e-53
 Match length
                    200
 % identity
                    64
                    (AF075597) Similar to 60S ribosome protein L19; coded for
 NCBI Description
                    by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                    H36046; coded for by A. thaliana cDNA T44067; coded for by
                    A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                    R90691 [Ara
                    121006
 Seq. No.
 Contig ID
                    5837_21.R1010
 5'-most EST
                    LIB3176-021-P1-K1-G2
 Method
                    BLASTX
 NCBI GI
                    g3377797
                   <u>.</u>271
- BLAST score
 E value
                    5.0e - 34
 Match length
                    152
 % identity
                    61
                    (AF075597) Similar to 60S ribosome protein L19; coded for
 NCBI Description
                    by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                    H36046; coded for by A. thaliana cDNA T44067; coded for by
                    A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                    R90691 [Ara
                    121007
 Seq. No.
 Contig ID
                    5838 2.R1010
                    jC-atXLIB327413P2b03b1
 5'-most EST
 Method
                    BLASTX
                    g3341679
 NCBI GI
                    290
 BLAST score
                    6.0e-26
 E value
 Match length
                    87
 % identity
                    69
 NCBI Description
                    (AC003672) dynamin-like protein phragmoplastin 12
                    [Arabidopsis thaliana]
                    121008
 Seq. No.
                    5841_1.R1010
 Contig ID
 5'-most EST
                    jC-atX22021Q1E1B08b1
 Seq. No.
                    121009
 Contig ID
                    5842 1.R1010
                    jC-a\(\bar{1}\)XLIB327434P4d12b1
 5'-most EST
 Method
                    BLASTN
 NCBI GI
                    q2618602
 BLAST score
                    283
 E value
                    1.0e-158
```

Contig ID

```
499
Match length
                   100 '
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSJ1, complete sequence [Arabidopsis thaliana]
                   121010
Seq. No.
                   5842 2.R1010
Contig ID
                  jC-atXLIB327432P4e01b1
5'-most EST
                   BLASTX
Method
                  g3724366
NCBI GI
                  146
BLAST score
                   5.0e-09
E value
Match length
                   71
% identity
                   38
                  (AB018379) unknown ORF [Thermus thermophilus]
NCBI Description
                   121011
Seq. No.
                   5843 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P2e09b2
Method
                  BLASTX
                   g1724114
NCBI GI
BLAST score
                   252
                   2.0e-21
E value
Match length
                  142
% identity
                   42
                  (U80041) Af10-protein [Avena fatua]
NCBI Description
Seq. No.
                   121012
Contig ID
                   5844 1.R1010
                  LIB3177-093-P1-K1-A4
5'-most EST
                  BLASTN
Method
                   q2351073
NCBI GI
BLAST score
                   175
                   2.0e-93
E value
Match length
                   657
% identity
                   97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYJ24, complete sequence [Arabidopsis thaliana]
                   121013
Seq. No.
Contig ID
                  5846 1.R1010
5'-most EST
                  jC-atXLIB327440P1d08b1
Seq. No.
                   121014
                   5850 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P3e09b1
                  BLASTN
Method
                                                                  4:19
NCBI GI
                  g3985934
BLAST score
                   313
E value
                   1.0e-176
Match length
                   427
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJE7, complete sequence [Arabidopsis thaliana]
                  121015
Seq. No.
```

5851 1.R1010

```
5'-most EST
                   jC-atX22033Q1E2B10b1
Method
                   BLASTX
NCBI GI
                   q1055161
BLAST score
                   204
                   9.0e-16
E value
Match length
                   153
% identity
                   25
                  (U40029) similar to human 100 kDa coactivator (U22055)
NCBI Description
                   [Caenorhabditis elegans]
Seq. No.
                   121016
Contig ID
                   5852 1.R1010
5'-most EST
                   jC-atXLIB327432P3e10b1
Seq. No.
                   121017
Contig ID
                   5855 1.R1010
                   jC-a\overline{t}XLIB327432P3e06b1
5'-most EST
Method
                   BLASTX
                  g3183274
NCBI GI
BLAST score
                   267
                   3.0e-23
E value
Match length
                   94
% identity
                   56
NCBI Description
                  HYPOTHETICAL 26.5 KD PROTEIN C15A10.05C IN CHROMOSOME I
                   >gi 2239182 emb CAB10102 (Z97208) hypothetical protein
                   [Schizosaccharomyces pombe]
                   121018
Seq. No.
Contig ID
                   5856 1.R1010
5'-most EST
                  jC-atXLIB327432P3e07b1
Method
                   BLASTX
NCBI GI
                   g2809257
BLAST score
                   132
E value
                   5.0e-55
Match length
                   114
% identity
                   59
NCBI Description
                  (AC002560) F21B7.26 [Arabidopsis thaliana]
                   121019
Seq. No.
Contig ID
                   5860 1.R1010
5'-most EST
                  LIB22-036-Q1-E1-D7
                   121020
Seq. No.
                   5861 1.R1010
Contig ID
5'-most EST
                   jC-a\(\bar{1}\)X24001Q1E1F10b1
Method
                   BLASTX
NCBI GI
                   g2344898
BLAST score
                   846
E value
                  6.0e-91
Match length
                  159
% identity
                  100
                  (AC002388) 60S ribosomal protein L30 isolog [Arabidopsis
NCBI Description
                  thaliana]
                  121021
Seq. No.
Contig ID
                  5862 1.R1010
5'-most EST
                  jC-atXLIB327440P2d11a1
```

```
Seq. No.
                  121022
Contig ID
                  5863 1.R1010
                  LIB3175-056-P1-K1-B1
5'-most EST
                  BLASTX
Method
                  g4235093
NCBI GI
BLAST score
                  333
                  8.0e-31
E value
                  166
Match length
                  45
% identity
                  (AF108944) beta-xylosidase [Aspergillus niger]
NCBI Description
Seq. No.
                  121023
                  5864 1.R1010
Contig ID
                  LIB3168-007-P1-K1-H4
5'-most EST
                  BLASTX
Method
                  g2129545
NCBI GI
BLAST score
                  733
                  6.0e-78
E value
                  136
Match length
                  99
% identity
                  beta-glucanase - Arabidopsis thaliana (fragment) >gi 600857
NCBI Description
                  (U17888) beta-glucanase [Arabidopsis thaliana]
                  121024
Seq. No.
                  5865 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P2f08b2
Method
                  BLASTX
NCBI GI
                  g4539322
BLAST score
                  403
                  5.0e-39
E value
Match length
                  164
                  55
% identity
NCBI Description (AL035679) putative protein [Arabidopsis thaliana]
                  121025
Seq. No.
                  5866_1.R1010
Contig ID
5'-most EST
                  LIB3175-039-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2702268
BLAST score
                  520
                  5.0e-53
E value
                  98
Match length
                  100
% identity
NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]
                  121026
Seq. No.
                  5867 1.R1010
Contig ID
5'-most EST
                  LIB3234-004-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q2499902
BLAST score
                  622
                  8.0e-65
E value
                  171
Match length
% identity
                  67
NCBI Description PUROMYCIN-SENSITIVE AMINOPEPTIDASE (PSA)
```

NCBI GI

```
121027
Seq. No.
                  5869 1.R1010
Contig ID
5'-most EST
                  LIB3176-098-P1-K1-D7
                  BLASTX
Method
                  g3402683
NCBI GI
BLAST score
                  176
E value
                  3.0e-12
                  180
Match length
                  26
% identity
                  (AC004697) patatin-like protein [Arabidopsis thaliana]
NCBI Description
                  121028
Seq. No.
Contig ID
                  5869 2.R1010
                  LIB3176-065-P1-K1-B11
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4678298
BLAST score
                  166
E value
                  3.0e-11
Match length
                  114
                  35
% identity
                  (AL049655) putative protein [Arabidopsis thaliana]
NCBI Description
                  121029
Seq. No.
                  5870_1.R1010
Contig ID
5'-most EST
                  jC-atXP73CF2G4T7d2
                  BLASTX
Method
                  g2507455
NCBI GI
BLAST score
                  896
E value
                  9.0e-97
                  195
Match length
                  87
% identity
                  FORMATE---TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE
NCBI Description
                  SYNTHETASE) (FHS) (FTHFS) >gi 322401 pir A43350
                  formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach
                  >gi 170145 (M83940) 10-formyltetrahydrofolate synthetase
                  [Spinacia oleracea]
                  121030
Seq. No.
Contig ID
                  5870 2.R1010
5'-most EST
                  jC-atXP79C231E24T7b1
Method
                  BLASTX
NCBI GI
                  g2507455
BLAST score
                  53
E value
                  1.0e-131
Match length
                  274
% identity
                  84
                  FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE
NCBI Description
                  SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350
                  formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach
                  >gi 170145 (M83940) 10-formyltetrahydrofolate synthetase
                  [Spinacia oleracea]
                  121031
Seq. No.
                  5870 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327431P2b07a1
Method
                  BLASTX
```

q2507455

NCBI GI

```
1490
BLAST score
E value
                  1.0e-166
                  322
Match length
                  89
% identity
                  FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE
NCBI Description
                  SYNTHETASE) (FHS) (FTHFS) >gi 322401 pir A43350
                  formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach
                  >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase
                  [Spinacia oleracea]
                  121032
Seq. No.
Contig ID
                  5870 4.R1010
5'-most EST
                  jC-atXLIB327438P3h03b1
Method
                  BLASTX
                  g1345633
NCBI GI
BLAST score
                  173
                  7.0e-48
E value
Match length
                  136
% identity
                  68
                  C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF
NCBI Description
                  SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE /
                  METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE /
                  FORMYLTETRAHYDROFOLATE SYNTHETASE >gi 901850 (J05519)
                  C1-tetrahydrofolate synthase [Rattus norvegicus]
Seq. No.
                  121033
Contig ID
                  5870 5.R1010
5'-most EST
                  LIB22-064-Q1-E1-D7
Method
                  BLASTX
                  g2507455
NCBI GI
BLAST score
                  589
                  1.0e-60
E value
                  149
Match length
% identity
                  76
                  FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE
NCBI Description
                  SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350
                  formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach
                  >gi 170145 (M83940) 10-formyltetrahydrofolate synthetase
                  [Spinacia oleracea]
                  121034
Seq. No.
Contig ID
                  5872 1.R1010
5'-most EST
                  jC-atXLIB327432P4f07b1
Method
                  BLASTN
NCBI GI
                  g3128143
BLAST score
                  199
                  1.0e-107
E value
Match length
                  421
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTI20, complete sequence [Arabidopsis thaliana]
                  121035
Seq. No.
                  5875 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P3f08b1
Method
                  BLASTN
```

q4753195

```
BLAST score
                  229
E value
                  1.0e-126
Match length
                  395
% identity
                  99
                  Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5
NCBI Description
                  cM, complete sequence
                  121036
Seq. No.
                  5877_2.R1010
Contig ID
                  jC-atXLIB327432P4f04b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3702323
BLAST score
                  1935
E value
                  0.0e + 00
Match length
                  460
% identity
                  86
NCBI Description
                  (AC005397) unknown protein [Arabidopsis thaliana]
                  121037
Seq. No.
Contig ID
                  5880_1.R1010
                  LIB22-021-Q1-E1-E8
5'-most EST
Seq. No.
                  121038
Contig ID
                  5884 1.RI010
5'-most EST
                  LIB3234-046-P1-K1-D12
                  BLASTN
Method
                  g3135250
NCBI GI
BLAST score
                  110
E value
                  9.0e-55
Match length
                  216
                  88
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F27F23 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  121039
Seq. No.
Contig ID
                  5889_1.R1010
                  LIB22-021-Q1-E1-G12
5'-most EST
                  121040
Seq. No.
Contig ID
                  5890 1.R1010
5'-most EST
                  LIB23-055-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  g2921823
BLAST score
                  446
                  6.0e-44
E value
Match length
                  147
% identity
                  65
NCBI Description
                  (AF046934) shoot-forming PKSF1 [Paulownia kawakamii]
Seq. No.
                  121041
                  5892_1.R1010
Contig ID
5'-most EST
                  g937264
Method
                  BLASTX
NCBI GI
                  q4678352
BLAST score
                  269
                  2.0e-23
E value
Match length
```

```
54
  % identity
 NCBI Description (AL049659) putative protein [Arabidopsis thaliana]
                    121042
 Seq. No.
                    5892 2.R1010
 Contig ID
                    LIB23-026-Q1-E1-F4
 5'-most EST
                    BLASTX
 Method
                    g4678352
 NCBI GI
 BLAST score
                    607
                    5.0e-63
 E value
                    166
 Match length
 % identity
                    73
 NCBI Description
                    (AL049659) putative protein [Arabidopsis thaliana]
 Seq. No.
                    121043
                    5895 1.R1010
 Contig ID
                    jC-atXLIB327432P2g10b2
 5'-most EST
 Method
                    BLASTX
                    g1246403
 NCBI GI
 BLAST score
                    232
                    4.0e-19
 E value
 Match length
                    84
 % identity
                    55
                    (X94698) TINY [Arabidopsis thaliana] >gi 3406035 (AC005405)
 NCBI Description
                    TINY [Arabidopsis thaliana]
 Seq. No.
                    121044
 Contig ID
                    5900 1.R1010
 5'-most EST
                    jC-atXLIB327432P3g11b1
Seq. No.
                    121045
 Contig ID
                    5901 1.R1010
 5'-most EST
                    jC-alXLIB327435P2e09b1
 Seq. No.
                    121046
 Contig ID
                    5901 2.R1010
 5'-most EST
                    jC-atXLIB327422P2h05a2
 Method
                    BLASTN
                    g531828
 NCBI GI
 BLAST score
                    58
 E value
                    1.0e-23
 Match length
                    62
                    98
 % identity
 NCBI Description Cloning vector pSport1, complete cds
                    121047
 Seq. No.
 Contig ID
                    5901 3.R1010
                    jC-atXP61C202B22T7d1
 5'-most EST
                    121048
 Seq. No.
 Contig ID
                    5902 1.R1010
 5'-most EST
                    ARABL1-019-Q1-B1-C7
 Method
                    BLASTN
                    g3367567
 NCBI GI
 BLAST score
                    301
                    1.0e-168
 E value
                    803
 Match length
```



```
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20
                  (ESSAII project)
                  121049
Seq. No.
Contig ID
                  5902 2.R1010
                  g2597583
5'-most EST
Method
                  BLASTN
                  g3805839
NCBI GI
BLAST score
                  246
E value
                  1.0e-135
Match length
                  870
% identity
                  95
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14
                  (ESSAII project)
                  121050
Seq. No.
                  5902 4.R1010
Contig ID
5'-most EST
                  jC-atXP111C123H2T7s1
                  BLASTX
Method
NCBI GI
                  g2496731
BLAST score
                  593
E value
                  3.0e-61
Match length
                  220
% identity
                  55
NCBI Description HYPOTHETICAL 30.2 KD PROTEIN Y40V >gi_2182566 (AE000089)
                  Y4oV [Rhizobium sp. NGR234]
                  121051
Seq. No.
                  5903 1.R1010
Contig ID
5'-most EST
                  LIB3175-003-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  g2911797
BLAST score
                  217
                  1.0e-17
E value
                  85
Match length
% identity
                  47
NCBI Description (AF008183) 4-coumarate:CoA ligase 2 [Populus balsamifera
                  subsp. trichocarpa X Populus deltoides]
                  121052
Seq. No.
                  5910_1.R1010
Contig ID
                  ARABL1-039-Q1-B1-D11
5'-most EST
Seq. No.
                  121053
Contig ID
                  5912_1.R1010
5'-most EST
                  g3228574
                  BLASTN
Method
NCBI GI
                  g4589412
BLAST score
                  37
                  6.0e-11
E value
Match length
                  105
                  84
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F6N7, complete sequence
```

```
Contig ID
                  5912 2.R1010
                  jC-alx24045Q1E1G05b1
5'-most EST
Seq. No.
                  121055
                  5912 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P2e05b1
                  BLASTN
Method
                  q4589412
NCBI GI
                  46
BLAST score
E value
                  2.0e-16
Match length
                  154
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F6N7, complete sequence
                  121056
Seq. No.
                  5912_7.R1010
Contig ID
5'-most EST
                  LIB23-001-Q1-E1-G4
                  BLASTN
Method
                  q4589412
NCBI GI
BLAST score
                  48
E value
                  7.0e-18
Match length
                  165
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F6N7, complete sequence
                  121057
Seq. No.
                  5915 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327407P3g06b1
                  BLASTX
Method
                  q2129755
NCBI GI
BLAST score
                   593
                   2.0e-61
E value
Match length
                   122
% identity
                  tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis
NCBI Description
                   thaliana >gi 619753 (U18993) tryptophan synthase alpha
                   chain [Arabidopsis thaliana] >gi 1585768 prf 2201482A Trp
                   synthase:SUBUNIT=alpha [Arabidopsis thaliana]
                   121058
Seq. No.
Contig ID
                   5916 1.R1010
                   jC-atXLIB327426P1g10b1
5'-most EST
                   121059
Seq. No.
                   5917 1.R1010
Contig ID
                   jC-atXLIB327430P1c06b1
5'-most EST
Method
                   BLASTN
                   g2618605
NCBI GI
                   205
BLAST score
                   1.0e-111
E value
                   1079
Match length
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MUK11, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  121060
Contig ID
                  5919 1.R1010
5'-most EST
                  jC-atXLIB327432P2f10a1
                  BLASTX
Method
                  g4586021
NCBI GI
BLAST score
                  1572
                  0.0e + 00
E value
Match length
                   492
                  100
% identity
                  (AC007170) putative cytoplasmic aconitate hydratase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  121061
                  5919 2.R1010
Contig ID
                  LIB3176-052-P1-K1-A2
5'-most EST
                  BLASTX
Method
                  g1351856
NCBI GI
BLAST score
                  365
                  7.0e-35
E value
                  129
Match length
                  89
% identity
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                   (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase
                   [Cucurbita sp.]
Seq. No.
                  121062
                  5924 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327413P4b11b1
Method
                  BLASTX
                  g1345655
NCBI GI
BLAST score
                  695
                  3.0e-73
E value
Match length
                  173
                  79
% identity
                  CINNAMYL-ALCOHOL DEHYDROGENASE 2 (CAD)
NCBI Description
                  >gi_757535_emb_CAA83508_ (Z31715) cinnamyl alcohol
                  dehydrogenase [Arabidopsis thaliana]
                  121063
Seq. No.
                  5927 1.R1010 ·
Contig ID
5'-most EST
                  jC-atXP17C110H13T7d3
Method
                  BLASTX
                  g3924602
NCBI GI
BLAST score
                  773
E value
                  3.0e-82
Match length
                  240
% identity
                  86
                  (AF069442) predicted OR23 protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  121064
                  5928 1.R1010
Contig ID
                  jC-atX22022Q1E1C11b1
5'-most EST
Method
                  BLASTX
                  g3877252
NCBI GI
BLAST score
                  285
E value
                  2.0e-25
```

```
121
Match length
                   48
% identity
NCBI Description
                  (Z93382) F45G2.10 [Caenorhabditis elegans]
                  121065
Seq. No.
                  5929 1.R1010
Contig ID
5'-most EST
                  jC-a\overline{1}XLIB327435P4d07b1
                  BLASTX
Method
                   g2352998
NCBI GI
BLAST score
                  244
                  2.0e-20 -
E value
Match length
                  162
% identity
                  31
NCBI Description (AF014461) EXO70 protein [Mus musculus]
Seq. No.
                  121066
                  5930 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P4e11b1
Method
                  BLASTX
                  g3243234
NCBI GI
BLAST score
                  317
                   4.0e-29
E value
                  86
Match length
% identity
                  72
NCBI Description (AF071477) isoflavone reductase related protein [Pyrus
                · communis]
                  121067
Seq. No.
                  5931 1.R1010
Contig ID
                  jC-atXLIB327432P3e11b1
5'-most EST
                  BLASTN
Method
                  g2462264
NCBI GI
BLAST score
                   44
E value
                  3.0e-15
Match length
                  56
                  95
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
                  121068
Seq. No.
                  5933 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P4e07b1
                  BLASTN
Method
NCBI GI
                  q2582640
BLAST score
                   66
E value
                  2.0e-28
Match length
                  74
                  97
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  121069
                  5935 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P4e08b1
Method
                  BLASTX
NCBI GI
                  q4262142
BLAST score
                  244
E value
                  1.0e-20
```

```
Match length
                   83
% identity
                   (AC005275) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   121070
Seq. No.
                   5936_1.R1010
Contig ID
                   LIB25-028-Q1-E1-F7
5'-most EST
                   BLASTN
Method
NCBI GI
                   q4581138
BLAST score
                   387
E value
                   0.0e + 00
                   426
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC F1011 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   121071
Contig ID
                   5944 2.R1010
                   LIB2\overline{2}-022-Q1-E1-E1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1684913
BLAST score
                   344
                   4.0e-32
E value
Match length
                   186
                   45
% identity
NCBI Description (U77888) receptor-like protein kinase [Ipomoea nil]
                   121072
Seq. No.
                   5948 1.R1010
Contig ID
                   jC-a\overline{t}XLIB327432P4f08b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2244895
BLAST score
                   535
E value
                   1.0e-54
Match length
                   137
                   79
% identity
                  (Z97338) similar to cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   121073
Seq. No.
                   5949_1.R1010
Contig ID
5'-most EST
                   LIB22-022-Q1-E1-E4
                   BLASTX
Method
NCBI GI
                   g1769895
                   191
BLAST score
                   2.0e-14
E value
                   94
Match length
% identity
                   43
                   (X96598) CaLB protein [Arabidopsis thaliana]
NCBI Description
                   121074
Seq. No.
Contig ID
                   5950 1.R1010
                   jC-atXLIB327432P3f09b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4467128
                   581
BLAST score
                   6.0e-60
E value
```

```
Match length
                  112
% identity
                  96
NCBI Description
                  (AL035538) putative protein [Arabidopsis thaliana]
                  121075
Seq. No.
                  5950 2.R1010
Contig ID
                  LIB23-008-Q1-E1-G6
5'-most EST
                  BLASTX
Method
                  g4467128
NCBI GI
                  983
BLAST score
                  1.0e-107
E value
                  218
Match length
                  89
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  121076
                  5952 1.R1010
Contig ID
                  LIB22-087-Q1-E1-F8
5'-most EST
                  BLASTN
Method
                  g2828278
NCBI GI
BLAST score
                  451
                  0.0e + 00
E value
                  451
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16
NCBI Description
                  (ESSAII project)
Seq. No.
                  121077
Contig ID
                  5955 1.R1010
5'-most EST
                  jC-atXLIB327409P2b08b1
Method
                  BLASTN
                  q4262221
NCBI GI
                  159
BLAST score
                  6.0e-84
E value
Match length
                  514
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F10A8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  121078
Seq. No.
                  5956 1.R1010
Contig ID
5'-most EST
                  LIB3168-027-P1-K1-F6
Method
                  BLASTX
                  g4160402
NCBI GI
BLAST score
                  849
                  5.0e-91
E value
Match length
                  348
                  57
% identity
                  (AJ132240) eukaryotic translation initiation factor 5 [Zea
NCBI Description
                  mays]
                  121079
Seq. No.
Contig ID
                  5958 1.R1010
5'-most EST
                  jC-atXLIB327424P2e01b2
                  BLASTN
Method
NCBI GI
                  g2582640
BLAST score
                  63
```

Contig ID

```
E value
                  1.0e-26
Match length
                  71
                  97
% identity
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  121080
                  5958_2.R1010
Contig ID
5'-most EST
                  LIB23-042-Q1-E1-F5
                  BLASTX
Method
NCBI GI
                  q3414809
BLAST score
                  195
E value
                  5.0e-15
Match length
                  123
% identity
                  3
NCBI Description (AF061529) rjs [Mus musculus]
                  121081
Seq. No.
                  5959 1.R1010
Contig ID
5'-most EST
                  g2748338
Method
                  BLASTN
NCBI GI
                  g4678705
BLAST score
                  257
E value
                  1.0e-142
Match length
                  409
% identity
                  98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
                  (ESSA project)
Seq. No.
                  121082
                  5960 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327426P2f08b1
Method
                  BLASTX
NCBI GI
                  g832876
BLAST score
                  407
E value
                  8.0e-47
Match length
                  156
% identity
                  64
NCBI Description
                  (L41345) ascorbate free radical reductase [Solanum
                  lycopersicum] >gi 1097368 prf 2113407A ascorbate free
                  radical reductase [Lycopersicon esculentum]
                  121083
Seq. No.
                  5962 1.R1010
Contig ID
5'-most EST
                  LIB22-022-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                  g3695389
BLAST score
                  217
                  3.0e-66
E value
Match length
                  126
% identity
                  47
NCBI Description
                  (AF096371) contains similarity to D-isomer specific
                  2-hydroxyacid dehydrogenases (Pfam: 2-Hacid DH.hmm, score:
                  19.11) [Arabidopsis thaliana]
                  121084
Seq. No.
```

5963_1.R1010

```
5'-most EST
                   iC-atXLIB327418P4h03b1
                   BLASTX
Method
NCBI GI
                   g2244841
BLAST score
                   306
                   1.0e-27
E value
Match length
                   137
                   53
% identity
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   121085
Contig ID
                   5965 1.R1010
5'-most EST
                   jC-atX22022Q1E1F08b1
                   BLASTN
Method
NCBI GI
                   q4589412
BLAST score
                   270
                   1.0e-150
E value
Match length
                   413
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   F6N7, complete sequence
                   121086
Seq. No.
Contig ID
                   5968 1.R1010
                   jC-aTXLIB327432P2g11b2
5'-most EST
Method
                   BLASTX
                   g3451075
NCBI GI
BLAST score
                   217
E value
                   2.0e-17
                   77
Match length
                   57
% identity
                   (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   121087
                   5970 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327420P4g03b1
Method
                   BLASTX
                   q2813966
NCBI GI
BLAST score
                   303
E value
                   4.0e-27
Match length
                   251
% identity
                   (Z97053) placental protein Diff33 [Homo sapiens]
NCBI Description
                   >gi 4545219 gb AAD22448.1 (AF112227) TDE homolog [Homo
                   sapīens]
                   121088
Seq. No.
Contig ID
                   5970 2.R1010
5'-most EST
                   q2747949
Method
                   BLASTX
NCBI GI
                   q3879145
BLAST score
                   187
E value
                   1.0e-13
Match length
                   73
% identity
                   49
                   (Z93386) predicted using Genefinder; Similarity to Human
NCBI Description
                   placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5
                   comes from this gene [Caenorhabditis elegans]
```

```
Seq. No.
                      121089
Contig ID
                     5971 1.R1010
5'-most EST
                      jC-atXLIB327440P4c01b2
Method
                     BLASTX
NCBI GI
                      g4758356
BLAST score
                      380
E value
                      2.0e-36
Match length
                      126
% identity
                      63
NCBI Description
                     flap structure-specific endonuclease 1; MATURATION FACTOR 1
                     (MF1); DNase IV; RAD2_HUMAN >gi_729475_sp_P39748_FEN1_HUMAN FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1)
                     >gi_1362788_pir__A56531 DNA structure-specific endonuclease
FEN1 - human >gi_704377_bbs_157592 DNase IV=nuclear 42 kda
5' -> 3' exonuclease [human, HeLa cells, Peptide, 380 aa]
                     >gi_642090 (L37374) endonuclease [Homo sapiens] >gi_3169155
                      (ACOO4770) FEN1 HUMAN; MATURATION FACTOR 1 (MF1); DNase IV;
                     RAD2_HUMAN [Homo sapiens] >gi_3980293_emb_CAA54166_(X76771) flap endonuclease-1 [Homo sapiens]
Seq. No.
                     121090
Contig ID
                     5974 1.R1010
5'-most EST
                     LIB22-022-Q1-E1-G5
                     BLASTX
Method
NCBI GI
                     q2980785
BLAST score
                      606
E value
                      4.0e-63
Match length
                     115
                     100
% identity
NCBI Description
                      (AL022198) SERINE CARBOXYPEPTIDASE II - like protein
                      [Arabidopsis thaliana]
                      121091
Seq. No.
                     5975 1.R1010
Contig ID
5'-most EST
                     jC-atXLIB327432P2q09b1
Method
                     BLASTN
NCBI GI
                     q2582640
BLAST score
                     45
E value
                      4.0e-16
Match length
                     52
% identity
                     96
NCBI Description
                     Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                     factor, RSp40
Seq. No.
                     121092
Contig ID
                     5978 1.R1010
                     LIB3175-065-P1-K1-G12
5'-most EST
Method
                     BLASTN
NCBI GI
                     g2828185
BLAST score
                     363
E value
                     0.0e + 00
Match length
                     411
% identity
                     97
                     Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MUD21, complete sequence [Arabidopsis thaliana]

E value

4.0e-80

```
121093
Seq. No.
                   5980 1.R1010
Contig ID
                   LIB22-022-Q1-E1-H10
5'-most EST
                   121094
Seq. No.
Contig ID
                   5986_1.R1010
                   LIB2\overline{2}-022-Q1-E1-H5
5'-most EST
                   BLASTX
Method
                   q3482921
NCBI GI
BLAST score
                   190
E value
                   2.0e-14
Match length
                   50
                   64
% identity
                   (AC003970) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   121095
Seq. No.
Contig ID
                   5987_1.R1010
5'-most EST
                   jC-atXLIB327432P3g07b1
Method
                   BLASTX
                   g3980410
NCBI GI
                   229
BLAST score
E value
                   9.0e-19
Match length
                   133
% identity
                   40
                   (AC004561) putative receptor-like protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   121096
Seq. No.
                   5990_1.R1010
Contig ID
5'-most EST
                   g2047803
Method
                   BLASTN
NCBI GI
                   g4165340
BLAST score
                   297
                   1.0e-166
E value
Match length
                   356
% identity
                   96
                  Arabidopsis thaliana chromosome I BAC F11M15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   121097
Seq. No.
Contig ID
                   5990_2.R1010
5'-most EST
                  LIB35-022-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                   q4510345
BLAST score
                   357
E value
                   2.0e-33
Match length
                   162
% identity
                   45
NCBI Description
                   (AC006921) unknown protein [Arabidopsis thaliana]
                   121098
Seq. No.
Contig ID
                   5991 1.R1010
5'-most EST
                   jC-atXLIB327432P4h03b1
Method
                  BLASTX
NCBI GI
                  g2213597
BLAST score
                   753
```

```
Match length
                  151
% identity
                  99
NCBI Description
                  (AC000348) T7N9.17 [Arabidopsis thaliana]
                  121099
Seq. No.
                  5997 1.R1010
Contig ID
                  jC-atXLIB327432P4h01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4220514
BLAST score
                  515
E value
                  2.0e-52
Match length
                  100
% identity
                  100
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                  121100
Seq. No.
                  6000 1.R1010 -
Contig ID
5'-most EST
                  LIB22-023-Q1-E1-B12
                  BLASTN
Method
NCBI GI
                  g2264314
BLAST score
                  301
                  1.0e-168
E value
Match length
                  470
% identity
                  67
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQK4, complete sequence [Arabidopsis thaliana]
                  121101
Seq. No.
Contig ID
                  6000 2.R1010
                  jC-atX22048Q1E1D06007a1
5'-most EST
                  BLASTN
Method
                  g2264314
NCBI GI
BLAST score
                  523
E value
                  0.0e + 00
Match length
                  523
                  70
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                  121102
                  6004 1.R1010
Contig ID
5'-most EST
                  LIB22-061-Q1-E2-C2
Method
                  BLASTX
NCBI GI
                  g4587530
                  297
BLAST score
                  8.0e-27
E value
Match length
                  99
                  59
% identity
NCBI Description
                  (AC007060) Strong similarity to F19I3.2 gi_3033375 putative
                  berberine bridge enzyme from Arabidopsis thaliana BAC
                  gb_AC004238
                  121103
Seq. No.
Contig ID
                  6005 1.R1010
5'-most EST
                  LIB3176-049-P1-K1-H11
                  BLASTX
Method
NCBI GI
                  g2879811
```

```
BLAST score
                  524
                  2.0e-53
E value
Match length
                  112
                  88
% identity
                  (AJ223316) ribosomal protein L30 [Lupinus luteus]
NCBI Description
                  121104
Seq. No.
                  6007 1.R1010
Contig ID
                  jC-atXLIB327413P4d12b1
5'-most EST
                  BLASTX
Method
                  g4538942
NCBI GI
BLAST score
                  265
E value
                  5.0e-23
Match length
                  129
                  52
% identity
                  (ALO49483) uncharacterized protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  121105
Contig ID
                  6010 1.R1010
5'-most EST
                  jC-atXLIB327433P1d10b1
Method
                  BLASTX
NCBI GI
                  g3367576
BLAST score
                  649
                  1.0e-67
E value
Match length
                  197
% identity
                  64
                  (ALO31135) NAM / CUC2 -like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  121106
Contig ID
                  6016 1.R1010
5'-most EST
                  LIB3234-046-P1-K1-D9
                  BLASTN
Method
NCBI GI
                  g4589421
BLAST score
                  36
E value
                  1.0e-10
Match length
                  70
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                  K5K13, complete sequence
                  121107
Seq. No.
                  6018 1.R1010
Contig ID
5'-most EST
                  LIB22-023-Q1-E1-D3
                  BLASTN
Method
NCBI GI
                  g4432829
BLAST score
                  113
                  1.0e-56
E value
                  445
Match length
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC T1B3 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  121108
Seq. No.
                  6028 1.R1010
Contig ID
5'-most EST
                  LIB22-048-Q1-E1-F1
Method
                  BLASTN
NCBI GI
                  q3128166
```

```
BLAST score
                   410
                   0.0e + 00
E value
                   450
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC F4I1 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   121109
Seq. No.
                   6030_1.R1010
Contig ID
                   LIB22-023-Q1-E1-F1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3738088
                   41
BLAST score
                   2.0e-13
E value
                   990
Match length
                   49
% identity
                   Arabidopsis thaliana chromosome II BAC T30L20 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   121110
Seq. No.
                   6031 1.R1010
Contig ID
5'-most EST
                   jC-a\overline{t}XLIB327419P2f04b2
Method
                   BLASTN
                   a4063730
NCBI GI
                   477
BLAST score
                   0.0e + 00
E value
                   1322
Match length
% identity
                   Arabidopsis thaliana BAC F21J6 from chromosome V,
NCBI Description
                   containing KNAT3 and mapping near 60.5 cM, complete
                   sequence [Arabidopsis thaliana]
                   121111
Seq. No.
                   6032 1.R1010
Contig ID
5'-most EST
                   LIB24-013-Q1-E1-F9
Method
                   BLASTX
                   q1495804
NCBI GI
                   159
BLAST score
E value
                   1.0e-10
                   118
Match length
                   40
% identity
                   (X96406) 13-lipoxygenase [Solanum tuberosum]
NCBI Description
                   121112
Seq. No.
                   6033 1.R1010
Contig ID
                   LIB22-023-Q1-E1-F12
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2253583
                   533
BLAST score
E value
                   1.0e-54
                   109
Match length
                   99
% identity
                   (U78721) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   121113
                   6034 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327410P1a08b1
```

```
Method
                  BLASTX
                  q2239089
NCBI GI
                  505
BLAST score
                  8.0e-51
E value
                  235
Match length
% identity
                  49
                  (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758)
                  anthranilate N-hydroxycinnamoyl/benzoyltransferase
                  [Dianthus caryophyllus]
Seq. No.
                  121114
Contig ID
                  6036 1.R1010
5'-most EST
                  jC-atXLIB327438P1g03a1
                  BLASTX
Method
                 g4416307
NCBI GI
BLAST score
                  174
                  3.0e-12
E value
                  187
Match length
% identity
                  29
                  (AF105716) hypothetical protein [Zea mays]
NCBI Description
Seq. No.
                  121115
                  6037 1.R1010
Contig ID
                  jC-atXLIB327440P4d10b2
5'-most EST
                  BLASTN
Method
                  q2264321
NCBI GI
BLAST score
                  263
                  1.0e-146
E value
                  457
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXM12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  121116
Contig ID
                  6041 1.R1010
5'-most EST
                  jC-alX22047Q1E1G04b1
                  BLASTX
Method
NCBI GI
                  q4559396
BLAST score
                  228
E value
                  9.0e-19
Match length
                  47
                  98
% identity
NCBI Description
                  (AC006526) unknown protein [Arabidopsis thaliana]
                  121117
Seq. No.
Contig ID
                  6052_1.R1010
                  LIB25-032-Q1-E1-D11
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3024898
BLAST score
                  338
E value
                  4.0e-39
Match length
                  203
% identity
                  61
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE KIAA0224 (HA4657) >gi 1504028 dbj BAA13213
```

(D86977) similar to putative ATP-dependent RNA helicase

```
KO3H1.2 of C.elegans(S41025) [Homo sapiens] >gi_3123906
                   (AF038391) pre-mRNA splicing factor [Homo sapiens]
                   121118
Seq. No.
                   6055 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P3h02b1
                   121119
Seq. No.
                   6056_1.R1010
Contig ID
5'-most EST
                   LIB2\overline{2}-024-Q1-E1-A11
                   BLASTX
Method
                   g3482910
NCBI GI
BLAST score
                   500
                   8.0e-51
E value
Match length
                   111
                   87
% identity
                   (AC003970) Similar to rice water stress induced protein
NCBI Description
                   gi 537404 [Arabidopsis thaliana]
                   121120
Seq. No.
                   6057_1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327403P1d05b1
Seq. No.
                   121121
Contig ID
                   6061 :1.R1010
5'-most EST
                   jC-atXLIB327413P2b04b1
Method
                   BLASTN
                   g3805839
NCBI GI
BLAST score
                   167
                   9.0e-89
E value
Match length
                   479
                   100
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14
NCBI Description
                   (ESSAII project)
                   121122
Seq. No.
Contig ID
                   6062 1.R1010
                   LIB3176-046-P1-K1-E2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3582436
BLAST score
                   242
E value
                   2.0e-20
Match length
                   100
% identity
                   54
NCBI Description
                   (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
                   121123
Seq: No.
                   6062_2.R1010
Contig ID
                   LIB2\overline{3}-068-Q1-E1-B10
5'-most EST
Method
                   BLASTX
                   g1203832
NCBI GI
                   229
BLAST score
                   5.0e-19
E value
                   75
Match length
                   63
% identity
                   (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                   [Hordeum vulgare] >gi 1588407 prf_ 2208395A beta-D-glucan
```

5'-most EST

exohydrolase [Hordeum vulgare]

```
121124
  Seq. No.
                    6063 1.R1010
  Contig ID
                    jC-atXP73CF3D11T7d2
  5'-most EST
                    BLASTX
  Method
                    q4325369
  NĊBI GI
                    598
  BLAST score
                    6.0e-62
  E value
  Match length
                    118
                    99
  % identity
  NCBI Description (AF128396) T3H13.3 gene product [Arabidopsis thaliana]
                    121125
  Seq. No.
  Contig ID
                    6063 2.R1010
                    jC-atXLIB327407P1b03b2
  5'-most EST
  Method
                    BLASTX
  NCBI GI
                    g4325369
                    623
  BLAST score
  E value
                    8.0e-65
  Match length
                    153
                    87
  % identity
  NCBI Description (AF128396) T3H13.3 gene product [Arabidopsis thaliana]
  Seq. No. -
                    121126
                    6065_1.R1010
  Contig ID
                    LIB22-024-Q1-E1-A9
  5'-most EST
                    121127
  Seq. No.
                    6068 1.R1010
  Contig ID
                    jC-atXLIB327413P2a09b1
  5'-most EST
  Method
                    BLASTX
  NCBI GI
                    q2598575
                    190
  BLAST score
  E value
                    4.0e-14
  Match length
                    112
  % identity
                    36
NCBI Description (Y15293) MtN21 [Medicago truncatula]
  Seq. No.
                    121128
                    6068 2.R1010
  Contig ID
  5'-most EST
                    LIB23-072-Q1-E1-F9
                    BLASTX
  Method
  NCBI GI
                    q2598575
  BLAST score
                    229
                    6.0e-19
  E value
  Match length
                    129
  % identity
  NCBI Description (Y15293) MtN21 [Medicago truncatula]
                    121129
  Seq. No.
                    6071 1.R1010
  Contig ID
  5'-most EST
                    jC-atXLIB327433P1a02b1
  Seq. No.
                    121130
                    6074 1.R1010
  Contig ID
```

jC-atXLIB327414P4e03a2

```
BLASTN
Method
NCBI GI
                  g4510338
BLAST score
                  431
                  0.0e + 00
E value
Match length
                  443
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F2H17 genomic
                  sequence, complete sequence
                  121131
Seq. No.
Contig ID
                  6074_2.R1010
                  jC-atXLIB327432P4h12b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4510338
BLAST score
                   371
                   0.0e + 00
E value
Match length
                  383
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC F2H17 genomic
NCBI Description
                  sequence, complete sequence
                  121132
Seq. No.
Contig ID
                   6075 1.R1010
                   jC-a\overline{t}XLIB327432P3h12b1
5'-most EST
                  121133
Seq. No.
                   6079 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327405P2h02b2
Method
                  BLASTX
NCBI GI
                   g3367522
BLAST score
                   769
E value
                   6.0e-82
Match length
                   153
% identity
                   99
                   (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   121134
Seq. No.
Contig ID
                   6085_1.R1010
                  LIB22-061-Q1-E2-D6
5'-most EST
Method
                   BLASTX
                   g2262111
NCBI GI
                   355
BLAST score
E value
                   1.0e-33
                   123
Match length
% identity
                   62
                   (AC002343) ribitol dehydrogenase isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   121135
                   6089_1.R1010
Contig ID
                   jC-atXLIB327405P3g01b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3695372
BLAST score
                   53
E value
                   1.0e-20
Match length
                   53
```

```
% identity
                  100
NCBI Description Arabidopsis thaliana BAC F1104
                  121136
Seq. No.
                  6092 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327408P4f03b1
Method
                  BLASTX
NCBI GI
                  q2497538
BLAST score
                  380
E value
                  1.0e-104
Match length
                  484
% identity
                  46
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 466350 (L08632)
NCBI Description
                  pyruvate kinase [Glycine max]
                  121137
Seq. No.
                  6092_3.R1010
Contig ID
5'-most EST
                  LIB3175-015-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q4581156
BLAST score
                  211
E value
                  7.0e-17
Match length
                  40
                  100
% identity
NCBI Description
                  (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
                  121138
Seq. No.
                  6093 1.R1010
Contig ID
                  jC-atXLIB327411P2b02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3355480
BLAST score
                  793
E value
                  2.0e-84
Match length
                  283
% identity
                  54
NCBI Description
                  (AC004218) Medicago nodulin N21-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  121139
                  6095 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P4f12b1
Method
                  BLASTN
NCBI GI
                  q4337186
BLAST score
                  180
E value
                  2.0e-96
Match length
                  446
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T28I24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  121140
Contig ID
                  6096 1.R1010
5'-most EST
                  LIB22-033-Q1-E2-C9
Method
                  BLASTX
NCBI GI
                  q4455276
BLAST score
                  161
E value
                  5.0e-11
```

```
Match length
                  71
% identity
                  49
                  (AL035527) peptide transporter-like protein [Arabidopsis
NCBI Description
                  thaliana]
                                                52 - 11 -
                  121141
Seq. No.
                  6102_1.R1010
Contig .ID
5'-most EST
                  LIB3168-001-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  g2564048
BLAST score
                  432
E value
                  0.0e + 00
                  444
Match length
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MKD15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  121142
Contig ID
                  6103 1.R1010
5'-most EST
                  LIB3175-022-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g3738284
BLAST score
                  613
E value
                  9.0e-64
Match length
                  114
% identity
                  97
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  121143
                  6104 1.R1010
Contig ID
5'-most EST
                  LIB22-024-Q1-E1-E2
Method
                  BLASTX
NCBI GI
                  g3450842
BLAST score
                  161
E value
                  1.0e-10
Match length
                  151
% identity
                  32
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                  satival
                  121144
Seq. No.
                  6106 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1b01b1
Method
                  BLASTN
NCBI GI
                  g4468976
BLAST score
                  203
E value
                  1.0e-110
Match length
                  393
% identity
                  98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18
                  (ESSA project)
                  121145
Seq. No.
Contig ID
                  6112 1.R1010
5'-most EST
                  LIB23-017-Q1-E1-A12
Method
                  BLASTX
NCBI GI
                  g2126240
```

BLAST score

378 .

```
BLAST score
                  270
                  1.0e-23
E value
Match length
                  105
                  52
% identity
                  Prolyl Aminopeptidase - Aeromonas sobria (fragment)
NCBI Description
Seq. No.
                  121146
                  6113_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1b08b1
                  BLASTX
Method
NCBI GI
                  g4539453
BLAST score
                  163
E value
                  5.0e-11
Match length
                  62
                  47
% identity
NCBI Description
                  (AL049500) putative protein [Arabidopsis thaliana]
                  121147
Seq. No.
                  6117 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327409P4e09b1
                  BLASTX
Method
NCBI GI
                  g3184258
BLAST score
                  242
E value
                  3.0e-20
Match length
                  96
% identity
                  46
                  (U82130) tumor susceptibility protein [Homo sapiens]
NCBI Description
                  121148
Seq. No.
Contig ID
                  6118 1.R1010
5'-most EST
                  jC-atX22024Q1E1F07b1
Method
                  BLASTN
NCBI GI
                  g4510323
BLAST score
                  223
E value
                  1.0e-122
Match length
                  397
% identity
                  97
NCBI Description
                  Arabidopsis thaliana BAC T7B11 from chromosome IV near 10
                  cM, complete sequence
                  121149
Seq. No.
                  6119 1.R1010
Contig ID
5'-most EST
                  jC-atX25047Q1E1A06b1
Method
                  BLASTX
NCBI GI
                  g3688186
BLAST score
                  1093
E value
                  1.0e-120
Match length
                  237
% identity
                  89
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
                  121150
Seq. No.
Contig ID
                  6119 2.R1010
5'-most EST
                  jC-atXLIB327433P1b07b1
Method
                  BLASTX
NCBI GI
                  g3075398
```

```
1.0e-48
E value
Match length
                   127
                   83
% identity
                   (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
                   121151
Seq. No.
                   6120 1.R1010
Contig ID
                   LIB22-086-Q1-E1-B1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2462825
BLAST score
                   478
E value
                   1.0e-47
Match length
                   184
                   59
% identity
                   (AF000657) contains Procite 'RNP1' putative RNA-binding
NCBI Description
                   region [Arabidopsis thaliana]
                   121152
Seq. No.
                   6123 1.R1010
Contig ID
5'-most EST
                   LIB3177-025-P1-K2-A10
                   BLASTX
Method
NCBI GI
                   g4510345
BLAST score
                   523
E value
                   7.0e-53
Match length
                   170
% identity
                   60
                   (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   121153
Seq. No.
                   6123 3.R1010
Contig ID
5'-most EST
                   g1158612
                   BLASTN
Method
NCBI GI
                   g4510338
BLAST score
                   59
E value
                   3.0e-24
Match length
                   139
% identity
                   86
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F2H17 genomic
                   sequence, complete sequence
                   121154
Seq. No.
                   6124 1.R1010
Contig ID
5'-most EST
                   LIB23-034-Q1-E1-G5
Method
                   BLASTN
NCBI GI
                   g2351062
BLAST score
                   438
E value
                   0.0e + 00
Match length
                   474
% identity
                   97
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MAH20, complete sequence [Arabidopsis thaliana]
                   121155
Seq. No.
Contig ID
                   6125 1.R1010
5'-most EST
                   LIB2\overline{2} - 024 - Q1 - E1 - G3
Method
                   BLASTX
NCBI GI
                   g266463
```

```
BLAST score
                   508
                   2.0e-51
E value
Match length
                   112
% identity
                   83
                   3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM
NCBI Description
                   DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_82259_pir__S25670
                   3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor -
                  potato >gi_22643_emb_CAA47720_ (X67310) 3-isopropylmalate
                   dehydrogenase [Solanum tuberosum] >gi_445064_prf__1908380A
                  beta isopropylmalate dehydrogenase [Solanum tuberosum]
Seq. No.
                   121156
                   6126 1.R1010
Contig ID
5'-most EST
                  g3449480
                  BLASTX
Method
NCBI GI
                  q100535
BLAST score
                   277
                   3.0e-24
E value
Match length
                   63
% identity
NCBI Description
                  hypothetical protein - swollen duckweed
                  >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna
                  gibba]
Seq. No.
                  121157
Contig ID
                  6126_2.R1010
5'-most EST
                  q936686
Method
                  BLASTX
                  q4164473
NCBI GI
BLAST score
                  216
                  3.0e-17
E value
Match length
                  51
% identity
                  76
                   (AF061157) negatively light-regulated protein [Vernicia
NCBI Description
                  fordii]
                  121158
Seq. No.
                  6126 3.R1010
Contig ID
                  jC-atXLIB327408P2a03b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q100535
BLAST score
                  294
E value
                  2.0e-26
Match length
                  71
                  83
% identity
                  hypothetical protein - swollen duckweed
NCBI Description
                  >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna
                  gibba]
Seq. No.
                  121159
                  6126_4.R1010
Contig ID
5'-most EST
                  q907\overline{1}55
Method
                  BLASTN
NCBI GI
                  g2618601
BLAST score
                  116
E value
                  2.0e-58
Match length
                  353
```

E value

```
98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MHJ24, complete sequence [Arabidopsis thaliana]
                   121160
Seq. No.
                   6127 1.R1010
Contig ID
                   jC-atXLIB327416P3d01b1
 5'-most EST
                   BLASTN
Method
                   g2582640
NCBI GI
                   55
BLAST score
                   9.0e-22
E value
                   59
Match length
                   98
% identity
                   Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                   121161
Seq. No.
                   6128 1.R1010
Contig ID
                   LIB2\overline{2} - 024 - Q1 - E1 - G6
 5'-most EST
                   BLASTX
Method
NCBI GI
                   g3522958
BLAST score
                   272
                   7.0e-24
E value
Match length
                   146
% identity
                   41
NCBI Description (AC004411) putative pectinesterase [Arabidopsis thaliana]
Seq. No.
                   121162
                   6129 1.R1010
Contig ID
                   LIB22-024-Q1-E1-G7
5'-most EST
                   BLASTN
Method
NCBI GI
                   q3821780
BLAST score
                   35
E value
                   6.0e-10
Match length
                   35
                   59
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   121163
                    6134 1.R1010
 Contig ID
                   LIB3175-066-P1-K1-B6
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3402745
BLAST score
                   188
                   1.0e-101
 E value
Match length
                   272
 % identity
                    96
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
NCBI Description
                    (ESSAII project)
                   121164
Seq. No.
                    6134 2.R1010
 Contig ID
                   LIB2\overline{5}-010-Q1-E1-F1
 5'-most EST
Method
                   BLASTX
                   q3080389
NCBI GI
BLAST score
                    654
```

2.0e-68

```
Match length
                   170
% identity
                  75
                   (AL022603) putative membrane associated protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  121165
Contig ID
                   6136 1.R1010
                   jC-aTXLIB327410P2c11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3881505
BLAST score
                   326
E value
                   9.0e-30
Match length
                  224
                  37
% identity
                  (247357) similar to the mouse hypothetical protein D15Kz1
NCBI Description
                   (PIR accession number A30222); cDNA EST EMBL:C08599 comes
                  from this gene; cDNA EST EMBL: C07385 comes from this gene;
                  cDNA EST EMBL: C08733 comes from this gene; cDNA EST
                  121166
Seq. No.
                  6137_1.R1010
Contig ID
5'-most EST
                  LIB2\overline{2}-024-Q1-E1-H4
Method
                  BLASTX
                  g285286
NCBI GI
BLAST score
                  295
                  8.0e-27
E value
Match length
                  111
                  50 -
% identity
NCBI Description flavonol 4'-sulfotransferase - Flaveria chloraefolia
                  121167
Seq. No.
                  6139 1.R1010
Contig ID
5'-most EST
                  LIB24-025-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  g4314378
BLAST score
                  283
E value
                  2.0e-25
Match length
                  64
% identity
                  83
NCBI Description
                  (AC006232) putative lipase [Arabidopsis thaliana]
                  121168
Seq. No.
                  6145 1.R1010
Contig ID
5'-most EST
                  jC-atXP15C106F9T7016a1
Method
                  BLASTX
NCBI GI
                  g1172873
BLAST score
                  455
E value
                  4.0e-45
Match length
                  135
% identity
                  58
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                   (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                  121169
                  6147 1.R1010
Contig ID
```

```
5'-most EST
                   jC-atXLIB327432P2h11b2
Method
                   BLASTN
                  q2582640
NCBI GI
BLAST score
                   66
E value
                   2.0e-28
                   70
Match length
                   99
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
Seq. No.
                   121170
                   6151 1.R1010
Contig ID
                  LIB22-025-Q1-E1-A9
5'-most EST
Method
                  BLASTN
NCBI GI
                  q3522932
BLAST score
                   33
E value
                   8.0e-09
Match length
                   69
% identity
                   94
                  Arabidopsis thaliana chromosome II BAC F14M4 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   121171
                   6153 1.R1010
Contig ID
5'-most EST
                  LIB22-025-Q1-E1-B10
                   BLASTX
Method
NCBI GI
                   q4376088
BLAST score
                   277
E value
                   1.0e-24
Match length
                   95
% identity
                   55
NCBI Description
                   (Z99707) cytochrome P450-like protein [Arabidopsis
                  thaliana]
Seq. No.
                   121172
Contig ID
                   6154 1.R1010
5'-most EST
                  jC-atXLIB327432P3h08b1
Method
                  BLASTN
NCBI GI
                   q4688614
BLAST score
                   367
E value
                   0.0e + 00
Match length
                   383
% identity
                   99
NCBI Description Arabidopsis thaliana mRNA for D-type cyclin
Seq. No.
                  121173
Contig ID
                  6155 1.R1010
5'-most EST
                  jC-atXLIB327432P4h09b1
Method
                  BLASTX
NCBI GI
                  q2842491
BLAST score
                   273
                   6.0e-24
E value
Match length
                  106
% identity
NCBI Description (ALO21749) putative protein [Arabidopsis thaliana]
Seq. No.
                  121174
```

```
6156 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327432P4h10a1
                   BLASTN
Method
                   g531828
NCBI GI
BLAST score
                   50
                   6.0e-19
E value
                   65
Match length
                   95
% identity
NCBI Description
                  Cloning vector pSport1, complete cds
Seq. No.
                   121175
                   6164 1.R1010
Contig ID
                   LIB22-025-Q1-E1-C11
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4006856
BLAST score
                   445
                   2.0e-44
E value
Match length
                   90
                   99
% identity
                   (Z99707) receptor kinase-like protein [Arabidopsis
NCBI Description
                   thaliana)
Seq. No.
                  121176
                   6165 1.R1010
Contig ID
                   jC-atXLIB327410P3f06b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3449316
BLAST score
                   309
                   1.0e-173
E value
Match length
                   453
                  92
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K9D7, complete sequence [Arabidopsis thaliana]
                   121177
Seq. No.
                   6168 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327407P1f03b2
Method
                   BLASTX
                   g4587685
NCBI GI
BLAST score
                   974
                   1.0e-106
E value
Match length
                  220
% identity
                   84
                   (AC007197) putative methylmalonate semi-aldehyde
NCBI Description
                  dehydrogenase [Arabidopsis thaliana]
                   121178
Seq. No.
                   6168 2.R1010
Contig ID
                  LIB25-043-Q1-E1-A3
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4587685
BLAST score
                   1667
E value
                  0.0e+00
Match length
                   413
                  81
% identity
                   (AC007197) putative methylmalonate semi-aldehyde
NCBI Description
                  dehydrogenase [Arabidopsis thaliana]
```

```
121179
  Seq. No.
                     6171 1.R1010
Contig ID
                     LIB3177-072-P1-K1-B10
  5'-most EST
  Method
                     BLASTX
  NCBI GI
                     g2062164
                     927
  BLAST score
                     1.0e-100
  E value
  Match length
                     201
                     88
  % identity
  NCBI Description
                     (ACO01645) jasmonate inducible protein isolog [Arabidopsis
                     thaliana]
                     121180 .
  Seq. No.
  Contig ID
                     6171 2.R1010
                     jC-aTXLIB327409P1h08b1
  5'-most EST
  Method
                     BLASTX
                     g2062164
  NCBI GI
  BLAST score
                     363
                     3.0e - 34
  E value
  Match length
                     85
                     89
  % identity
  NCBI Description
                     (AC001645) jasmonate inducible protein isolog [Arabidopsis
                     thaliana]
  Seq. No.
                     121181
  Contig ID
                     6171 3.R1010
  5'-most EST
                     jC-atXLIB327438P1d12a1
  Method
                     BLASTX
  NCBI GI
                     g2062163
  BLAST score
                     1135
  E value
                     1.0e-124
  Match length
                     214
  % identity
                     98
  NCBI Description
                     (AC001645) jasmonate inducible protein isolog [Arabidopsis
                     thaliana]
                     121182
  Seq. No.
  Contig ID
                     6174 1.R1010
  5'-most EST
                     jC-atXLIB327433P1a11b1
  Method
                     BLASTN
                     g3243255
  NCBI GI
  BLAST score
                     37
                     4.0e-11
  E value
  Match length
                     37
  % identity
                     100
  NCBI Description
                     Vigna unguiculata phosphoribosylpyrophosphate
                     amidotransferase (purl) mRNA, complete cds
  Seq. No.
                     121183
  Contig ID
                     6178_1.R1010
  5'-most EST
                     LIB22-086-Q1-E1-C2
  Seq. No.
                     121184
  Contig ID
                     6180 1.R1010
  5'-most EST
                     jC-atXLIB327408P1a08b1
```

BLASTN

```
NCBI GI
                   q3702731
BLAST score
                   259
                   1.0e-143
E value
                   378
Match length
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFC19, complete sequence [Arabidopsis thaliana]
                   121185
Seq. No.
                   6181 1.R1010
Contig ID
5'-most EST
                  LIB24-070-Q1-E1-F8
Method
                   BLASTX
                   q4588001
NCBI GI
BLAST score
                   514
                   7.0e-52
E value
                   223
Match length
% identity
                   (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   121186
Seq. No.
Contig 'ID
                   6182_1.R1010
5'-most EST
                  LIB22-031-Q1-E1-F12
Method
                  BLASTX
                   q4585978
NCBI GI
                   1341
BLAST score
                   1.0e-149
E value
Match length
                   261
% identity
                   (AC005287) NADP specific isocitrate dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   121187
Contig ID
                   6184 1.R1010
                  LIB2\overline{2}-025-Q1-E1-E11
5'-most EST
Method
                   BLASTX
                  g4587556
NCBI GI
BLAST score
                   414
E value
                   3.0e-64
                   144
Match length
% identity
                   (AC006577) Similar to gi_1653162 (p)ppGpp
NCBI Description
                   3-pyrophosphohydrolase from Synechocystis sp genome
                   gb_D90911. EST gb_W43807 comes from this gene.
                   [Arabidopsis thaliana]
                   121188
Seq. No.
Contig ID
                   6187 1.R1010
                   LIB3234-089-P1-K1-B1
5'-most EST
Method
                   BLASTN
NCBI GI
                  q2673901
BLAST score
                   316
E value
                   1.0e-178
Match length
                   348
% identity
                   97
                  Arabidopsis thaliana chromosome II BAC T24P15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

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121189
Seq. No.
Contig ID
                  6189 1.R1010
                  LIB22-025-Q1-E1-E5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4206110
BLAST score
                  238
E value
                  5.0e-20
Match length
                  74
% identity
                  53
NCBI Description
                  (AF097661) cytochrome [Mesembryanthemum crystallinum]
Seq. No.
                  121190
                  6193 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1b03b1
Method
                  BLASTX
NCBI GI
                  q4467126
BLAST score
                  719
E value
                  5.0e-76
Match length
                  238
                  60
% identity
NCBI Description
                  (AL035538) guanine nucleotide-exchange protein-like
                  [Arabidopsis thaliana]
                  121191
Seq. No.
                  6196 1.R1010
Contig ID
                  LIB22-083-Q1-E2-F3
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4335760
BLAST score
                  122
                  2.0e-06
E value
                  123
Match length
% identity
                  (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  121192
                  6198_1.R1010
Contig ID
5'-most EST
                  q905764
Method
                  BLASTX
                                                   Ŀ.
NCBI GI
                  a2459443
BLAST score
                  169
E value
                  6.0e-97
Match length
                  183
% identity
                  98
                  (AC002332) putative NAD(P)-dependent cholesterol
NCBI Description
                  dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  121193
Contig ID
                  6198_3.R1010
5'-most EST
                  LIB22-025-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                  a2459443
BLAST score
                  828
E value
                  7.0e-89
Match length
                  218
% identity
                  85
                  (AC002332) putative NAD(P)-dependent cholesterol
NCBI Description
```

dehydrogenase [Arabidopsis thaliana] 121194 Seq. No. Contig ID 6201 1.R1010 jC-aTXLIB327433P1b02b1 5'-most EST Method BLASTX q3785987 NCBI GI 215 BLAST score 4.0e-17 E value Match length 94 % identity 47 NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana] 121195 Seq. No. 6203 1.R1010 Contig ID LIB3234-013-P1-K1-A8 5'-most EST Method BLASTX g2104949 NCBI GI BLAST score 716 E value 8.0e-76 Match length 159 % identity 86 NCBI Description (U96716) MAP kinase-like protein [Selaginella lepidophylla] Seq. No. 121196 6205 1.R1010 Contig ID 5'-most EST LIB22-025-Q1-E1-G10 BLASTX Method g3915070 NCBI GI BLAST score 682 E value 7.0e-72Match length 175 72 % identity NCBI Description HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS) >gi_1841704_emb_CAB06653_ (Z85984) histidyl tRNA Synthetase [Oryza sativa] 121197 Seq. No. Contig ID 6206 1.R1010 5'-most EST jC-atXLIB327433P1b11b1 121198 Seq. No. Contig ID 6207 1.R1010 5'-most EST $LIB2\overline{2}-025-Q1-E1-G12$ Method BLASTX NCBI GI g4503593 BLAST score 140 E value 1.0e-08 Match length 81 % identity 14 NCBI Description

Seq. No. 121199 Contig ID 6213 1.R1010

>gi_631069_pir__S43074 AF-1p protein - human

eps 15 GB A.N. L221768 [Homo sapiens]

epidermal growth factor receptor pathway substrate 15

>gi_470035_emb_CAA82305_ (Z29064) Highly similar to murine

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LIB3168-073-P1-K1-D1
5'-most EST
                  BLASTX
Method
                  g4469003
NCBI GI
                 ··· 658
BLAST score
                  9.0e-69
E value
                  257
Match length
                  54
% identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
                  121200
Seq. No.
                  6215 1.R1010
Contig ID
                  LIB3175-081-P1-K1-G4
5'-most EST
                  BLASTX
Method
                  g3193297
NCBI GI
BLAST score
                  571
                  2.0e-59
E value
                  130
Match length
                  89
% identity
                  (AF069298) similar to epoxide hydrolases [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  121201
                  6215 2.R1010
Contig ID
                  LIB22-025-Q1-E1-H10
5'-most EST
                  BLASTX
Method
                  q3193297
NCBI GI
                  474
BLAST score
                  9.0e-48
E value
                  113
Match length
% identity
                  88
                  (AF069298) similar to epoxide hydrolases [Arabidopsis
NCBI Description
                  thaliana]
                  121202
Seq. No.
                  6216 1.R1010
Contig ID
                  jC-aTXLIB327406P3c07b2
5'-most EST
                  BLASTX
Method
                 · q2244977
NCBI GI
                  1168
BLAST score
                  1.0e-128
E value
                  225
Match length
                  95
% identity
NCBI Description (Z97340) cysteine proteinase [Arabidopsis thaliana]
                  121203
Seq. No.
                  6216 2.R1010
Contig ID
                  LIB23-033-Q1-E1-B1
5'-most EST
                  BLASTX
Method
                  g2244977
NCBI GI
                  750
BLAST score
                  1.0e-79
E value
                  191
Match length
                  80
% identity
                  (Z97340) cysteine proteinase [Arabidopsis thaliana]
NCBI Description
                  121204
Seq. No.
```

6216_3.R1010

Contig ID

```
5'-most EST
                  jC-a1X24094Q1E1G12b1
Method
                  BLASTX
                  q2244977
NCBI GI
BLAST score
                  924
                  1.0e-100
E value
Match length
                  202
                  86
% identity
                  (Z97340) cysteine proteinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  121205
Contig ID
                  6216 4.R1010
5'-most EST
                  q2733445
                  BLASTN
Method
NCBI GI
                  q2244950
BLAST score
                  253
E value
                  1.0e-140
Match length
                  340
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  121206
Contig ID
                  6216_5.R1010
5'-most EST
                  jC-atXP68C218B14T7d1
Method
                  BLASTX
NCBI GI
                  a2244977
BLAST score
                  449
E value
                  2.0e-44
Match length
                  215
% identity
                  49
NCBI Description
                  (Z97340) cysteine proteinase [Arabidopsis thaliana]
Seq. No.
                  121207
Contig ID
                  6224 1.R1010
5'-most EST
                  LIB22-026-Q1-E1-A10
Method
                  BLASTX
NCBI GI
                  q416758
BLAST score
                  714
E value
                  1.0e-75
Match length
                  138
% identity
                  100
                  SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)
NCBI Description
                  carboxypeptidase Y-like protein [Arabidopsis thaliana]
                  >gi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis
                  thaliana]
Seq. No.
                  121208
Contiq ID
                  6225 1.R1010
5'-most EST
                  jC-atXLIB327407P4b11b1
Method
                  BLASTN
NCBI GI
                  q4589950
BLAST score
                  158
E value
                  2.0e-83
Match length
                  282
% identity
                  97
                  Arabidopsis thaliana chromosome II BAC T28P16 genomic
NCBI Description
```

sequence, complete sequence

```
121209
Seq. No.
                  6225 2.R1010
Contig ID
                  LIB24-106-Q1-E1-C10
5'-most EST
                . BLASTX
Method
NCBI GI
                  q4589965
BLAST score
                  993
E value
                  1.0e-108
Match length
                  190
% identity
                  100
NCBI Description (AC007169) putative glyoxalase II [Arabidopsis thaliana]
                  121210
Seq. No.
                  6225_3.R1010
Contig ID
                  LIB25-065-Q1-E1-C10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4589965
BLAST score
                  409
E value
                  5.0e-40
Match length
                  117
                  72
% identity
NCBI Description
                  (AC007169) putative glyoxalase II [Arabidopsis thaliana]
Seq. No.
                  .121211
                                                 e) = 1.
Contig ID
                  6226 1.R1010
5'-most EST
                  jC-atXLIB327411P3a08b1
Method
                  BLASTX
NCBI GI
                  q4587989
BLAST score
                  248
E value
                  7.0e-21
Match length
                  79
                  62
% identity
NCBI Description
                  (AF085279) hypothetical Cys-3-His zinc finger protein
                  [Arabidopsis thaliana]
Seq. No.
                  121212
                  6228 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327410P1d04b1
Method
                  BLASTN
                  q3702731
NCBI GI
BLAST score
                  792
E value
                  0.0e + 00
Match length
                  1240
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFC19, complete sequence [Arabidopsis thaliana].
Seq. No.
                  121213
                  6232 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P2h08b2
Method
                  BLASTX
NCBI GI
                  g2829903
BLAST score
                  659
E value
                  4.0e-69
Match length
                  170
% identity
                  81
NCBI Description (AC002311) unknown protein [Arabidopsis thaliana]
```

NCBI GI

```
Seq. No.
                  121214
                  6235 1.R1010
Contig ID
                  jC-atXLIB327432P4h08b1
5'-most EST
                  121215
Seq. No.
                  6238 1.R1010
Contig ID
                  jC-atXLIB327432P3h10b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4056453
BLAST score
                  531
E value
                  4.0e-54
Match length
                  123
                  85
% identity
                  (AC005990) EST gb AA597511 comes from this gene.
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  121216
                  6239_1.R1010
Contig ID
                  jC-atXLIB327432P4h11b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4589969
BLAST score
                  198
                  1.0e-107
E value
                  473
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F1P15 genomic
                  sequence, complete sequence
                  121217
Seq. No.
                  6241_1.R1010 ·
Contig ID
                  jC-atXLIB327421P1g03b1
5'-most EST
Method
                  BLASTX
                  g3738324
NCBI GI
BLAST score
                  749
E value
                  3.0e-79
                  246
Match length
                  59
% identity
NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]
                  121218
Seq. No.
                  6243 1.R1010
Contig ID
                  LIB25-026-Q1-E1-A11
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2088643
BLAST score
                  1009
                  1.0e-110
E value
Match length
                  200
                  93
% identity
NCBI Description
                  (AF002109) transcription factor SF3 isolog [Arabidopsis
                  thaliana]
                 -121219
Seq. No.
                  6244 1.R1010
Contig ID
                  jC-atXLIB327431P3h12a1
5'-most EST
Method
                  BLASTX
```

q4539327

```
770
BLAST score
E value
                  3.0e-85
Match length
                  204
% identity
NCBI Description
                  (AL035679) putative proton pump [Arabidopsis thaliana]
                  121220
Seq. No.
                  6244 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327432P4h07b1
Method
                  BLASTX
NCBI GI
                  q4567273
BLAST score
                  761
                  3.0e-81
E value
Match length
                  143
% identity
                  100
NCBI Description
                   (AC006841) putative vacuolar proton ATPase subunit
                   [Arabidopsis thaliana]
Seq. No.
                  121221
                   6247 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1a04b1
Method
                  BLASTX
NCBI GI
                  g1350930
BLAST score
                   766
                  2.0e-81
E value
Match length
                  150
                  100
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S13
                  121222
Seq. No.
                   6251 1.R1010
Contig ID
                  LIB23-033-Q1-E1-H8
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4220468
BLAST score
                   337
                   0.0e + 00
E value
Match length
                   358
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC T8011 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   121223
                   6252 1.R1010
Contig ID
                   jC-atX22086Q1E1C10b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4539322
BLAST score
                   571
                   6.0e-59
E value
Match length
                   137
% identity
                  (AL035679) putative protein [Arabidopsis thaliana]
NCBI Description
                  121224
Seq. No.
                   6254 1.R1010
Contig ID
                   jC-atXLIB327433P1a03b1
5'-most EST
                  BLASTN
Method
```

q2275194

NCBI GI

% identity

68

```
BLAST score
                    263
· E value
                    1.0e-145
 Match length
                    1036
 % identity
                    98
 NCBI Description
                    Arabidopsis thaliana chromosome II BAC T08I13 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
                    121225
 Seq. No.
                    6255 1.R1010
 Contig ID
                    LIB3\overline{5}-042-Q1-E1-D7
 5'-most EST
 Seq. No.
                    121226
                    6256 1.R1010
 Contig ID
                    jC-atXLIB327428P1c07b2
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g1888357
 BLAST score
                    550
 E value
                    3.0e-56
 Match length
                    241
 % identity
                    46
 NCBI Description
                    (X98130) alpha-mannosidase [Arabidopsis thaliana]
                    >qi 1890154 emb CAA72432_ (Y11767) alpha-mannosidase
                    precursor [Arabidopsis thaliana]
                    121227
 Seq. No.
 Contig ID
                    6260 1.R1010
 5'-most EST
                    LIB23-005-Q1-E1-B6
 Method
                    BLASTX
 NCBI GI
                    g2062156
 BLAST score
                    914
 E value
                    8.0e-99
 Match length
                    234
 % identity
                    33
 NCBI Description
                    (AC001645) jasmonate inducible protein isolog [Arabidopsis
                    thaliana]
                    121228
 Seq. No.
 Contig ID
                    6260 2.R1010
 5'-most EST
                    jC-atXP44C170J16T7d1
                    BLASTX
 Method
 NCBI GI
                    g2062156
 BLAST score
                    824
 E value
                    2.0e-88
 Match length
                    246
 % identity
                    29
 NCBI Description
                     (AC001645) jasmonate inducible protein isolog [Arabidopsis
                    thaliana]
 Seq. No.
                    121229
                    6262 1.R1010
 Contig ID
                    LIB3176-067-P1-K1-D10
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g2559012
 BLAST score
                    857
 E value
                    1.0e-102
 Match length
                    289
```

Contig ID

```
(AF026293) chaperonin containing t-complex polypeptide 1,
NCBI Description
                  beta subunit; CCT-beta [Homo sapiens] >gi 4090929
                  (AF026166) chaperonin-containing TCP-1 beta subunit homolog
                  [Homo sapiens]
                  121230
Seq. No.
                  6263 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1a08b1
Method
                  BLASTN
NCBI GI
                  g2582640
                  42
BLAST score
                  3.0e-14
E value
Match length
                  54
                  94
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  121231
                  6265 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327414P2d06a1
Method
                  BLASTX
NCBI GI
                  g4586117
BLAST score
                  279
E value
                  1.0e-24
Match length
                  93
% identity
                  62
NCBI Description (AL049638) putative protein [Arabidopsis thaliana]
                  121232
Seq. No.
                  6266 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1a09b1
Method
                  BLASTX
NCBI GI
                  g3242062
BLAST score
                  391
E value
                  8.0e-38
Match length
                  131
% identity
                  64
NCBI Description
                  (Z97058) NRT2;1p [Arabidopsis thaliana] >gi 3608362
                  (AF019748) high-affinity nitrate transporter ACH1
                  [Arabidopsis thaliana] >gi_3747058 (AF093754)
                  trans-membrane nitrate transporter protein AtNRT2:1
                  [Arabidopsis thaliana]
Seq. No.
                  121233
                  6268 1.R1010
Contig ID
                  LIB22-082-Q1-E2-E9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3757524
BLAST score
                  533
E value
                  2.0e-54
Match length
                  143
% identity
                  78
NCBI Description
                  (AC005167) tetracycline transporter-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  121234
```

6270 1.R1010

5'-most EST

```
5'-most EST
                    jC-atXP17C110E22T7d3
                    BLASTX
Method
NCBI GI
                    g3122572 ·
BLAST score
                    1646
                    0.0e + 00
E value
                    433
Match length
% identity
                    72
                   NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
NCBI Description
                    (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
                   SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
                    >gi 758340 emb CAA59818 (X85808) 76 kDa mitochondrial
                    complex I subunit [Solanum tuberosum]
                    121235
Seq. No.
                    6270 2.R1010
Contig ID
5'-most EST
                    jC-atXP71CF1D9T7072d1
                    BLASTX
Method
NCBI GI
                   q3122572
BLAST score
                    705
E value
                    2.0e-74
                   206
Match length
                    67
% identity
                   NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
NCBI Description
                    (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
                   SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
                    >gi 758340 emb CAA59818 (X85808) 76 kDa mitochondrial
                   complex I subunit [Solanum tuberosum]
Seq. No.
                   121236
                   6270 3.R1010
Contig ID
5'-most EST
                   q2446053
Method
                   BLASTN
NCBI GI
                   q4589436
BLAST score
                    356
E value
                   0.0e + 00
Match length
                    437
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MPA22, complete sequence
Seq. No.
                   121237
                   6271 1.R1010
Contig ID
5'-most EST
                   LIB3175-036-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q1076450
BLAST score
                   269
E value
                   3.0e-23
Match length
                   142
                   42
% identity
                   hypothetical protein - rape >gi 508373 (L34287) unnamed
NCBI Description
                   protein product [Brassica napus]
Seq. No.
                   121238
Contig ID
                   6272 1.R1010
```

jC-atX22026Q1E1E03b1

```
BLASTX
Method
NCBI GI
                    g2342738
BLAST score
                    259
                    2.0e-22
E value
Match length
                    52
                    100
% identity
                   (AC002341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    121239
                    6273 1.R1010
Contig ID
                   LIB22-035-Q1-E1-A9
5'-most EST
                   BLASTX
Method
NCBI GI
                    q1402900
BLAST score
                    352
                    2.0e-33
E value
Match length
                    109
% identity
                    67
                    (X98322) peroxidase [Arabidopsis thaliana]
NCBI Description
                    >gi 1429219 emb CAA67312 (X98776) peroxidase ATP13a
                    [Arabidopsis thaliana]
Seq. No.
                    121240
                   6276_1.R1010
LIB22-026-Q1-E1-E8
Contig ID
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4512685
BLAST score
                    543
                    4.0e-72
E value
Match length
                    173
% identity
                    78
                   (AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087)
NCBI Description
                   hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    121241
                    6278 1.R1010
Contig ID
                   LIB2\overline{2}-026-Q1-E1-F1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2245031
BLAST score
                   229
                   1.0e-126
E value
Match length
                   360
% identity
                   99
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
Seq. No.
                   121242
                   6281 3.R1010
Contig ID
5'-most EST
                   jC-atXP108C174G13T7s1
                   BLASTX
Method
NCBI GI
                   q461812
BLAST score
                    47
                   8.0e-40
E value
Match length
                   145
% identity
                   52
                   CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
NCBI Description
                   GERANIOL-10-HYDROXYLASE) (GE10H) >gi 167484 (L10081)
```

```
roseus]
                   121243
Seq. No.
                   6283 1.R1010
Contig ID
                   jC-atXLIB327433P1b05b1
5'-most EST
                   BLASTN
Method
                   q4757388
NCBI GI
BLAST score
                   255
E value
                   1.0e-141
                   322
Match length
% identity
                   96
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   F15L12, complete sequence
                   121244
Seq. No.
                   6284 1.R1010
Contig ID
                   LIB2\overline{2}-026-Q1-E1-F4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3132470
BLAST score
                   406
E value
                   1.0e-39
Match length
                   83
% identity
                   100
NCBI Description
                   (AC003096) unknown protein [Arabidopsis thaliana]
Seq. No.
                   121245
                   6286 1.R1010
Contig ID
                   LIB3234-019-P1-K1-F2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3702315
BLAST score
                   250
E value
                   1.0e-138
Match length
                   550
% identity
                   99
                   Arabidopsis thaliana chromosome II BAC T3F17 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   121246
                   6288 1.R1010
Contig ID
                   jC-a\(\bar{1}\)XLIB327435P4b01b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4835226
BLAST score
                   302
E value
                   6.0e-27
Match length
                   184
% identity
NCBI Description
                   (AL049862) putative protein [Arabidopsis thaliana]
                   121247
Seq. No.
                   6288 2.R1010
Contig ID
                   LIB22-026-Q1-E1-F9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4006891
BLAST score
                   507
```

Cytochrome P-450 protein [Catharanthus roseus]

>qi 445604 prf 1909351A cytochrome P450 [Catharanthus

2.0e-55

E value

NCBI GI

```
Match length
                   145
% identity
                   80
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   121248
                   6294 1.R1010
Contig ID
                   jC-atXP110C117B14T7d1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4757395
BLAST score
                   470
                   0.0e + 00
E value
                   497
Match length
% identity
                   98
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K21L13, complete sequence
                   121249
Seq. No.
                   6295 1.R1010
Contig ID
                   LIB2\overline{2}-042-Q1-E1-D11
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3450842
BLAST score
                   327
E value
                   3.0e-30
Match length
                   95
% identity
                   62
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   121250
                   6296 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327416P3h02b1
Method
                   BLASTX
NCBI GI
                   q4262147
BLAST score
                   190
E value
                   3.0e-14
Match length
                   61
                   57
% identity
NCBI Description
                   (AC005275) putative homolog of transport inhibitor response
                   1 [Arabidopsis thaliana]
Seq. No.
                   121251
                   6296 2.R1010
Contig ID
5'-most EST
                   LIB3175-021-P1-K1-B10
Method
                   BLASTN
NCBI GI
                   q4519191
BLAST score
                   294
E value
                   1.0e-164
Match length
                   341
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K9P8, complete sequence
                   121252
Seq. No.
Contig ID
                   6298 1.R1010
                   LIB22-026-Q1-E1-G9
5'-most EST
                   BLASTN
Method
```

q4454022

```
BLAST score
                   399
E value
                 0.0e+00
Match length
                  403
% identity
                   100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
NCBI Description
                   (ESSAII project)
                   121253
Seq. No.
Contig ID
                   6300 1.R1010
                   g2722849
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3868723
                   28
BLAST score
E value
                   8.0e-06
Match length
                   185
                   35
% identity
                  Arabidopsis thaliana chromosome V map 60.5 cM, complete
NCBI Description
                   sequence [Arabidopsis thaliana]
                   121254
Seq. No.
                   6301 1.R1010
Contiq ID
                   LIB23-073-Q1-E1-D4
5'-most EST
                  BLASTX
Method
NCBI GI
                   q2655926
BLAST score
                   328
                   2.0e-30
E value
Match length
                   98
% identity
                   60
NCBI Description (Y09057) sf21 [Helianthus annuus]
Seq. No.
                   121255
                   6303 1.R1010
Contig ID
                   LIB2\overline{2}-026-Q1-E1-H2
5'-most EST
Method
                   BLASTX
                   q1208875
NCBI GI
BLAST score
                   102
E value
                   2.0e-03
Match length
                   114
% identity
                   (U50071) C. elegans ankyrin-related unc-44 (GB:U21734)
NCBI Description
                   [Caenorhabditis elegans] >gi_1814195 (U39847) AO49 ankyrin
                   [Caenorhabditis elegans]
                   121256
Seq. No.
                   6307 1.R1010
Contig ID
                   LIB3175-070-P1-K-B12
5'-most EST
                   121257
Seq. No.
                   6311 1.R1010
Contig ID
                  LIB23-051-Q1-E1-B2
5'-most EST
                  BLASTX
Method
                   g1899188
NCBI GI
BLAST score
                  100
                   2.0e-03
E value
                   89
Match length
                  23
% identity
NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]
```

5'-most EST

```
121258
Seq. No.
Contig ID
                  6311 2.R1010
5'-most EST
                  LIB22-027-Q1-E1-A12
                  121259
Seq. No.
                  6312 1.R1010
Contig ID
5'-most EST
                  LIB25-047-Q1-E1-H4
                  121260
Seq. No.
                  6312 2.R1010
Contig ID
                  LIB22-027-Q1-E1-A2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3668086
BLAST score
                  220
                  6.0e-18
E value
                  60
Match length
                  67
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                  121261
Seq. No.
                  6316 1.R1010
Contig ID
                  LIB3176-112-P1-K1-B11
5'-most EST
                  BLASTX
Method
                  g1708971
NCBI GI
                  160
BLAST score
                  3.0e-10
E value
                  236
Match length
                  32
% identity
                  (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
NCBI Description
                  (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                  >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) -
                  black cherry >gi_288116_emb_CAA51194_ (X72617)
                  mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
                  (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
                  serotina] >gi 1090776 prf 2019441A mandelonitrile lyase
                  [Prunus serotina]
Seq. No.
                  121262
                  6316 2.R1010
Contig ID
5'-most EST
                  g2446066
                  121263
Seq. No.
Contig ID
                  6317 1.R1010
                  LIB24-086-Q1-E1-D9
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3892051
BLAST score
                  622
E value
                  7.0e-65
                  134
Match length
                  92
% identity
                  (AC002330) predicted NADH dehydrogenase 24 kD subunit
NCBI Description
                  [Arabidopsis thaliana]
                  121264
Seq. No.
Contig ID
                  6318 3.R1010
```

jC-atXLIB327433P1c02b1

E value

4.0e-51

```
121265
Seq. No.
Contig ID
                  6319 1.R1010
5'-most EST
                  jC-atXLIB327433P1c12b1
Seq. No.
                  121266
                  6323 1.R1010
Contig ID
5'-most EST
                  jC-atXP44C171E15T7008a1
                  BLASTX
Method
NCBI GI
                  q2851508
BLAST score
                  355
E value
                  3.0e-33
Match length
                  90
                  78
% identity
                  60S RIBOSOMAL PROTEIN L21 >qi 2160162 (AC000132) Similar to
NCBI Description
                  ribosomal protein L21 (gb_L38826). ESTs
                  gb AA395597, gb ATTS5197 come from this gene. [Arabidopsis
                  thaliana] >gi 3482935 (AC003970) Putative ribosomal protein
                  L21 [Arabidopsis thaliana]
Seq. No.
                  121267
Contig ID
                  6323 2.R1010
5'-most EST
                  jC-alXLIB327435P2a11b1
Method
                  BLASTX
                  a2851508
NCBI GI
BLAST score
                  868
                  2.0e-93
E value
Match length
                  164
                  100
% identity
                  60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to
NCBI Description
                  ribosomal protein L21 (gb_L38826). ESTs
                  gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis
                  thaliana] >gi_3482935 (AC003970) Putative ribosomal protein
                  L21 [Arabidopsis thaliana]
Seq. No.
                  121268
Contig ID
                  6323 3.R1010
5'-most EST
                  jC-atXLIB327427P1b10b1
Method
                  BLASTX
NCBI GI
                  q2851508
BLAST score
                  620
E value
                  2.0e-64
Match length
                  164
% identity
                  83
NCBI Description
                  60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to
                  ribosomal protein L21 (gb_L38826). ESTs
                  gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis
                  thaliana] >gi_3482935 (AC003970) Putative ribosomal protein
                  L21 [Arabidopsis thaliana]
                  121269
Seq. No.
                  6323 5.R1010
Contig ID
5'-most EST
                  LIB35-027-Q1-E1-G12
Method
                  BLASTX
NCBI GI
                  q4587600
BLAST score
                  507
```

```
Match length
                   99
                   96
% identity
NCBI Description
                   (AC006951) putative translation initiation factor EIF-1A
                   [Arabidopsis thaliana]
Seq. No.
                   121270
                   6323_6.R1010 ***
Contig ID
5'-most EST
                   jC-atXmonuni27Df12b1
Method
                   BLASTX
                   q4587600
NCBI GI
BLAST score
                   567
E value
                   2.0e-58
Match length
                   119
% identity
                   92
                   (AC006951) putative translation initiation factor EIF-1A
NCBI Description
                   [Arabidopsis thaliana]
                   121271
Seq. No.
                   6323_7.R1010
Contig ID
                   q872<del>0</del>05
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2851508
BLAST score
                   70
                   7.0e-40
E value
Match length
                   97
                   86
% identity
                   60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to
NCBI Description
                   ribosomal protein L21 (qb L38826). ESTs
                   gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis
                   thaliana] >gi_3482935 (AC003970) Putative ribosomal protein
                   L21 [Arabidopsis thaliana]
Seq. No.
                   121272
Contig ID
                   6323 8.R1010
                   LIB3177-009-P1-K2-D2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2851508
BLAST score
                   379
E value
                   4.0e-50
Match length
                   137
% identity
                   67
                   60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to
NCBI Description
                   ribosomal protein L21 (gb L38826). ESTs
                   gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein
                   L21 [Arabidopsis thaliana]
Seq. No.
                   121273
Contig ID
                   6325_1.R1010
5'-most EST
                   LIB24-054-Q1-E1-D9
Method
                   BLASTX
NCBI GI
                   q3914740
BLAST score
                   583
E value
                   5.0e-60
Match length
                   145
% identity
                   81
NCBI Description 60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_
```

(D78495) ribosomal protein [Brassica rapa]

```
121274
Seq. No.
                  6325 2.R1010
Contig ID
5'-most EST
                  LIB25-056-Q1-E1-H3
Method
                  BLASTN
                  q4589969
NCBI GI
BLAST score
                  432
E value
                  0.0e + 00
                  460
Match length
% identity
                  98
                  Arabidopsis thaliana chromosome II BAC F1P15 genomic
NCBI Description
                  sequence, complete sequence
                  121275
Seq. No.
                  6325 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327414P1e11a1
Method
                  BLASTX
NCBI GI
                  g3914740
BLAST score
                  429
E value
                  3.0e-42
Match length
                  127
% identity
                  70
NCBI Description 60S RIBOSOMAL PROTEIN L26 >qi 2160300 dbj BAA18941
                  (D78495) ribosomal protein [Brassica rapa]
Seq. No.
                  121276
                  6325 7.R1010
Contig ID
5'-most EST
                  jC-atXLIB327439P3g10b2
Method
                  BLASTX
NCBI GI
                  g3914740
BLAST score
                  367
E value
                  9.0e-35
Match length
                  99
% identity
                  75
                  60S RIBOSOMAL PROTEIN L26 >qi 2160300 dbj BAA18941
NCBI Description
                  (D78495) ribosomal protein [Brassica rapa]
                  121277
Seq. No.
                  6328 1.R1010
Contig ID
                  LIB22-027-Q1-E1-B8
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4063737
BLAST score
                  368
                  0.0e + 00
E value
Match length
                  526
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC F24D13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  121278
Seq. No.
                  6329 1.R1010
Contig ID
                  jC-atXLIB327405P3e10b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g116527
BLAST score
                  257
```

6.0e-22

E value

```
Match length
                   88
% identity
                   48
                   PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196)
NCBI Description
                  >gi 1143166 (U32397) ClpP protease [Nicotiana tabacum]
                   >gi_2924270_emb_CAA77422_ (Z00044) ATP-dependent protease
                  proteolytic subuni [Nicotiana tabacum]
                  121279
Seq. No.
Contig ID
                  6331 1.R1010
5'-most EST
                   jC-atX23018Q1E1E01a1
                   121280
Seq. No.
                   6337 1.R1010
Contig ID
5'-most EST
                   g244<del>6</del>087
Method
                   BLASTN
                   g3868722
NCBI GI
                   47
BLAST score
                   3.0e-17
E value
Match length
                   83
                   89
% identity
NCBI Description
                  Arabidopsis thaliana BAC T19G15, from chromosome V near
                   60.5 cM, complete sequence [Arabidopsis thaliana]
                   121281
Seq. No.
                   6341 1.R1010
Contig ID
                  LIB2\overline{2}-027-Q1-E1-D11
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4587530
BLAST score
                   390
                   8.0e-38
E value
Match length
                   126
% identity
                   56
                   (AC007060) Strong similarity to F19I3.2 gi 3033375 putative
NCBI Description
                  berberine bridge enzyme from Arabidopsis thaliana BAC
                   gb AC004238
Seq. No.
                   121282
                   6345 1.R1010
Contig ID
                  g1215998
5'-most EST
Method
                   BLASTX
NCBI GI
                  q3914403
BLAST score
                   231
E value
                   2.0e-57
Match length
                   173
                   66
% identity
                  PROTOPORPHYRINOGEN OXIDASE, MITOCHONDRIAL (PPO II)
NCBI Description
                   (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME II) (PPX II)
                   >gi 2370335 emb CAA73866 (Y13466) protoporphyrinogen
                  oxidase [Nicotiana tabacum] >gi_3929920_dbj_BAA34712_
                   (AB020500) mitochondrial protoporphyrinogen oxidase
                   [Nicotiana tabacum] >gi 4105188 (AF044129)
                  protoporphyrinogen oxidase PX-2 [Nicotiana tabacum]
Seq. No.
                   121283
                  6346 1.R1010
Contig ID
5'-most EST
                  LIB3175-057-P1-K1-E9
Method
                  BLASTX
```

```
NCBI GI
                  g3511285
BLAST score
                  319
                  2.0e-29
E value
Match length
                  113
                  52
% identity
                  (AF081534) cellulose synthase [Populus alba x Populus
NCBI Description
                  tremula]
                  121284
Seq. No.
                  6350 1.R1010
Contig ID
                  LIB3175-004-P1-K1-C2
5'-most EST
                  BLASTN
Method
NCBI GI
                  g1707006
BLAST score
                  315
                  1.0e-177
E value
                  705
Match length
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T1B8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  121285
Seq. No.
Contig ID
                  6351 1.R1010
                  LIB3168-098-P1-K1-F3
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3643085
BLAST score
                  291
                  8.0e-26
E value
Match length
                  135
                  50
% identity
NCBI Description
                  (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
                  crystallinum]
Seq. No.
                  121286
Contig ID
                  6355 1.R1010
5'-most EST
                  jC-atXLIB327433P1d12b1
Seq. No.
                  121287
Contig ID
                  6356 1.R1010
5'-most EST
                  jC-atXLIB327421P2g09b1
                  BLASTX
Method
NCBI GI
                  q2497702
BLAST score
                  246
E value
                  2.0e-20
Match length
                  142
% identity
                  42
                  OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR
NCBI Description
                  >gi_2121019_pir__I40710 outer membrane lipoprotein -
                  Citrobacter freundii >gi_717136 (U21727) lipocalin
                  precursor [Citrobacter freundii]
                  121288
Seq. No.
Contig ID
                  6356 2.R1010
5'-most EST
                  jC-atXP73C223J11T7b1
Method
                  BLASTX
NCBI GI
                  g2497702
BLAST score
                  246
E value
                  2.0e-20
```

```
Match length
                  142
                  42
% identity
NCBI Description
                  OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR
                  >gi_2121019 pir I40710 outer membrane lipoprotein -
                  Citrobacter freundii >gi 717136 (U21727) lipocalin
                  precursor [Citrobacter freundii]
                  121289
Seq. No.
Contig ID
                  6356 3.R1010
5'-most EST
                  jC-atXP96C248H15T7b1
Method
                  BLASTX
NCBI GI
                  q2497702
BLAST score
                  238
E value
                  1.0e-19
Match length
                  141
                  40
% identity
                  OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR
NCBI Description
                  >gi 2121019 pir I40710 outer membrane lipoprotein -
                  Citrobacter freundii >gi_717136 (U21727) lipocalin
                  precursor [Citrobacter freundii]
                  121290
Seq. No.
                  6356 5.R1010
Contig ID
5'-most EST
                  LIB35-042-Q1-E1-E12
Method
                  BLASTN
NCBI GI
                  q4519188
BLAST score
                  318
E value
                  1.0e-179
Match length
                  383
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21L19, complete sequence
                  121291
Seq. No.
                  6357 1.R1010
Contig ID
                  LIB22-027-Q1-E1-F1
5'-most EST
Method
                  BLASTX
                  g4678924
NCBI GI
BLAST score
                  660
                  3.0e-69
E value
Match length
                  157
% identity
                  85
NCBI Description
                  (ALO49711) putative protein [Arabidopsis thaliana]
                  121292
Seq. No.
                  6358 1.R1010
Contig ID
                  LIB23-065-Q1-E1-E12
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4249390
BLAST score
                  577
                  5.0e-69
E value
Match length
                  166
% identity
                  86
NCBI Description
                  (AC005966) Similar to gb_AF039182 probable aldo-keto
                  reductase from Fragaria x ananassa. This gene may be cut
                  off. EST gb U74151 comes from this gene. [Arabidopsis
```

thaliana]

```
121293
Seq. No.
Contig ID
                  6361 1.R1010
5'-most EST
                  LIB23-040-Q1-E1-D10
Seq. No.
                  121294
                  6363 1.R1010
Contig ID
                  jC-atXLIB327432P4f09b1
5'-most EST
Method
                  BLASTX
                  g3123295
NCBI GI
BLAST score
                  336
                  5.0e-31
E value
Match length
                  137
% identity
                  48
NCBI Description
                  CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi 2583169
                   (AF026473) calmodulin-related protein [Arabidopsis
                  thalianal
Seq. No.
                  121295
Contig ID
                  6368 1.R1010
5'-most EST
                  jC-atXLIB327433P1e06b1
                  BLASTX
Method
NCBI GI
                  q320552
BLAST score
                  329
                                                                          · ...
E value
                  1.0e-42
Match length
                  124
% identity
                  80
                  anthranilate synthase (EC 4.1.3.27) alpha-1 chain -
NCBI Description
                  Arabidopsis thaliana
                  121296
Seq. No.
                  6369 1.R1010
Contig ID
                  jC-aTXLIB327433P1e07b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q401213
BLAST score
                  516
                  3.0e-52
E value
Match length
                  126
% identity
                  84
NCBI Description
                  ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >qi 166792
                  (M96073) phosphoribosylanthranilate transferase
                  [Arabidopsis thaliana] >gi 445600 prf 1909347A
                  phosphoribosylanthranilate transferase [Arabidopsis
                  thaliana]
Seq. No.
                  121297
                  6372 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327415P2b09b2
Method
                  BLASTX
NCBI GI
                  g4455223
BLAST score
                  1255
E value
                  1.0e-138
Match length
                  343
% identity
NCBI Description
                  (AL035440) putative DNA binding protein [Arabidopsis
```

thalianal

5'-most EST

g1217113

```
Seq. No.
                  121298
                  6378 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327440P1e03b1
Method
                  BLASTX
NCBI GI
                  g1531758
BLAST score
                  386
                  4.0e-37
E value
                  107
Match length
% identity
                  72
                  (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
NCBI Description
                  unknown protein [Arabidopsis thaliana]
                  121299
Seq. No.
                  6383 1.R1010
Contig ID
5'-most EST
                  LIB3177-081-P1-K1-C7
                  121300
Seq. No.
                  6388 1.R1010
Contig ID
                  LIB25-062-Q1-E1-F8
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2245031
BLAST score
                  299
                  1.0e-167
E value
Match length
                  735
% identity
                  98
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  121301
Seq. No.
                  6389 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1c03b1
Seq. No.
                  121302
                  6390 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1c04b1
Method
                  BLASTX
NCBI GI
                  q3759184
BLAST score
                  416
                  2.0e-40
E value
Match length
                  104
                  77
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                  121303
Seq. No.
                  6391 1.R1010
Contig ID
5'-most EST
                  LIB22-028-Q1-E1-A2
Method
                  BLASTX
NCBI GI
                  q4512666
BLAST score
                  165
                  2.0e-11
E value
                  96
Match length
                  42
% identity
NCBI Description
                  (AC006931) putative mei2 protein [Arabidopsis thaliana]
                  121304
Seq. No.
Contig ID
                  6396 1.R1010
```

Seq. No.

121309

```
Method
                  BLASTX
NCBI GI
                  g2829923
BLAST score
                  1191
                  1.0e-131
E value
                  231
Match length
                  58
% identity
                  (AC002291) Similar to uridylyl transferases [Arabidopsis
NCBI Description
                  thaliana]
                  121305
Seq. No.
                  6396 2.R1010
Contig ID
                  jC-atXP82CG2D5T7d3
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2829923
                  582
BLAST score
                  4.0e-64
E value
                  124
Match length
                  50
% identity
                  (AC002291) Similar to uridylyl transferases [Arabidopsis
NCBI Description
                  thaliana)
                  121306
Seq. No.
                  6399 1.R1010
Contig_ID
5'-most EST
                  q2763305
Method
                  BLASTX
NCBI GI
                  q2347188
BLAST score
                  658
                  1.0e-130
E value
Match length
                  241
                  92
% identity
NCBI Description
                  (AC002338) laccase isolog [Arabidopsis thaliana]
                  >gi 3150401 (AC004165) putative laccase [Arabidopsis
                  thaliana]
                  121307
Seq. No.
                  6400 1.R1010
Contig ID
5'-most EST
                  jC-atXP31C144I5T7d2
                  BLASTX
Method
                  g2245037
NCBI GI
BLAST score
                  331
E value
                  1.0e-30
                  162
Match length
                  50
% identity
NCBI Description (Z97342) nuclear antigen homolog [Arabidopsis thaliana]
                  121308
Seq. No.
Contig ID
                  6404 1.R1010
5'-most EST
                  g905<del>5</del>89
                  BLASTX
Method
                  g2102691
NCBI GI
BLAST score
                  431
E value
                  1.0e-42
Match length
                  102
% identity
NCBI Description (U64817) fructokinase [Lycopersicon esculentum]
```

Match length

286

```
6408 1.R1010
Contig ID
                  jC-atXLIB327424P1d12b2
5'-most EST
Method
                  BLASTX
                  g4522009
NCBI GI
BLAST score
                   577
                  2.0e-59
E value
                  118
Match length
                  99
% identity
                  (AC007069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  121310
Seq. No.
                  6412 1.R1010
Contig ID
                  g2733625
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4455214
BLAST score
                  987
E value
                  1.0e-124
                  273
Match length
% identity
                  88
                   (AL035440) putative dihydrolipoamide succinyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                  121311
Seq. No.
                  6412 2.R1010
Contig ID
                  jC-atXLIB327429P4a10a2
5'-most EST
Method
                  BLASTN
                  q4756963
NCBI GI
BLAST score
                  390
E value
                  0.0e+00
Match length
                  415
                  99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
                  121312
Seq. No.
                  6413 1.R1010
Contig ID
                  LIB22-028-Q1-E1-C5
5'-most EST
                  121313
Seq. No.
                  6414 1.R1010
Contig ID
                  LIB3175-035-P1-K1-E9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1418990
BLAST score
                  627
E value
                  3.0e-65
Match length
                  171
                  67
% identity
NCBI Description (Z75524) unknown [Lycopersicon esculentum]
                  121314
Seq. No.
                  6415 1.R1010
Contiq ID
5'-most EST
                  jC-atXLIB327413P2c07b1
Method
                  BLASTX
NCBI GI
                  g2398679
BLAST score
                  708
E value
                  2.0e-80
```

Seq. No.

121320

•;

```
% identity
                   63
NCBI Description
                   (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
                  synthase [Morinda citrifolia]
Seq. No.
                  121315
                   6415 2.R1010
Contig ID
                  ARABL1-041-Q1-B1-E1
5'-most EST
Seq. No.
                  121316
                   6419 1.R1010
Contig ID
5'-most EST
                  jC-atX22028Q1E1D04a1
Method
                  BLASTN
NCBI GI
                  q2656028
BLAST score
                   414
                  0.0e + 00
E value
Match length
                  454
% identity
                  93
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
Seq. No.
                  121317
Contig ID
                  6419 2.R1010
                  jC-atXLIB327404P4c11b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2459445
BLAST score
                  186
E value
                  9.0e-14
Match length
                  77
                  21
% identity
NCBI Description
                   (AC002332) putative ribonucleoprotein [Arabidopsis
                  thaliana]
Seq. No.
                  121318
Contig ID
                  6424 1.R1010
5'-most EST
                  jC-atXLIB327433P1d03b1
Method
                  BLASTX
NCBI GI
                  g2651310
BLAST score
                  266
E value
                  4.0e-23
Match length
                  126
% identity
                  43
                   (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
                  121319
Seq. No.
Contig ID
                  6425 1.R1010
5'-most EST
                  jC-atXLIB327408P2e12b1
Method
                  BLASTN
NCBI GI
                  g2651294
BLAST score
                  375
E value
                  0.0e + 00
Match length
                  438
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T2P4 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

Method

```
6426 1.R1010
Contig ID
                  LIB3234-022-P1-K1-C8
5'-most EST
                  121321
Seq. No.
                  6428 1.R1010
Contig ID
                  jC-atXLIB327412P3f06b1
5'-most EST
                  BLASTN
Method
                  g4589434
NCBI GI
                  355
BLAST score
                  0.0e + 00
E value
                  507
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNJ7, complete sequence
                  121322
Seq. No.
                  6430 1.R1010
Contig ID
                  LIB22-028-Q1-E1-E4
5'-most EST
                  BLASTN
Method
NCBI GI
                  g4185128
BLAST score
                  143
                  2.0e-74
E value
                   410
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II P1 MSF3 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  121323
Seq. No.
                   6438 1.R1010
Contig ID
                  LIB25-062-Q1-E1-A6
5'-most EST
Seq. No.
                  121324
                   6439 1.R1010
Contig ID
                  q122\overline{3}590
5'-most EST
                  BLASTX
Method
                   q4586105
NCBI GI
BLAST score
                   172
                   4.0e-12
E value
Match length
                   65
                   49
% identity
                  (AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
                  121325
Seq. No.
                   6443 1.R1010
Contig ID
                   jC-atXLIB327419P3a10b2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4580531
                   839
BLAST score
E value
                   5.0e-90
Match length
                  170
                   96
% identity
NCBI Description (AF036309) scarecrow-like 14 [Arabidopsis thaliana]
                  121326
Seq. No.
                   6443 2.R1010
Contig ID
                  LIB22-028-Q1-E1-F9
5'-most EST
```

BLASTX

Method

```
NCBI GI
                   q4580531
BLAST score
                   1112
                   1.0e-122
E value
Match length
                   259
% identity
                   87
NCBI Description
                  (AF036309) scarecrow-like 14 [Arabidopsis thaliana]
Seq. No.
                  121327
Contig ID
                   6445 1.R1010
                  LIB22-028-Q1-E1-G10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2911055
BLAST score
                   295
                  2.0e-70
E value
Match length
                   167
% identity
                   91
NCBI Description
                   (AL021961) putative protein [Arabidopsis thaliana]
                   121328
Seq. No.
                   6445 2.R1010
Contig ID
5'-most EST
                  LIB3177-038-P1-K2-C1
Method
                  BLASTX
NCBI GI
                  q2583116
BLAST score
                   415
E value
                   1.0e-40
Match length
                  107
% identity
                  79
NCBI Description
                  (AC002387) unknown protein [Arabidopsis thaliana]
                   121329
Seq. No.
                   6445_3.R1010
Contig ID
5'-most EST
                  LIB25-039-Q1-E1-B8
Method
                  BLASTX
NCBI GI
                   g2911055
BLAST score
                   568
E value
                   2.0e-66
Match length
                  156
% identity
                  87
NCBI Description
                  (AL021961) putative protein [Arabidopsis thaliana]
                  121330
Seq. No.
                  6447 1.R1010
Contig ID
5'-most EST
                   jC-atXP27C130D20T7d2
Method
                  BLASTX
NCBI GI
                  g3236235
BLAST score
                  790
E value
                   2.0e-84
Match length
                  204
% identity
                  51
                   (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4056501 (AC005896) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                  121331
                  6448 1.R1010
Contig ID
5'-most EST
                  jC-aTXLIB327433P1e08b1
```

BLASTX

```
NCBI GI
                  q2384673
BLAST score
                  426
E value
                  7.0e-42
Match length
                  81
                  100
% identity
NCBI Description
                   (AF012658) putative potassium transporter AtKT3p
                   [Arabidopsis thaliana]
Seq. No.
                  121332
                  6450 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1e09b1
Method
                  BLASTN
NCBI GI
                  q4589428
BLAST score
                  184
E value
                  6.0e-99
Match length
                  344 .
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFH8, complete sequence
Seq. No.
                  121333
Contig ID
                  6451 1.R1010
5'-most EST
                  jC-atXLIB327433P1e04b1
                  121334
Seq. No.
                  6455 1.R1010
Contig ID
5'-most EST
                  q905853
Method
                  BLASTX
NCBI GI
                  g3033375
BLAST score
                  293
E value
                  4.0e-26
Match length
                  99
% identity
                  51
NCBI Description
                  (AC004238) putative berberine bridge enzyme [Arabidopsis
                  thaliana]
                  121335
Seq. No.
Contig ID
                  6459 1.R1010
5'-most EST
                  LIB3177-072-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g3212877
BLAST score
                  1554
E value
                  1.0e-173
Match length
                  316
% identity
                  68
NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]
                  121336
Seq. No.
                  6465 1.R1010
Contig ID
                  LIB22-029-Q1-E1-A11
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3426041
BLAST score
                  543
                  8.0e-56
E value
Match length
                  152
% identity
                  72
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
```

```
121337
Seq. No.
Contig ID
                  6467 1.R1010
5'-most EST
                  jC-atXLIB327433P1c01b1
Method /
                  BLASTX
NCBI GI
                  g4539342
BLAST score
                  899
E value
                  3.0e-97
Match length
                  173
% identity
                  66
NCBI Description
                  (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                  121338
                  6471 1.R1010
Contig ID
5'-most EST
                  jC-atX22029Q1E1B01b1
Method
                  BLASTN
NCBI GI
                  g2191126
BLAST score
                  230
E value
                  1.0e-126
Match length
                  400
                  99
% identity
NCBI Description Arabidopsis thaliana BAC IG002N01
                  121339
Seq. No.
Contig [ID
                  6472 1.R1010
5'-most EST
                  jC-atXLIB327433P1c09b1
Method
                  BLASTN
NCBI GI
                  g4756963
BLAST score
                  128
E value
                  2.0e-65
Match length
                  472
                  98
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
Seq. No.
                  121340
                  6475 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1c11b1
Method
                  BLASTN
NCBI GI
                  q4559344
BLAST score
                  270
                  1.0e-150
E value
Match length
                  424
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F27C12 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  121341
                  6476 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1c07b1
Method
                  BLASTN
NCBI GI
                  g2529657
BLAST score
                  349
E value
                  0.0e + 00
Match length
                  361
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T30B22 genomic
```

NCBI GI

sequence, complete sequence [Arabidopsis thaliana] 121342 Seq. No. 6478 1.R1010 Contig ID LIB35-019-Q1-E1-H10 5'-most EST Method BLASTN . . . NCBI GI q4220645 BLAST score 213 1.0e-116 E value Match length 410 % identity 99 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana] 121343 Seq. No. Contig ID 6482 1.R1010 5'-most EST LIB23-015-Q1-E1-G4 121344 Seq. No. 6483 1.R1010 Contig ID LIB3175-033-P1-K1-G12 5'-most EST Method BLASTX NCBI GI q4678309 BLAST score 921 1.0e-99 E value 194 Match length 95 % identity NCBI Description (ALO49655) small GTP-binding protein-like (fragment) [Arabidopsis thaliana] Seq. No. 121345 6485 1.R1010 Contig ID jC-atXP115C248N22T7084d1 5'-most EST BLASTX Method NCBI GI q4584832 BLAST score 258 E value 6.0e-22 Match length 91 % identity 53 NCBI Description (AL031764) hypothetical protein [Schizosaccharomyces pombe] Seq. No. 121346 6491 1.R1010 Contig ID 5'-most EST LIB24-061-Q1-E1-C1 Method BLASTX NCBI GI - q2739376 BLAST score 1261 E value 1.0e-139 Match length 283 % identity 89 NCBI Description (AC002505) putative permease [Arabidopsis thaliana] 121347 Seq. No. Contig ID 6493 1.R1010 5'-most EST jC-atXLIB327414P4g02b2 Method BLASTN

q3241927

```
BLAST score
                  295
                  1.0e-165
E value
                  738
Match length
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTE17, complete sequence [Arabidopsis thaliana]
                  121348
Seq. No.
Contig ID
                  6494 1.R1010
                  LIB22-078-01-E1-E7
5'-most EST
Method
                  BLASTN
NCBI GI
                  q1707006
BLAST score
                  204
E value
                  1.0e-111
Match length
                  410
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T1B8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  121349
Seq. No.
                  6497 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327412P1d03a1
Seq. No.
                  121350
                  6500 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1d09b1
Seq. No.
                  121351
                  6502 1.R1010
Contig ID
5'-most EST
                  jC-a1X25089Q1E1A11b1
                  BLASTX
Method
NCBI GI
                  q2191177
BLAST score
                  625
                  3.0e-65
E value
Match length
                  128
% identity
                  100
NCBI Description
                  (AF007270) belongs to the SPOU family of rRNA methylases.
                  [Arabidopsis thaliana]
Seq. No.
                  121352
Contig ID
                  6504 1.R1010
5'-most EST
                  jC-atXLIB327433Pld11b1
Method
                  BLASTX
NCBI GI
                  q2829923
BLAST score
                  1061
E value
                  1.0e-116
Match length
                  202
% identity
NCBI Description
                  (AC002291) Similar to uridylyl transferases [Arabidopsis
                  thalianal
Seq. No.
                  121353
                  6504 2.R1010
Contig ID
5'-most EST
                  g2445958
Method
                  BLASTN
                  g2477521
NCBI GI
BLAST score
                  344
```

Contig ID

```
E value
                   0.0e + 00
Match length
                   375
% identity
                   98
                  Arabidopsis thaliana chromosome I BAC F22K2O genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                  121354
Seq. No.
                   6507 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327402P1g09b1
Method
                   BLASTX
NCBI GI
                   g2827536
BLAST score
                   184
                   2.0e-13
E value
Match length
                   45
% identity
                   60
NCBI Description
                  (AL021633) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   121355
                   6507 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327433P1d08b1
Seq. No.
                   121356
Contig ID
                   6507_3.R1010
5'-most EST
                   jC-atXLIB327422P4d08b1
                   BLASTX
Method
NCBI GI
                  a2827536
BLAST score
                   175
E value
                   4.0e-12
Match length
                   45
                   58
% identity
NCBI Description
                  (AL021633) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   121357
Contig ID
                   6509 1.R1010
5'-most EST
                  LIB22-064-Q1-E1-B11
                  121358
Seq. No.
Contig ID
                   6509 2.R1010
5'-most EST
                  LIB3234-015-P1-K1-C12
                   121359
Seq. No.
Contig ID
                   6517 1.R1010
5'-most EST
                  LIB22-029-Q1-E1-G10
                   121360
Seq. No.
                   6518 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1e01b1
Method
                  BLASTX
NCBI GI
                   q3928089
BLAST score
                   716
E value
                   1.0e-75
Match length
                  134
                   97
% identity
                  (AC005770) putative osr40 [Arabidopsis thaliana]
NCBI Description
                   121361
Seq. No.
```

6520_1.R1010

Method

BLASTX

```
5'-most EST
                  LIB3175-075-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g1916290
BLAST score
                  185
                  1.0e-13
E value
                  79
Match length
                  52
% identity
NCBI Description
                  (U89876) ALY [Mus musculus]
                  121362
Seq. No.
                  6521 1.R1010
Contig ID
5'-most EST
                  q2047839
Method
                  BLASTX
NCBI GI
                  g462147
BLAST score
                  101
E value
                  3.0e-25
Match length
                  72
% identity
                  88
                  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)
NCBI Description
                   (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
                   (PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase
                   (EC 5.3.1.9) - Arabidopsis thaliana
                  >gi 415923 emb CAA48940 (X69195) glucose-6-phosphate
                  isomerase [Arabidopsis thaliana]
                  121363
Seq. No.
                  6525 1.R1010
Contig ID
                  LIB2\overline{2}-029-Q1-E1-G8
5'-most EST
                  BLASTN
Method
NCBI GI
                  g2244950
BLAST score
                  211
E value
                  1.0e-115
Match length
                  365
% identity
                  96
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  121364
                  6529 1.R1010
Contig ID
                  LIB25-031-Q1-E1-B12
5'-most EST
                  121365
Seq. No.
                  6536 1.R1010
Contig ID
5'-most EST
                  g671759
                  BLASTN
Method
NCBI GI
                  g2264318
BLAST score
                  222
E value
                  1.0e-122
Match length
                  353
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  121366
                  6538 1.R1010
Contig ID
                  LIB24-114-Q1-E1-A10
5'-most EST
```

```
NCBI GI
                  q3122139
BLAST score
                  897
                  1.0e-96
E value
Match length
                  329
% identity
                  52
                  GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE)
NCBI Description
                   (GLYCEROKINASE) (GK) (ATP-STIMULATED
                  GLUCOCORTICOID-RECEPTOR TRANSLOCATON PROMOTER) (ASTP)
                  >gi 484372_pir__JN0606 ATP-stimulated
                  qlucocorticoid-receptor translocation promoter protein -
                  rat >gi 433211 dbj BAA03677 (D16102) ATP-stimulated
                  qlucocorticoid-receptor translocaton promoter [Rattus
                  rattusl
                  121367
Seq. No.
                  6540 1.R1010
Contig ID
                  jC-atXLIB327421P3b10b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3449327
BLAST score
                  220
E value
                  1.0e-120
Match length
                  541
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCA23, complete sequence [Arabidopsis thaliana]
Seq. No.
                  121368
                  6545 1.R1010
Contig ID
                  LIB3175-057-P1-K1-E3
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2656024
BLAST score
                  287
E value
                  1.0e-160
Match length
                  703
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K15E6
                  121369
Seq. No.
                  6546 1.R1010
Contig ID
                  jC-atXLIB327421P2b06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2245030
BLAST score
                  309
                  7.0e-28
E value
Match length
                  194
% identity
                  43
                  (Z97341) apetala2 domain TINY homolog [Arabidopsis
NCBI Description
                  thalianal
                  121370
Seq. No.
                  6551 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327411P1g05b1
Method
                  BLASTX
NCBI GI
                  g4559331
BLAST score
                  818
```

9.0e-88

1.

E value

5'-most EST

```
Match length
                  148
% identity
                  100
NCBI Description
                  (AC007087) unknown protein [Arabidopsis thaliana]
                  121371
Seq. No.
                  6553 1.R1010
Contig ID
                  jC-atXLIB327409P3f12b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3912953
BLAST score
                  371
E value
                  4.0e-35
Match length
                  189
% identity
                  43
                  PUTATIVE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE DEAMINASE (ACC
NCBI Description
                  DEAMINASE) >gi_3256439_dbj_BAA29122.1 (AP000001) 328aa
                  long hypothetical 1-aminocyclopropane-1-carboxylate
                  deaminase [Pyrococcus horikoshii]
                  121372
Seq. No.
Contig ID
                  6554 1.R1010
5'-most EST
                  jC-atXLIB327411P1c03b1
Method
                  BLASTX
NCBI GI
                  q4467138
BLAST score
                  681
E value
                  9.0e-72
Match length
                  135
                  99.
% identity
NCBI Description
                  (AL035540) probable H+-transporting ATPase (Arabidopsis
                  thaliana]
Seq. No.
                  121373
Contig ID
                  6555 1.R1010
5'-most EST
                  LIB3175-006-P1-K1-A12
Method
                  BLASTX
                  q3360289
NCBI GI
BLAST score
                  458
E value
                  2.0e-45
Match length
                  171
% identity
                  56
                  (AF023164) leucine-rich repeat transmembrane protein kinase
NCBI Description
                  1 [Zea mays]
Seq. No.
                  121374
Contig ID
                  6560 1.R1010
5'-most EST
                  jC-atXLIB327410P3c11b1
Method
                  BLASTN
NCBI GI
                  q2564051
BLAST score
                  308
E value
                  1.0e-173
Match length
                  599
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  121375
                  6562 1.R1010
Contig ID
```

jC-atXLIB327431P2c04a1

Method

BLASTN

```
Method
                  BLASTX
NCBI GI
                  g1621268
BLAST score
                  666
                  1.0e-71
E value
                  198
Match length
                  70
% identity
NCBI Description (Z81012) unknown [Ricinus communis]
Seq. No.
                  121376
                  6562 2.R1010
Contig ID
                  jC-atXLIB327414P2e10a1
5'-most EST
                  BLASTX
Method
                  g1621268
NCBI GI
BLAST score
                  570
                  1.0e-58
E value
                  123
Match length
                  88
% identity
NCBI Description (Z81012) unknown [Ricinus communis]
Seq. No.
                  121377
                  6562 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327416P3f10b1
Method
                  BLASTX
NCBI GI
                  q4049348
BLAST score
                  424
E value
                  1.0e-41
Match length
                  97
                  77
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                  121378
Contig ID
                  6562 4.R1010
5'-most EST
                  jC-atXLIB327429P1a06b2
                  BLASTX
Method
NCBI GI
                  g1621268
BLAST score
                  42
                  2.0e-91
E value
Match length
                  207
                  83
% identity
NCBI Description (Z81012) unknown [Ricinus communis]
                  121379
Seq. No.
Contig ID
                  6564 1.R1010
5'-most EST
                  jC-atXLIB327419P2f10b2
Method
                  BLASTX
NCBI GI
                  g4263791
BLAST score
                  389
                  1.0e-126
E value
Match length
                  302
                  77
% identity
                  (AC006068) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  121380
Seq. No.
Contig ID
                  6570 1.R1010
                  LIB24-023-Q1-E1-H10
5'-most EST
```

```
NCBI GI
                  q3461810
                  237
BLAST score
                  1.0e-130
E value
                  388
Match length
                  98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T17M13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  121381
Seq. No.
Contig ID
                  6571 1.R1010
5'-most EST
                  jC-atXLIB327422P3b07b2
Method
                  BLASTX
NCBI GI
                  q2702281
BLAST score
                  816
                  2.0e-87
E value
                  176
Match length
% identity
                  58
NCBI Description
                   (AC003033) putative protein disulfide isomerase precursor
                   [Arabidopsis thaliana]
                  121382
Seq. No.
                  6573 1.R1010
Contig ID
5'-most EST
                  LIB22-030-Q1-E1-E11
Seq. No.
                  121383
                  6574 1.R1010
Contig ID
5'-most EST
                  LIB22-030-Q1-E1-E2
Method
                  BLASTX
                  g2160176
NCBI GI
                  272
BLAST score
                  6.0e-24
E value
Match length
                  117
% identity
                  51
NCBI Description
                  (AC000132) F21M12.25 gene product [Arabidopsis thaliana]
                  121384
Seq. No.
Contig ID
                  6578_1.R1010
5'-most EST
                  jC-atXP49C178K1T7070a1
Method
                  BLASTX
                  q4454051
NCBI GI
BLAST score
                  76
                  2.0e-64
E value
Match length
                  135
% identity
                  93
                  (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  121385
                  6582 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327427P3g04b2
Method
                  BLASTX
                  g2623303
NCBI GI
BLAST score
                  1441
                  1.0e-160
E value
Match length
                  301
% identity
                  (AC002409) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
```

```
Seq. No.
                  121386
                   6583 1.R1010
Contig ID
                   jC-atXP15C106P2T7031a1
5'-most EST
Method
                  BLASTN
                  q4587641
NCBI GI
BLAST score
                   629
                  0.0e + 00
E value
Match length
                  865
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
Seq. No.
                  121387
                  6597 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327427P4b10b2
Method
                  BLASTX
NCBI GI
                  g2252840
BLAST score
                  405
E value
                  3.0e-39
Match length
                  124
% identity
                  63
NCBI Description
                  (AF013293) contains regions of similarity to Haemophilus
                  influenzae permease (SP:P38767) [Arabidopsis thaliana]
                  121388
Seq. No.
Contig' ID
                  6602 1.R1010
                  jC-atX22030Q1E1H10b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3548806
BLAST score
                  545
E value
                  5.0e-74
Match length
                  178
% identity
                  77
NCBI Description
                  (AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.
                  121389
Contig ID
                  6604 1.R1010
5'-most EST
                  jC-atXLIB327418P4a04b1
Method
                  BLASTN
NCBI GI
                  g4220510
BLAST score
                  559
E value
                  0.0e+00
Match length
                  1215
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
                   (ESSAII project)
Seq. No.
                  121390
                  6604 2.R1010
Contig ID
5'-most EST
                  g2048220
Method
                  BLASTN
NCBI GI
                  g4220510
BLAST score
                  380
E value
                  0.0e + 00
Match length
                  560
% identity
                  97
```

5'-most EST

g2758442

```
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
                   (ESSAII project)
                  121391
Seq. No.
                   6607 1.R1010
Contig ID
                   jC-aTXLIB327433P1e10b1
5'-most EST
                   BLASTN
Method
NCBI GI
                  g2337888
BLAST score
                  336
                  0.0e + 00
E value
                   407
Match length
                   99
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14J16,
                 complete sequence [Arabidopsis thaliana]
                  121392
Seq. No.
                   6609 1.R1010
Contig ID
                  LIB22-031-Q1-E1-A1
5'-most EST
                  BLASTN
Method
                  g2435510
NCBI GI
BLAST score
                   404
                  0.0e+00
E value
Match length
                   464
                   97
% identity .
NCBI Description Arabidopsis thaliana BAC TM017A05
Seq. No.
                  121393
                  6610 1.R1010
Contig ID
                  LIB2\overline{2}-031-Q1-E1-A10
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3176694
BLAST score
                   257
E value
                  1.0e-142
Match length
                   400
% identity
                   99
                  Arabidopsis thaliana chromosome I BAC T14N5 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  121394
Seq. No.
                   6611 1.R1010
Contig ID
5'-most EST
                  ARABLI-16-Q1-B1-E7
Method
                  BLASTN
                  g4538918
NCBI GI
BLAST score
                  356
                   0.0e + 00
E value
Match length
                  544
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18
NCBI Description
                   (ESSA project)
Seq. No.
                  121395
                  6612 1.R1010
Contig ID
5'-most EST
                  LIB22-058-Q1-E1-G12
                  121396
Seq. No.
Contig ID
                  6617 1.R1010
```

Contig ID

```
Method
                   BLASTN
NCBI GI
                   q4587986
BLAST score
                   361
E value
                   0.0e + 00
Match length
                   394
% identity
                   98
                  Arabidopsis thaliana ABA-regulated gene cluster, complete
NCBI Description
                  sequence
Seq. No.
                   121397
                   6618 1.R1010
Contig ID
                   LIB23-044-Q1-E2-F11
5'-most EST
Method
                  BLASTX
NCBI GI
                   q2462925
BLAST score
                   808
E value
                   2.0e-86
Match length
                   184
                   89
% identity
NCBI Description
                   (AJ000053) GTP cyclohydrolase II /
                   3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                   thaliana]
                   121398
Seq. No.
Contig ID
                   6619 1.R1010
                  jC-atXLIB327427P3h03b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2244749
BLAST score
                   1262
E value
                   1.0e-146
                   278
Match length
% identity
                   93
NCBI Description
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                   121399
                   6619 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327408P2d10b1
Method
                  BLASTX
NCBI GI
                   g2244749
BLAST score
                   679
                   2.0e-71
E value
Match length
                  165
% identity
                   83
NCBI Description
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
                  121400
Seq. No.
                   6620 1.R1010
Contig ID
5'-most EST
                  LIB3176-118-P2-K1-H12
Method
                  BLASTX
NCBI GI
                   g4510345
BLAST score
                   505
E value
                   6.0e-51
Match length
                  125
% identity
                  81
NCBI Description
                  (AC006921) unknown protein [Arabidopsis thaliana]
                  121401
Seq. No.
```

6620 2.R1010

```
5'-most EST
                   ARABLI-04-Q1-B1-A12
Method
                   BLASTX
NCBI GI
                   q4510345
BLAST score
                   768
E value
                   1.0e-81
                   161
Match length
% identity
                   89
NCBI Description
                   (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   6621 1.R1010
5'-most EST
                   jC-atXLIB327433P1f10b1
Method
                   BLASTX
NCBI GI
                   q2435511
BLAST score
                   160
                   9.0e-11
E value
Match length
                   59
                   56
% identity
NCBI Description
                   (AF024504) contains similarity to prolyl 4-hydroxylase
                   alpha subunit [Arabidopsis thaliana]
                  121403
Seq. No.
Contig ID
                   6624 1.R1010
5'-most EST
                   jC-atXP98CH2G2T7b1
                   BLASTN
Method
                   q3510347
NCBI GI
BLAST score
                   55
                   8.0e-22
E value
Match length
                   227
% identity
                   87
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSJ11, complete sequence [Arabidopsis thaliana]
                   121404
Sea. No.
Contig ID
                   6624 2.R1010
5'-most EST
                   jC-atXP94CH4G4T7091d1
Method
                   BLASTN
NCBI GI
                   g474407
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
% identity
                   100
NCBI Description
                   Z.mais (KW5330) mRNA for nonphosphorylating
                   glyceraldehyde-3-phosphate dehydrogenase
Seq. No.
                   121405
Contig ID
                   6627 1.R1010
5'-most EST
                   jC-atXLIB327410P1e01b1
Method
                   BLASTN
NCBI GI
                   g4559375
BLAST score
                   271
E value
                   1.0e-150
Match length
                   636
% identity
                   97
                  Arabidopsis thaliana chromosome II BAC F11C10 genomic
NCBI Description
```

sequence, complete sequence

```
121406
Seq. No.
Contig ID
                  6627 3.R1010
                  LIB22-069-Q1-E1-C6
5'-most EST
Method
                  BLASTN
NCBI GI
                  g4559375
BLAST score
                  182
                  7.0e-98
E value
Match length
                  391
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC F11C10 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  121407
Contig ID
                  6630 1.R1010
5'-most EST
                  jC-atX22031Q1E1C01b2
Seq. No.
                  121408
                  6631 1.R1010
Contig ID
5'-most EST
                  LIB3175-064-P1-K1-C12
                  121409
Seq. No.
                  6634 1.R1010
Contig ID
                  LIB24-071-Q1-E1-F11
5'-most EST
Method
                  BLASTX
                  g4455314
NCBI GI
BLAST score
                  408
                  6.0e-40
E value
Match length
                  111
% identity
                  71
NCBI Description
                  (AL035528) glycine-rich RNA-binding protein AtGRP2-like
                  [Arabidopsis thaliana]
Seq. No.
                  121410
                  6635 1.R1010
Contia ID
5'-most EST
                  jC-atXLIB327414P2c09a1
Method
                  BLASTX
NCBI GI
                  q4056480
BLAST score
                  842
E value
                  2.0e-90
Match length
                  256
                  76
% identity
NCBI Description
                  (AC005896) putative adenylate kinase [Arabidopsis thaliana]
Seq. No.
                  121411
Contig ID
                  6635 2.R1010
5'-most EST
                  LIB3177-018-P1-K2-D12
Method
                  BLASTX
NCBI GI
                  q4056480
BLAST score
                  662
E value
                  1.0e-69
Match length
                  146
```

% identity

NCBI Description (AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No. 121412 Contig ID 6640 1.R1010

5'-most EST LIB24-122-Q1-E1-B10

Seq. No.

121417

```
Method
                   BLASTX
                   g3875368
NCBI GI
BLAST score
                   342
                   9.0e-32
E value
                   192
Match length
% identity
                   35
NCBI Description
                   (Z36948) similar to polypyrimidine tract binding protein
                   [Caenorhabditis elegans]
                   121413
Seq. No.
                   6641 1.R1010
Contiq ID
                   LIB22-031-Q1-E1-D1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3395432
BLAST score
                   766
                   1.0e-82
E value
                   223
Match length
% identity
                   63
NCBI Description
                   (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   121414
                   6643 1.R1010
Contig ID
                   jC-atXLIB327433P1g03b1
5'-most EST
Method
                   BLASTX
                   g3047013
NCBI GI
BLAST score
                   174
                   2.0e-12
E value
Match length
                   113
                   42
% identity
                  (AF057032) DNA topoisomerase III [Caenorhabditis elegans]
NCBI Description
Seq. No.
                   121415
                   6644 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327433P1g04b1
Method
                   BLASTX
NCBI GI
                   q4249384
BLAST score
                   149
                   2.0e-09
E value
Match length
                   138
% identity
                   22
                   (AC005966) Similar to gi 4056506 F3G5.25 nodulin-like
NCBI Description
                   protein from Arabidopsis thaliana BAC gb AC005896.
                   [Arabidopsis thaliana]
Seq. No.
                   121416
                   6645 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327419P2b02b2
                   BLASTN
Method
                   q3785968
NCBI GI
BLAST score
                   258
E value
                   1.0e-143
Match length
                   432
                   97
% identity
                  Arabidopsis thaliana chromosome II BAC F2I9 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

```
6646 1.R1010
Contig ID
5'-most EST
                  LIB25-099-Q1-E1-B2
Method
                  BLASTX
                  g3894178
NCBI GI
BLAST score
                   426
                   8.0e-42
E value
                  108
Match length
                   75
% identity
NCBI Description
                   (AC005312) putative nucleic acid binding protein
                   [Arabidopsis thaliana]
                  121418
Seq. No.
Contig ID
                   6649 1.R1010
5'-most EST
                   jC-atXP111C122K10T7d1
                  BLASTX
Method
NCBI GI
                  g3779024
BLAST score
                  1100
E value
                  1.0e-120
Match length
                  227
% identity
                  100
                  (AC005171) unknown protein [Arabidopsis thaliana]
NCBI Description
                  121419
Seq. No.
Contig ID
                   6650 1.R1010
5'-most EST
                  g496819
Method
                  BLASTX
NCBI GI
                  g4455210
BLAST score
                   407
                  1.0e-39
E value
Match length
                  78
% identity
                  100
                   (AL035440) putative aspartate-tRNA ligase [Arabidopsis
NCBI Description
                  thaliana]
                  121420
Seq. No.
Contig ID
                  6652 1.R1010
5'-most EST
                  jC-atXLIB327417P1b08b1
Method
                  BLASTN
NCBI GI
                  g3264774
BLAST score
                  618
E value
                  0.0e+00
Match length
                  670
                  98
% identity
NCBI Description
                  Arabidopsis thaliana BAC T8A17 chromosome IV, complete
                  sequence [Arabidopsis thaliana]
Seq. No.
                  121421
                  6655 1.R1010
Contig ID
5'-most EST
                  LIB25-025-Q1-E1-B12
                  BLASTN
Method
NCBI GI
                  g2262135
BLAST score
                  166
E value
                  4.0e-88
Match length
                  495
% identity
                  99
NCBI Description
                  Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
                  cM, complete sequence
```

```
Seq. No.
                   121422
                   6655-2.R1010
Contig ID
                   g2597660
5'-most EST
Method
                   BLASTX
                   g2281115
NCBI GI
BLAST score
                   651
                   3.0e-68
E value
Match length
                   203
% identity
                   (ACO02330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   121423
                   6659 1.R1010
Contig ID
5'-most EST
                   LIB3175-068-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q3096930
BLAST score
                   302
E value
                   5.0e-27
Match length
                   137
% identity
NCBI Description
                   (AL023094) Homeodomain - like protein [Arabidopsis
                  thalianal
Seq. No.
                   121424
Contig ID
                   6663 1.R1010
5'-most EST
                   q2393438
Seq. No.
                   121425
                   6663_2.R1010
Contig ID
5'-most EST
                   q115\overline{8}746
Method
                   BLASTX
NCBI GI
                   q1946372
BLAST score
                   177
E value
                   9.0e-13
Match length
                   83
% identity
                  41
NCBI Description
                   (U93215) yeast hypothetical protein YDB1 SCHPO isolog
                   [Arabidopsis thaliana]
Seq. No.
                   121426
Contig ID
                   6663 3.R1010
5'-most EST
                   jC-atXLIB327422P1f03b1
Method
                   BLASTN
NCBI GI
                   q3882354
BLAST score
                   398
E value
                   0.0e + 00
Match length
                   462
% identity
NCBI Description
                  Arabidopsis thaliana 12-oxophytodienoate reductase OPR1 and
                  12-oxophytodienoate reductase OPR2 genes, complete cds
Seq. No.
                  121427
                   6663 4.R1010
Contig ID
5'-most EST
                  LIB3176-112-P1-K1-D5
Method
                  BLASTN
```

Seq. No.

121432

```
g3882354
NCBI GI
BLAST score
                   31.6
                   1.0e-178
E value
Match length
                   392
                   9.7
% identity
NCBI Description
                  Arabidopsis thaliana 12-oxophytodienoate reductase OPR1 and
                   12-oxophytodienoate reductase OPR2 genes, complete cds
                   121428
Seq. No.
Contig ID
                   6666_1.R1010
5'-most EST
                   jC-atX22076Q1E1G05b1
Method
                   BLASTN
                   q2351061
NCBI GI
BLAST score
                   178
                   2.0e-95
E value
Match length
                   465
% identity
                   54
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAF19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   121429
                   6668_1.R1010
Contig ID
5'-most EST
                   LIB35-009-Q1-E1-B12
Method
                   BLASTX
NCBI GI
                   g2213583
BLAST score
                   369
E value
                   3.0e-35
Match length
                   119
% identity
                   67
                   (AC000348) T7N9.3 [Arabidopsis thaliana]
NCBI Description
                   121430
Seq. No.
Contig ID
                   6669_1.R1010
5'-most EST
                   jC-atXLIB327433P1h02b1
Method
                   BLASTN
NCBI GI
                  g3702723
BLAST score
                   354
                   0.0e + 00
E value
Match length
                   358
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K14B20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   121431
                   6670_1.R1010
Contig ID
5'-most EST
                   jC-atXP92C246M11T7049d1
Method
                   BLASTX
                  g233598
NCBI GI
BLAST score
                   203
E value
                   2.0e-15
                   96
Match length
% identity
                   43
                  13 kDa-B polypeptide of iron-sulfur protein fraction of
NCBI Description
                  NADH: ubiquinone oxidoreductase [cattle, heart, Peptide
                  Mitochondrial Partial, 114 aa]
```

```
6670 2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327426P3h05b1
                   BLASTN
Method
NCBI GI
                   g2656031
BLAST score
                   253
E value
                   1.0e-140
Match length
                   612
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC20
Seq. No.
                   121433
                   6674 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327430P4c05b1
                   121434
Seq. No.
Contig ID
                   6680 1.R1010
                   g1159723
5'-most EST
Method
                   BLASTN
NCBI GI
                   g4263762
BLAST score
                   256
E value
                   1.0e-142
Match length
                   292
% identity
                  98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F17L24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                   121435
Seq. No.
                   6683 1.R1010
Contig ID
5'-most EST
                  LIB2\overline{2}-031-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                   g4325344
BLAST score
                   1424
E value
                  1.0e-158
Match length
                   305
% identity
                   91
                   (AF128393) similar to beta-transducins (Pfam: PF00400,
NCBI Description
                  Score=71.7, E=1.5e-17, N=6) [Arabidopsis thaliana]
Seq. No.
                  121436
Contig ID
                   6683 2.R1010
5'-most EST
                  LIB3234-017-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  q4325340
BLAST score
                   330
E value
                   0.0e + 00
Match length
                   363
% identity
                   97
NCBI Description Arabidopsis thaliana BAC T1J1
                  121437
Seq. No.
                  6684_1.R1010
Contig ID
5'-most EST
                  g502129
Method
                  BLASTX
NCBI GI
                  g2739368
BLAST score
                   499
E value
                  3.0e-50
```

Match length

```
Match length
                  142
% identity
                  77
NCBI Description
                  (AC002505) cyclin-like protein [Arabidopsis thaliana]
                  121438
Seq. No.
                  6686 1.R1010
Contig ID
                  jC-atXP86CG9E2T7d2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2827139
BLAST score
                  1286
E value
                  1.0e-142
Match length
                  257
% identity
                  94
NCBI Description
                   (AF027172) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana] >gi_4049343_emb_CAA22568
                                                                     (AL034567)
                  cellulose synthase catalytic subunit (RSW1) [Arabidopsis
                  thaliana]
                  121439
Seq. No.
                  6686_2.R1010
Contig ID
                  jC-atXP8C92K17T7s1
5'-most EST
                  BLASTX
Method
                  g2827139
NCBI GI
BLAST score
                  489
E value
                  2.0e-49
Match length
                  110
% identity
                  84
                  (AF027172) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana] >gi 4049343 emb CAA22568
                                                                     (AL034567)
                  cellulose synthase catalytic subunit (RSW1) [Arabidopsis
                  thaliana]
                  121440
Seq. No.
Contig ID
                  6687 1.R1010
5'-most EST
                  jC-aTXLIB327402P1d04b1
Method
                  BLASTX
                  g102525
NCBI GI
BLAST score
                  161
E value
                  8.0e-11
Match length
                  108
% identity
                  33
NCBI Description
                  lin-10 protein - Caenorhabditis elegans (fragment)
                  >gi_829166_emb_CAA35704.1_ (X51321) hypothetical protein
                  [Caenorhabditis elegans]
Seq. No.
                  121441
                  6688 1.R1010
Contig ID
5'-most EST
                  LIB23-073-Q1-E1-D7
Seq. No.
                  121442
                  6689 1.R1010
Contig ID
5'-most EST
                  LIB22-086-Q1-E1-B11
Method
                  BLASTX
NCBI GI
                  q3540195
BLAST score
                  152
E value
                  8.0e-10
```

```
% identity
                  19
NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  121443
                  6692 1.R1010
Contig ID
5'-most EST
                  jC-atX22032Q1E1A03b1
                  BLASTX
Method
                  g4056461
NCBI GI
BLAST score
                  892
                  1.0e-96
E value
                  168
Match length
% identity
                  100
NCBI Description
                 (AC005990) F508.34 [Arabidopsis thaliana]
                  121444
Seq. No.
                  6693 1.R1010
Contig ID
5'-most EST
                  LIB3176-101-P1-K1-C4
                  BLASTN
Method
NCBI GI
                  q3510247
BLAST score
                  233
                  1.0e-128
E value
                  403
Match length
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC F19D11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  121445
Seq. No.
                  6694_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327401P4h07b2
Method
                  BLASTN
NCBI GI
                  q3869069
BLAST score
                  203
E value
                  1.0e-110
Match length
                  601
% identity
                  95
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  121446
                  6695 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327415P3d08b1
Method
                  BLASTN
NCBI GI
                  g4757403
BLAST score
                  273
E value
                  1.0e-152
Match length
                  455
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJL12, complete sequence
Seq. No.
                  121447
Contig ID
                  6696 1.R1010
5'-most EST
                  jC-atXP124C121C17T7d1
                  BLASTN
Method
NCBI GI
                  q3047060
BLAST score
                  434
E value
                  0.0e+00
```

```
Match length
                    514
 % identity
                    99
 NCBI Description Arabidopsis thaliana BAC F7N22
                    121448
 Seq. No.
                    6703 1.R1010
 Contig ID
                    jC-atXLIB327421P3f07b1
 5'-most EST
                    BLASTX
 Method
                    g3420047
 NCBI GI
 BLAST score
                    514
                    3.0e-52
 E value
                    106
 Match length
                    93
 % identity
 NCBI Description
                    (AC004680) putative protein kinase [Arabidopsis thaliana]
 Seq. No.
                    121449
                    6707 1.R1010
 Contig ID
 5'-most EST
                    jC-atX24056Q1E1H01b1
                    BLASTX
 Method
                    g2145358
 NCBI GI
 BLAST score
                    302
                    2.0e-27
 E value
                    58
 Match length
                    98
 % identity
. NCBI Description
                    (Y10922) HD-Zip protein [Arabidopsis thaliana]
 Seq. No.
                    121450
 Contig ID
                    6713 1.R1010
 5'-most EST
                    LIB22-032-Q1-E1-C3
 Seq. No.
                    121451
                    6715 1.R1010
 Contig ID
                    LIB24-013-Q1-E1-E11
 5'-most EST
 Method
                    BLASTN
 NCBI GI
                    g3108025
                    243
 BLAST score
                    1.0e-134
 E value
 Match length
                    398
                    98
 % identity
                    Arabidopsis thaliana chromosome 1 BAC T13D8, complete
 NCBI Description
                    sequence [Arabidopsis thaliana]
                    121452
 Seq. No.
                    6717 1.R1010
 Contig ID
 5'-most EST
                    LIB22-032-Q1-E1-C7
 Method
                    BLASTX
 NCBI GI
                    g3063694
 BLAST score
                    466
 E value
                    2.0e-46
 Match length
                    121
 % identity
                    79
                   (AL022537) putative protein [Arabidopsis thaliana]
 NCBI Description
                    121453
 Seq. No.
 Contig ID
                    6718_1.R1010
                    LIB22-032-Q1-E1-C8
 5'-most EST
```

```
NCBI GI
                  g2224901
BLAST score
                  237
                  5.0e-20
E value
Match length
                  68
                  68
% identity
                  (U67134) PcMYB1 protein [Petroselinum crispum]
NCBI Description
Seq. No.
                  121454
                  6720 1.R1010
Contig ID
5'-most EST
                  LIB3177-010-P1-K2-G3
                  BLASTX
Method
NCBI GI
                  g4544456
BLAST score
                  623
                  4.0e-65
E value
Match length
                  132
% identity
                  92
                  (AC006592) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  121455
                  6721 1.R1010
Contig ID
5'-most EST
                  jC-a\(\bar{1}\)XLIB327435P2b05a1
Method
                  BLASTX
                  g3024898
NCBI GI
BLAST score
                  397
E value
                  2.0e-38
Match length
                  141
% identity
                  54
NCBI Description
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
                  HELICASE KIAA0224 (HA4657) >gi 1504028 dbj BAA13213
                  (D86977) similar to putative ATP-dependent RNA helicase
                  K03H1.2 of C.elegans(S41025) [Homo sapiens] >gi 3123906
                  (AF038391) pre-mRNA splicing factor [Homo sapiens]
                  121456
Seq. No.
Contig ID
                  6724_1.R1010
5'-most EST
                  jC-atXLIB327417P4h03b1
Method.
                  BLASTX
NCBI GI
                  g116923
BLAST score
                  472
                  4.0e-47
E value
Match length
                  197
% identity
                  54
                  COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                  >gi 111414 pir S13520 beta-COP protein - rat
                  >gi 55819 emb CAA40505 (X57228) beta COP [Rattus
                  norvegicus]
                  121457
Seq. No.
                  6724 2.R1010
Contig ID
5'-most EST
                  LIB3168-073-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1169014
BLAST score
                  270
                  2.0e-23
E value
Match length
                  184
% identity
                  36
NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
```

Seq. No.

Contig ID

5'-most EST

121462

6740 1.R1010

jC-atXLIB327429P1e03b2

>gi 472343 (L31852) bcop [Drosophila melanogaster] Seq. No. 121458 Contig ID 6729 1.R1010 jC-atXLIB327427P2b07b1 5'-most EST BLASTX Method g3176687 NCBI GI 745 BLAST score E value 6.0e-79 221 Match length % identity 62 (AC003671) Strong similarity to trehalose-6-phosphate NCBI Description synthase homolog from A. thaliana chromosome 4 contig gb Z97344. ESTs gb H37594, gb R65023, gb H37578 and gb R64855 come from this gene. [Arabidopsis thaliana] Seq. No. 121459 Contig ID 6735 1.R1010 5'-most EST jC-atXLIB327433P1g12b1 Method BLASTX NCBI GI q2760324 BLAST score 813 E value 3.0e-87 Match length 167 % identity 92 NCBI Description (AC002130) F1N21.9 [Arabidopsis thaliana] Seq. No. 121460 Contig ID 6736 1.R1010 5'-most EST jC-atXP35C151L2T7d1 Method BLASTX a2498943 NCBI GI BLAST score 287 E value 1.0e-25 Match length 123 % identity 38 PUTATIVE SPERMIDINE SYNTHASE (PUTRESCINE NCBI Description AMINOPROPYLTRANSFERASE) (SPDSY) >gi 2129288 pir B64339 spermidine synthase (EC 2.5.1.16) - Methanococcus jannaschii > gi 1591033 (U67486) spermidine synthase (speE) [Methanococcus jannaschii] Seq. No. 121461 Contig ID 6737 1.R1010 5'-most EST LIB22-032-Q1-E1-E3 BLASTX Method NCBI GI q4741929 BLAST score 111 6.0e-38 E value Match length 116 % identity 66 NCBI Description (AF130253) membrane related protein CP5 [Arabidopsis thaliana]

g315722

```
Method
                  BLASTN
NCBI GI
                  q2582640
BLAST score
                  66
E value
                  2.0e-28
Match length
                  70
                  99
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                  121463
Seq. No.
                  6742 1.R1010
Contig ID
                  jC-atXmonuni26Ad02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q586145
BLAST score
                  274
                  2.0e-74
E value
                  259
Match length
% identity
                  62
                  UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT
NCBI Description
                  PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP)
                  >qi 488848 emb CAA55894 (X79332) Rieske iron sulphur
                  protein [Solanum tuberosum]
                  121464
Seq. No.
Contig ID
                 . 6742 2.R1010
                  LIB35-001-Q1-E1-H7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1717949
BLAST score
                  692
E value
                  7.0e-73
Match length
                  137
% identity
                  92
                  UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 1
NCBI Description
                  PRECURSOR (RIESKE IRON-SULFUR PROTEIN 1) (RISP1)
                  >gi 100375 pir B41607 ubiquinol--cytochrome-c reductase
                  (EC 1.10.2.2) iron-sulfur protein precursor - common
                  tobacco (fragment) >gi 170322 (M77225) Rieske Fe-S protein
                  [Nicotiana tabacum]
               121465
Seq. No.
Contig ID
                  6742 3.R1010
5'-most EST
                  LIB3176-026-P1-K1-A5
Method
                  BLASTX
                  q586145
NCBI GI
BLAST score
                  210
                  5.0e-20
E value
Match length
                  119
                  53
% identity
                  UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT
NCBI Description
                  PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP)
                  >gi 488848 emb CAA55894 (X79332) Rieske iron sulphur
                  protein [Solanum tuberosum]
                  121466
Seq. No.
                  6742 7.R1010
Contig ID
```

```
121467
Seq. No.
                  6742 8.R1010
Contig ID
                  jC-atXLIB327430P4g08b1
5'-most EST
                  BLASTN
Method
                  q2582640
NCBI GI
BLAST score
                  54
E value
                  1.0e-21
Match length
                  70
                  94
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
Seq. No.
                  121468
                  6744 1.R1010
Contig ID
                  LIB22-032-Q1-E1-F1
5'-most EST
Method
                  BLASTX
                  g4406809
NCBI GI
BLAST score
                  444
                  6.0e-44
E value
                  190
Match length
% identity
                  46
                  (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  121469
                  6749 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327417P2b05b1
                  BLASTN
Method
                  g4589412
NCBI GI
BLAST score
                  221
                  1.0e-121
E value
                  683
Match length
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F6N7, complete sequence
                  121470
Seq. No.
Contig ID
                  6750 1.R1010
5'-most EST
                  LIB24-133-Q1-E1-G8
                  BLASTX
Method
NCBI GI
                  q4115936
BLAST score
                  855
E value
                  5.0e-92
Match length
                  189
                  87
% identity
NCBI Description
                  (AF118223) No definition line found [Arabidopsis thaliana]
                  121471
Seq. No.
                  6754 1.R1010
Contig ID
5'-most EST
                  LIB24-022-Q1-E1-H7
Method
                  BLASTX
                  g1086252
NCBI GI
BLAST score
                  173
E value
                  3.0e-12
Match length
                  63
% identity
                  54
NCBI Description
                  sucrose cleavage protein - Potato >gi 707001 bbs 157931
                  (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum
```

```
tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]
                   [Solanum tuberosum]
Seq. No.
                   121472
                  6760 1.R1010
Contig ID
5'-most EST
                  LIB22-032-Q1-E1-G3
                  121473
Seq. No.
Contig ID
                  6762 1.R1010
                  LIB22-032-Q1-E1-G5
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4678320
BLAST score
                   171
E value
                   2.0e-81
Match length
                  159
% identity
                   96
                   (AL049658) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  121474
Contig ID
                  6764 1.R1010
5'-most EST
                  LIB3168-096-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g4507657
BLAST score
                - 851
E value
                   4.0e-91
                  523
Match length
% identity
                  38
NCBI Description
                  tripeptidyl peptidase II >gi 136107 sp P29144 TPP2 HUMAN
                  TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL
                  AMINOPEPTIDASE) >gi 1082875 pir S54376
                  tripeptidyl-peptidase II (EC 3.4.14.10) - human >qi 339880
                   (M73047) tripeptidyl peptidase II [Homo sapiens]
                  121475
Seq. No.
Contig ID
                   6765 1.R1010
5'-most EST
                  LIB25-033-Q1-E1-G4
Method
                  BLASTN
NCBI GI
                  q3080430
BLAST score
                  272
E value
                  1.0e-151
Match length
                  500
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19
                   (ESSAII project)
                  121476
Seq. No.
Contig ID
                  6766 1.R1010
5'-most EST
                  LIB3175-032-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g1161926
BLAST score
                  1047
E value
                  1.0e-114
Match length
                  412
% identity
                  54
NCBI Description
                  (U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine
```

```
121477
 Seq. No.
                   6768 1.R1010
Contig ID
                   jC-atXLIB327410P3d09b1
 5'-most EST
                   BLASTX
Method
NCBI GI
                   q2827546
BLAST score
                   1614
E value
                   0.0e+00
Match length
                   344
                   93
 % identity
                   (AL021635) cytochrome P450 like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   121478
                   6768 2.R1010
Contig ID
 5'-most EST
                   g17129
Method
                   BLASTX
NCBI GI
                   q2827548
· BLAST score
                   149
E value
                   3.0e-41
Match length
                   101
 % identity
                   90
NCBI Description
                   (AL021635) cytochrome P450 - like protein [Arabidopsis
                   thaliana]
                   121479
Seq. No.
Contig ID
                   6770_1.R1010
 5'-most EST .
                   jC-atXP86CG9G12T7d2
                   BLASTX
Method
NCBI GI
                   q1653767
BLAST score
                   482
E value
                   3.0e-48
Match length
                   210
 % identity
                   46
                   (D90916) oligopeptidase A [Synechocystis sp.]
NCBI Description
                   121480
Seq. No.
                   6770_2.R1010
Contig ID
 5'-most EST
                   jC-atXLIB327408P3e01b1
Method
                   BLASTX
                   q1653767
NCBI GI
BLAST score
                   506
                   4.0e-51
E value
                   203
Match length
 % identity
                   51
NCBI Description
                   (D90916) oligopeptidase A [Synechocystis sp.]
                   121481
Seq. No.
Contig ID
                   6770_3.R1010
 5'-most EST
                   LIB22-066-Q1-E1-C7
Method
                   BLASTN
NCBI GI
                   g4757395
BLAST score
                   196
E value
                   1.0e-106
Match length
                   547
 % identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
```

K21L13, complete sequence

```
Seq. No.
                  121482
Contig ID
                  6771 1.R1010
5'-most EST
                  LIB24-077-Q1-E1-E5
Method
                  BLASTX
NCBI GI
                  g2317907
                  690
BLAST score
E value
                  1.0e-72
Match length
                  150
                  90
% identity
NCBI Description
                  (U89959) Mago Nashi-like protein [Arabidopsis thaliana]
Seq. No.
                  121483
                  6772 1.R1010
Contig ID
5'-most EST
                  ARABL1-039-Q1-B1-E5
                  121484
Seq. No.
Contig ID
                  6777 1.R1010
5'-most EST
                  LIB3234-094-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g4220535
BLAST score
                  495
E value
                  4.0e-50
Match length
                  97
% identity
                  99
                  (AL035356) clathrin coat assembly like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  121485
Contig ID
                  6778 1.R1010
5'-most EST
                  LIB23-055-Q1-E1-H9
                  121486
Seq. No.
Contig ID
                  6779_1.R1010
5'-most EST
                  LIB24-002-Q1-E1-C12
Method
                  BLASTX
                  g3786005
NCBI GI
                  477
BLAST score
E value
                  7.0e-48
Match length
                  119
                  51
% identity
NCBI Description
                  (AC005499) putative phosphoethanolamine
                  cytidylyltransferase [Arabidopsis thaliana]
                  121487
Seq. No.
                  6780_1.R1010
Contig ID
                  LIB22-033-Q1-E2-A2
5'-most EST
Method
                  BLASTX
                  q3114968
NCBI GI
BLAST score
                  331
E value
                  8.0e-31
Match length
                  143
% identity
                  46
                  (Y14997) prolidase [Suberites domuncula]
NCBI Description
                  121488
Seq. No.
                  6781 1.R1010
Contig ID
```

```
5'-most EST
                 g935442
Seq. No.
                   121489
Contig ID
                   6783 1.R1010
                   LIB2\overline{5}-024-Q1-E1-H9
5'-most EST
Method
                   BLASTX
                   q4097585
NCBI GI
BLAST score
                   552
E value
                   2.0e~56
                   189
Match length
% identity
                   59
                  (U64925) NTGP4 [Nicotiana tabacum]
NCBI Description
Seq. No.
                   121490
Contig ID
                   6786 1.R1010
5'-most EST
                   jC-atXLIB327433P1f05b1
Seq. No.
                   121491
Contig ID
                   6788 1.R1010
5'-most EST
                   jC-atXLIB327433P1f08b1
Method
                   BLASTN
NCBI GI
                   g2760172
BLAST score
                   212
                   1.0e-115
E value
Match length
                   420
% identity
                   96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUB3, complete sequence [Arabidopsis thaliana]
                   121492
Seq. No.
                   6789 1.R1010
Contig ID
5'-most EST
                   LIB22-033-Q1-E1-B4
Method
                   BLASTN
NCBI GI
                   q2924653
BLAST score
                   123
E value
                   1.0e-62
Match length
                   335
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDA7, complete sequence [Arabidopsis thaliana]
                   121493
Seq. No.
                   6790 1.R1010
Contig ID
5'-most EST
                  LIB24-056-Q1-E2-G3
Method
                  BLASTX
NCBI GI
                   g4559339
BLAST score
                   160
                   7.0e-11
E value
Match length
                   61
                   59
% identity
NCBI Description
                   (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
                  thaliana]
                   121494
Seq. No.
                   6797 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327401P4h12b2
```

```
NCBI GI
                   g3098571
BLAST score
                   876
E value
                   3.0e-94
Match length
                   200
% identity
                   80
                   (AF049028) BURP domain containing protein [Brassica napus]
NCBI Description
Seq. No.
                   121495
Contig ID
                   6797 2.R1010
                   LIB22-033-Q1-E1-C5
5'-most EST
                   BLASTN
Method
                   g3098570
NCBI GI
BLAST score
                   76
E value
                   2.0e-34
Match length
                   220
% identity
                   84
                  Brassica napus BURP domain containing protein mRNA,
NCBI Description
                  complete cds
Seq. No.
                   121496
Contig ID
                   6798 1.R1010
                   LIB2\overline{2}-033-Q1-E2-C6
5'-most EST
Method
                   BLASTX
                   g2827139
NCBI GI
BLAST score
                   143
                   1.0e-46
E value
Match length
                   91
% identity
                   97
                   (AF027172) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana] >gi 4049343 emb CAA22568 (AL034567)
                   cellulose synthase catalytic subunit (RSW1) [Arabidopsis
                   thaliana]
                   121497
Seq. No.
Contig ID
                   6799 1.R1010
5'-most EST
                   LIB22-033-Q1-E2-C7
                   BLASTN
Method
NCBI GI
                   g3600029
BLAST score
                   414
                   0.0e + 00
E value
Match length
                   414
% identity
                   100
                  Arabidopsis thaliana BAC T12H2O
NCBI Description
                   121498
Seq. No.
                   6800 1.R1010
Contig ID
5'-most EST
                  LIB22-086-Q1-E1-H7
Method
                  BLASTX
NCBI GI
                   g4038030
BLAST score
                   92
E value
                   1.4e-02
Match length
                   225
% identity
                   (AC005936) putative protein kinase, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
```

121499

Seq. No.

```
Contig ID
                   6801 1.R1010
5'-most EST
                   jC-atXP87CG8H11T7b1
Method
                   BLASTX
NCBI GI
                   g3157931
BLAST score.
                   603
                   3.0e-83
E value
Match length
                   161
% identity
                   100
NCBI Description
                   (AC002131) Similar to pyrophosphate-dependent
                  phosphofuctokinase beta subunit gb Z32850 from Ricinus
                   communis. ESTs gb N65773, gb N649\overline{2}5 and gb F15232 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                  121500
Contig ID
                   6801 2.R1010
                  LIB3176-054-P1-K1-G6
5'-most EST
Method
                  BLASTX
                   q3157931
NCBI GI
BLAST score
                  884
E value
                  1.0e-107
Match length
                   299
% identity
                  73
                   (AC002131) Similar to pyrophosphate-dependent
NCBI Description
                  phosphofuctokinase beta subunit gb Z32850 from Ricinus
                  communis. ESTs gb N65773, gb N64925 and gb F15232 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                   121501
                   6802 1.R1010
Contig ID
                  LIB22-033-Q1-E2-D2
5'-most EST
Seq. No.
                   121502
                  6803 1.R1010
Contig ID
5'-most EST
                   jC-atXP100CE3D10T7b1
Method
                  BLASTX
NCBI GI
                   g4455256
BLAST score
                   542
E value
                   2.0e-55
Match length
                  131
% identity
                   76
NCBI Description
                   (AL035523) protein-methionine-S-oxide reductase
                   [Arabidopsis thaliana]
                  121503
Seq. No.
Contig ID
                   6803 2.R1010
5'-most EST
                  g2759219
Method
                  BLASTX
NCBI GI
                  g1136793
BLAST score
                  337
                  1.0e-54
E value
Match length
                  200
% identity
                  59
NCBI Description
                  (X91486) PMSR protein [Brassica napus]
                  121504
Seq. No.
                  6805 1.R1010
Contig ID
```

LIB22-033-Q1-E2-D5

```
121505
Seq. No.
                  6806 1.R1010
Contig ID
                  jC-atXP54C186E21T7007d1
5'-most EST
                  BLASTX
Method
                  g629602
NCBI GI
BLAST score
                  1539
                  1.0e-172
E value
                  331
Match length
                  87
% identity
                  probable imbibition protein - wild cabbage
NCBI Description
                  >gi 488787 emb CAA55893 (X79330) putative imbibition
                  protein [Brassica oleracea]
                  121506
Seq. No.
                  6806 2.R1010
Contig ID
5'-most EST
                  jC-atXLIB327408P1g01b1
Method
                  BLASTX
NCBI GI
                  q629602
BLAST score
                  1887
                  0.0e + 00
E value
                  363
Match length
                  96
% identity
NCBI Description
                  probable imbibition protein - wild cabbage
                  >gi 488787 emb CAA55893 (X79330) putative imbibition
                  protein [Brassica oleracea]
Seq. No.
                  121507
                  6806 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327406P3g12b2
Method
                  BLASTX
NCBI GI
                  q629602
BLAST score
                  782
                  1.0e-83
E value
Match length
                  158
% identity
                  91
NCBI Description probable imbibition protein - wild cabbage
                  >gi 488787 emb CAA55893 (X79330) putative imbibition
                  protein [Brassica oleracea]
Seq. No.
                  121.508
Contig ID
                  6806 4.R1010
5'-most EST
                  jC-atXLIB327425P1d08b1
Method
                  BLASTX
NCBI GI
                  g629602
BLAST score
                  1035
                  1.0e-113
E value
                  213
Match length
% identity
                  92
NCBI Description
                  probable imbibition protein - wild cabbage
                  >gi 488787 emb CAA55893 (X79330) putative imbibition
                  protein [Brassica oleracea]
                  121509
Seq. No.
Contig ID
                  6806 6.R1010
5'-most EST
                  jC-atXLIB327405P3h11b1
```

```
NCBI GI
                  g629602
                  253
BLAST score
                  2.0e-42
E value
                  136
Match length
                  6.4
% identity ~
                  probable imbibition protein - wild cabbage
NCBI Description
                 .>gi 488787 emb CAA55893 (X79330) putative imbibition
                  protein [Brassica oleracea]
                  121510
Seq. No.
                  6806 9.R1010
Contig ID
5'-most EST
                  jC-atXLIB327418P2e09b2
Method
                  BLASTX
                  g629602
NCBI GI
BLAST score
                  435
                  7.0e-43
E value
                  91
Match length
                  91
% identity
NCBI Description
                  probable imbibition protein - wild cabbage
                  >gi 488787 emb CAA55893 (X79330) putative imbibition
                  protein [Brassica oleracea]
                  121511
Seq. No.
                  6808 1.R1010
Contig ID
5'-most EST
                  LIB22-033-Q1-E1-D8
                  BLASTX
Method
NCBI GI
                  q2583129
BLAST score
                  697
                  9.0e-74
E value
Match length
                  128
% identity
                  100
                  (AC002387) putative methionine aminopeptidase [Arabidopsis
NCBI Description
                  thaliana]
                  121512
Seq. No.
Contig ID
                  6809 1.R1010
5'-most EST
                  jC-atXLIB327433P1g07b1
Method
                  BLASTX
NCBI GI
                  g4585993
BLAST score
                  328
E value
                  3.0e-30
Match length
                  94
% identity
                  66
                  (AC005287) Similar to serine/threonine kinases [Arabidopsis
NCBI Description
                  thaliana]
                  121513
Seq. No.
                  6810 1.R1010
Contig ID
5'-most EST
                  jC-alX22046Q1E1A10b1
Method
                  BLASTN
NCBI GI
                  g2832611
BLAST score
                  507
                  0.0e + 00
E value
Match length -
                  507
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5
NCBI Description
```

...

(ESSAII project)

BLAST score

```
121514
Seq. No.
                   6812 1.R1010
Contig ID
5'-most EST
                   LIB3168-070-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   q2564114
BLAST score
                   326
E value
                   3.0ė-30
Match length
                   105
% identity
                   63
NCBI Description
                   (AF000372) UDP glucose:flavonoid 3-o-glucosyltransferase
                   [Vitis vinifera]
                   121515
Seq. No.
Contig ID
                   6813 1.R1010
5'-most EST
                   jC-atXLIB327433P1g05b1
Method
                   BLASTN
NCBI GI
                   q3785968
BLAST score
                   405
E value
                   0.0e + 00
Match length
                   413
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F2I9 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   121516
Contig ID
                   6815_1.R1010
5'-most EST
                   jC-atXP71C221H24T7050d1
Method
                   BLASTX
NCBI GI
                   q3738309
BLAST score
                   1197
E value
                   1.0e-132
Match length
                   241
% identity
                   98
NCBI Description
                   (AC005309) unknown protein [Arabidopsis thaliana]
                  121517
Seq. No.
                   6816 1.R1010
Contig ID
5'-most EST
                  LIB24-085-Q1-E1-C8
Method
                   BLASTX
NCBI GI
                   q1906830
BLAST score
                   901
E value
                   1.0e-97
Match length
                  179
                   98
% identity
NCBI Description
                  (Y11829) heat shock protein [Arabidopsis thaliana]
Seq. No.
                   121518
Contig ID
                   6817 1.R1010
5'-most EST
                  LIB22-033-Q1-E2-F3
                  121519
Seq. No.
Contig ID
                   6818 1.R1010
5'-most EST
                  LIB22-033-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  q461812
```

% identity

```
E value
                   2.0e-22
Match length
                   107
                   42
% identity
                  CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
NCBI Description
                   GERANIOL-10-HYDROXYLASE) (GE10H) >gi 167484 (L10081)
                   Cytochrome P-450 protein [Catharanthus roseus]
                  >gi_445604_prf__1909351A cytochrome P450 [Catharanthus
                roseus]
Seq. No.
                   121520
Contig ID
                   6819 1.R1010
5'-most EST
                  LIB22-033-Q1-E1-F5
Method
                  BLASTN
NCBI GI
                   q2477521
BLAST score
                   357
E value
                   0.0e + 00
Match length
                   357
                   100
% identity
                  Arabidopsis thaliana chromosome I BAC F22K2O genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   121521
Contig ID
                   6821_1.R1010
5'-most EST
                  LIB22-033-Q1-E1-F7
Method
                  BLASTN
                  q3582315
NCBI GI
BLAST score
                   419
E value
                   0.0e + 00
                   419
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T27A16 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  121522
Contig ID
                   6822_1.R1010
5'-most EST
                  LIB22-033-Q1-E2-F8
Seq. No.
                   121523
Contig ID
                   6823 1.R1010
5'-most EST
                  jC-atXLIB327414P1g09b1
Method
                  BLASTX
NCBI GI
                  q4220481
BLAST score
                   567
E value
                   3.0e-58
Match length
                   108
% identity
                  100
NCBI Description
                   (AC006069) unknown protein [Arabidopsis thaliana]
                   121524
Seq. No.
Contig ID
                   6824 1.R1010
5'-most EST
                  LIB22-033-Q1-E2-G2
Method
                  BLASTX
NCBI GI
                  q3522939
BLAST score
                  471
E value
                  4.0e-47
Match length
                  183
```

NCBI GI

```
(AC004411) putative squamosa-promoter binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  121525
Seq. No.
Contig ID
                   6825 1.R1010
5'-most EST
                   LIB22-033-Q1-E2-G3
Method
                   BLASTX
                   q4587572
NCBI GI
                   692
BLAST score
E value
                   3.0e-73
Match length
                   131
% identity
                   100
                   (AC006550) Similar to gb_U70015 lysosomal trafficking
NCBI Description
                   regulator from Mus musculus and contains 2 PF 00400 WD40,
                   G-beta repeats. ESTs gb T43386 and gb AA3952\overline{3}6 come from
                   this gene. [Arabidopsis thaliana]
                  121526
Seq. No.
Contig ID
                   6826 1.R1010
                  LIB3176-015-P1-K1-G5
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2181180
BLAST score
                   346
                  3.0e-32
E value
Match length
                   215
% identity
                   36
NCBI Description (Z84377) xylosidase [Aspergillus niger]
                  121527
Seq. No.
                  6827 1.R1010
Contig ID
                  LIB22-033-Q1-E1-G5
5'-most EST
                  121528
Seq. No.
Contig ID
                   6831 1.R1010
5'-most EST
                  937\overline{1}30
Seq. No.
                  121529
                   6831 2.R1010
Contig ID
5'-most EST
                   jC-atXP112C130B24T7a1
Method
                  BLASTX
NCBI GI
                  g2244993
BLAST score
                   248
E value
                  9.0e-21
Match length
                  108
% identity
                   47
NCBI Description
                  (Z97341) similarity to AMP-activated protein kinase beta
                   [Arabidopsis thaliana]
Seq. No.
                  121530
Contig ID
                   6831_3.R1010
5'-most EST
                  g2762827
Seq. No.
                  121531
Contig ID
                  6831 4.R1010
5'-most EST
                  jC-atXLIB327406P3f04b2
Method
                  BLASTX
```

g2244993

Match length

```
BLAST score
                  427
E value
                  8.0e-54
Match length
                  198
% identity
                  54
NCBI Description
                  (Z97341) similarity to AMP-activated protein kinase beta
                  [Arabidopsis thaliana]
                  121532
Seq. No.
                  6832 1.R1010
Contig ID
                  LIB2\overline{2}-033-Q1-E1-H3
5'-most EST
Seq. No.
                  121533
Contig ID
                  6835_1.R1010
                  LIB22-033-Q1-E2-H6
5'-most EST
                  121534
Seq. No.
Contig ID
                  6836 1.R1010
5'-most EST
                  jC-atXP11C97N14T7018d1
Method
                  BLASTN
                  g3800746
NCBI GI
BLAST score
                  39
E value
                  3.0e-12
Match length
                  43
% identity
                  98
NCBI Description
                  Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA,
                  complete cds
                  121535
Seq. No.
Contig ID
                  6836 2.R1010
5'-most EST
                  jC-atXLIB327433P1h07b1
                  BLASTX
Method
NCBI GI
                  g4049341
BLAST score
                  220
E value
                  9.0e-18
Match length
                  88
                  47
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
                  121536
Seq. No.
Contig ID
                  6839 1.R1010
5'-most EST
                  jC-atXLIB327421P3c02b1
Method
                  BLASTX
NCBI GI
                  q3047104
BLAST score
                  506
E value
                  4.0e-51
Match length
                  148
% identity
                  66
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
                  121537
Seq. No.
Contig ID
                  6841 1.R1010
5'-most EST
                  jC-alXLIB327434P2g05b1
Method
                  BLASTX
                  g3098603
NCBI GI
BLAST score
                  219
                  2.0e-17
E value
```

```
% identity
                   32
 NCBI Description
                   (AF052191) katanin p60 subunit [Strongylocentrotus
                   purpuratus]
                   121538
 Seq. No.
                   6852 1.R1010
 Contig ID
 5'-most EST
                   jC-atXLIB327433P1f07b1
                   BLASTN
 Method
 NCBI GI
                   q3702731
 BLAST score
                   216
                   1.0e-118
 E value
Match length
                   399
 % identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                   MFC19, complete sequence [Arabidopsis thaliana]
                   121539
 Seq. No.
 Contig ID
                   6860 2.R1010
 5'-most EST
                   LIB25-105-Q1-E1-G11
Method
                   BLASTX
 NCBI GI
                   g4539452
 BLAST score
                   415
E value
                   2.0e-40
Match length
                   1.10
                   43
 % identity
NCBI Description
                   (AL049500) putative phosphoribosylanthranilate transferase
                   [Arabidopsis thaliana]
                   121540
Seq. No.
Contig ID
                   6879 1.R1010
                   jC-atXLIB327408P1d06b1
 5'-most EST
Method
                   BLASTX
NCBI GI
                   g416730
BLAST score
                   573
                   8.0e-59
E value
Match length
                   216
 % identity
                   53
                   BETA-UREIDOPROPIONASE (BETA-ALANINE SYNTHASE)
NCBI Description
                   (N-CARBAMOYL-BETA-ALANINE AMIDOHYDROLASE)
                   >gi 285064 pir S27881 beta-alanine synthase - rat
                   >gi 203106 (M97662) beta-alanine synthase [Rattus
                   norvegicus]
                   121541
Seq. No.
Contig ID
                   6881 1.R1010
 5'-most EST
                   jC-atX22033Q1E2E12b1
                   BLASTX
Method
NCBI GI
                   g4432845
BLAST score
                   199
· E value
                   3.0e-15
Match length
                   114
% identity
NCBI Description
                   (AC006283) unknown protein [Arabidopsis thaliana]
                   121542
Seq. No.
Contig ID
                   6888 1.R1010
```

jC-atX22033Q1E2E09b1

```
Method
                   BLASTX
NCBI GI
                   g4468990
BLAST score
                   1115
                   1.0e-122
E value
Match length
                   217
                   100
% identity
                   (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
                   121543
Seq. No.
                   6889_1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327405P2h05b2
Method
                   BLASTX
                   q2194137
NCBI GI
BLAST score
                   319
E value
                   3.0e-29
Match length
                   140
                   54
% identity
NCBI Description
                   (AC002062) ESTs gb R29947, gb H76702 come from this gene.
                   [Arabidopsis thaliana]
                   121544
Seq. No.
                   6901 1.R1010
Contig ID
5'-most EST
                   g1053717
Method
                   BLASTX
NCBI GI
                   g3549674
BLAST score
                   702
                   5.0e-74
E value
Match length
                   160
% identity
                   85
                   (AL031394) pathogenesis-related protein 1 precursor, 19.3K
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   121545
                   6914 1.R1010
Contig ID
5'-most EST
                   jC-aTXLIB327408P3d01b1
Method
                   BLASTN
                   g4757403
NCBI GI
BLAST score
                   326
E value
                   0.0e + 00
Match length
                   434
                   97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJL12, complete sequence
Seq. No.
                   121546
                   6914 2.R1010
Contig ID
5'-most EST
                   g906050
Method
                   BLASTN
                   g4757403
NCBI GI
BLAST score
                   417
E value
                  0.0e + 00
Match length
                  1007
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MJL12, complete sequence
```

 σ

121547

Seq. No.

```
6932_1.R1010
Contig ID
                  LIB3177-099-P1-K1-G2
5'-most EST
                BLASTX
Method
NCBI GI
                  q1914683
BLAST score
                  281
E value
                  9.0e-25
                  75
Match length
                  73
% identity
NCBI Description
                  (Y12013) RAD23, isoform I [Daucus carota]
Seq. No.
                  121548
Contig ID
                  6934 1.R1010
                  jC-atXLIB327424P1e01b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  a4049335
BLAST score
                  1105
E value
                  1.0e-121
Match length
                  242
% identity
                  92
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
                  121549
Seq. No.
Contig ID
                  6938_1.R1010
5'-most EST
                  jC-atX22074Q1E1G04b1
Method
                  BLASTX
NCBI GI
                  g3763925
BLAST score
                  549
E value
                  4.0e-56
Match length
                  121
% identity
                  .90
NCBI Description (AC004450) putative Af10-protein [Arabidopsis thaliana]
Seq. No.
                  121550
Contig ID
                  6938_2.R1010
5'-most EST
                  LIB3234-015-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q3763925
                  423
BLAST score
E value
                  1.0e-41
Match length
                  80
% identity
                  100
                 (AC004450) putative Af10-protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  121551
                  6939_1.R1010
Contig ID
5'-most EST
                  jC-atX22034Q1E2B05b1
Method
                  BLASTX
NCBI GI
                  q2842486
BLAST score
                  50
E value
                  2.0e-54
Match length
                  151
% identity
NCBI Description
                  (AL021749) putative protein [Arabidopsis thaliana]
Seq. No.
                  121552
Contig ID
                  6940 1.R1010
5'-most EST
                  jC-atXLIB327433P1f03b1
```

Seq. No.

```
Method
                   BLASTX
NCBI GI
                  q4432863
BLAST score
                   234
                   2.0e-19
E value
                   106
Match length
                   41
% identity
                   (AC006300) putative phosphate/phosphoenolpyruvate
NCBI Description
                   translocator protein [Arabidopsis thaliana]
                   121553
Seq. No.
                  6943 1.R1010
Contig ID
5'-most EST
                   jC-atX22034Q1E2B09b1
Method
                   BLASTX
NCBI GI
                   g2239178
BLAST score
                   468
                   6.0e-47
E value
                  143
Match length
                   62
% identity
NCBI Description
                  (Z97208) hypothetical transport protein
                   [Schizosaccharomyces pombe]
                   121554
Seq. No.
                   6944 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327411P1e02b1
Method
                   BLASTN
NCBI GI
                   g4490291
BLAST score
                   492
E value
                  0.0e + 00
Match length
                   492
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5
                   (ESSA project)
                  121555
Seq. No.
Contig ID
                  6944_2.R1010
5'-most EST
                   jC-atXLIB327416P4c12b1
Method
                  BLASTN
NCBI GI
                  g4490291
                  420
BLAST score
                  0.0e + 00
E value
Match length
                   612
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5
NCBI Description
                   (ESSA project)
Seq. No.
                  121556
                   6944 3.R1010
Contig ID
5'-most EST
                  jC-atXLIB327433P1f12b1
Method
                  BLASTX
NCBI GI
                  g4490297
BLAST score
                  362
                  1.0e-54
E value
Match length
                  125
% identity
                  90
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
```

```
Contig ID
                  6947 1.R1010
                  jC-atXLIB327418P1f07b1
5'-most EST
Method
                  BLASTN
                  q473877
NCBI GI
BLAST score
                  58
                  2.0e-23
E value
                  131
Match length
                  92
% identity
                  Arabidopsis thaliana Columbia calnexin homolog gene,
NCBI Description
                  complete cds
                  121558
Seq. No.
                  6947 2.R1010
Contig ID
5'-most EST
                  LIB24-123-Q1-E1-E7
Method
                  BLASTX
                  q473878
NCBI GI
BLAST score
                  702
E value
                  3.0e-74
Match length
                  146
% identity
                  88
                  (U08315) calnexin homolog [Arabidopsis thaliana]
NCBI Description
                  121559.
Seq. No.
                  6950 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327423P3a10b1
                  BLASTX
Method
                  q2062157
NCBI GI
BLAST score
                  652
                  3.0e-68
E value
Match length
                  128
% identity
                  34
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  121560
Seq. No.
Contig ID
                  6953 1.R1010
5'-most EST
                  g2047833
Method
                  BLASTN
NCBI GI
                  q4096078
BLAST score
                  239
E value
                  1.0e-131
Match length
                  452
                  100
% identity
                  Arabidopsis thaliana chromosome I BAC T5A14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  121561
Seq. No.
                  6953 2.R1010
Contig ID
5'-most EST
                  g2047373
Method
                  BLASTX
                  g4204271
NCBI GI
BLAST score
                  512
                  6.0e-52
E value
Match length
                  115
% identity
                  90
NCBI Description (AC005223) Unknown protein [Arabidopsis thaliana]
```

E value

```
121562
 Seq. No.
                    6954 1.R1010
 Contig ID
                    LIB3176-065-P1-K1-C11
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q2160168
 BLAST score
                    2556
                    0.0e + 00
 E value
                    547
 Match length
                    90
 % identity
 NCBI Description
                    (AC000132) Strong similarity to R. communis
                    phosphoglycerate mutase (gb_X70652). ESTs
                    gb T41853, gb T76648 come from this gene. [Arabidopsis
                    thaliana]
 Seq. No.
                    121563
 Contig ID
                    6954 2.R1010
 5'-most EST
                    LIB3176-116-P2-K1-A7
                    BLASTX
 Method
 NCBI GI
                    q2160168
 BLAST score
                    289
 E value
                    6.0e-26
                    71
 Match length
 % identity
                    (AC000132) Strong similarity to R. communis
 NCBI Description
                    phosphoglycerate mutase (gb X70652). ESTs
                    gb T41853, gb T76648 come from this gene. [Arabidopsis
                    thaliana]
 Seq. No.
                    121564
                    6956 1.R1010
 Contig ID
 5'-most EST
                    LIB24-086-01-E1-C8
 Method
                    BLASTX
 NCBI GI
                    a4115375
 BLAST score
                    81
 E value
                    2.0e-49
                    123
 Match length
 % identity
                    77
                   (AC005967) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    121565
 Seq. No.
 Contig ID
                    6958 1.R1010
 5'-most EST
                    jC-alXLIB327434P3f11b1
 Method
                    BLASTX
 NCBI GI
                    q3702339
 BLAST score
                    645
 E value
                    4.0e-67
 Match length
                    232
 % identity
                    57
 NCBI Description
                    (AC005397) unknown protein [Arabidopsis thaliana]
                    121566
 Seq. No.
 Contig ID
                    6958 2.R1010
 5'-most EST
                    LIB24-094-Q1-E1-C4
 Method
                    BLASTX
 NCBI GI
                    q3702339
 BLAST score
                    427
```

7.0e-42

```
Match length
                   119
% identity
NCBI Description
                  (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                   121567
Contig ID
                   6958 3.R1010
5'-most EST
                  jC-atXLIB327402P4d08b1
Method
                   BLASTN
NCBI GI
                   g2505873
BLAST score
                   332
                   0.0e + 00
E value
                   385
Match length
% identity
                   96
NCBI Description
                  Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus
Seq. No.
                   121568
Contig ID
                   6959 1.R1010
5'-most EST
                  LIB22-034-Q1-E2-D3
Method
                  BLASTN
NCBI GI
                   q4678340
BLAST score
                   171
E value
                   3.0e - 91
Match length
                   315
% identity
                   100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11
                   (ESSA project)
Seq. No.
                   121569
Contig ID
                  6962 1.R1010
5'-most EST
                   jC-atXLIB327426P2b12b1
Method
                  BLASTN
NCBI GI
                   g3869069
BLAST score
                   285
E value
                   1.0e-159
Match length
                   553
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   121570
Contig ID
                   6965 1.R1010
5'-most EST
                   jC-atX22026Q1E1H12b1
Method
                  BLASTX
NCBI GI
                  g3152660
BLAST score
                  71
E value
                   2.0e-30
Match length
                  337
% identity
                  28
NCBI Description
                  (AF064603) GA17 protein [Homo sapiens]
Seq. No.
                  121571
Contig ID
                   6965 2.R1010
5'-most EST
                  LIB25-067-Q1-E1-B7
                  121572
Seq. No.
Contig ID
                  6966 1.R1010
5'-most EST
                  jC-atXP8C92G20T7s1
```

% identity

```
Method
                  BLASTN
NCBI GI
                  q4469002
BLAST score
                   481
E value
                  0.0e + 00
Match length
                   513
% identity
                   58
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
NCBI Description
                   (ESSA project)
                  121573
Seq. No.
                   6972 1.R1010
Contig ID
                  jC-atXLIB327433P1g06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3269293
BLAST score
                  188
                   8.0e-14
E value
Match length
                  156
% identity
                   35
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
Sea. No.
                  121574
Contig ID
                   6972 2.R1010
5'-most EST
                  g2581630
Seq. No.
                  121575
Contig ID
                   6977 1.R1010
5'-most EST
                  jC-aIXLIB327436P4c03b1
Method
                  BLASTX
NCBI GI
                   g2190554
BLAST score
                  819
E value
                   3.0e-87
Match length
                   426
% identity
                  39
                  (AC001229) Similar to Arabidopsis cytochrome P450 CYP90
NCBI Description
                   (gb X87367). [Arabidopsis thaliana]
                  121576
Seq. No.
Contig ID
                   6978 1.R1010
5'-most EST
                  jC-atXLIB327424P2h10b2
Method
                  BLASTN
NCBI GI
                  q2582640
BLAST score
                  51
                  2.0e-19
E value
Match length
                  70
% identity
                   94
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                   factor, RSp40
                  121577
Seq. No.
Contig ID
                   6979 1.R1010
5'-most EST
                  LIB3176~101-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  q3236234
BLAST score
                  40
                  9.0e-13
E value
Match length
                  80
```

E value

1.0e-40

```
NCBI Description Arabidopsis thaliana chromosome II BAC F13M22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  121578
                  6981 1.R1010
Contig ID
                  LIB22-034-Q1-E2-F7
5'-most EST
                  BLASTN
Method
                  g2245073
NCBI GI
BLAST score
                  226
                  1.0e-124
E value
                  318
Match length
                  97
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  121579
Seq. No.
Contig ID
                  6982 1.R1010
                  LIB23-023-Q1-E1-F8
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4199934
BLAST score
                  302
E value
                  1.0e-169
Match length
                  353
% identity.
                  33
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  121580
                  6987 1.R1010
Contig ID
                  g2739504
5'-most EST
Method
                  BLASTX
                  q4538978
NCBI GI
BLAST score
                  305
                  8.0e-28
E value
Match length
                  71
% identity
                  79
                  (AL049487) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  121581
Seq. No.
Contig ID
                  6990 1.R1010
5'-most EST
                  LIB23-046-Q1-E1-H11
Method
                  BLASTX
NCBI GI
                  q421855
BLAST score
                  1770
E value
                  0.0e + 00
Match length
                  367
% identity
                  95
                  alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana
NCBI Description
                  (fragment)
                  121582
Seq. No.
Contig ID
                  6995 1.R1010
5'-most EST
                  jC-atXP82CG2C1T7b1
Method
                  BLASTX
NCBI GI
                  q2541876
BLAST score
                  417
```

```
Match length
                  137
% identity
                   59
NCBI Description
                  (D26015) CND41, chloroplast nucleoid DNA binding protein
                   [Nicotiana tabacum]
Seq. No.
                  121583
Contig ID
                  6999 1.R1010
                  jC-atX24071Q1E1F09a1
5'-most EST
Method
                  BLASTX
                  g2342727
NCBI GI
BLAST score
                  58
                  2.0e-15
E value
Match length
                  80
% identity
                  52
NCBI Description
                  (AC002341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  121584
Contig ID
                  7000 1.R1010
5'-most EST
                  LIB24-097-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  q2827536
BLAST score
                  195
E value
                  9.0e-15
Match length
                  65
% identity
                  51
NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  121585
Contig ID
                  7001 1.R1010
5'-most EST
                  jC-atXLIB327410P2c12b1
Method
                  BLASTX
                  g2959370
NCBI GI
BLAST score
                  195
                  1.0e-14
E value
Match length
                  91
% identity
                  37
                  (AL022117) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  121586
Seq. No.
Contig ID
                  7002 1.R1010
5'-most EST
                  LIB22-034-Q1-E2-H7
Method
                  BLASTX
                  q3063451
NCBI GI
BLAST score
                  585
                  2.0e-60
E value
Match length
                  113
% identity
                  99
NCBI Description (AC003981) F22013.13 [Arabidopsis thaliana]
                  121587
Seq. No.
                  7007 1.R1010
Contig ID
                  jC-atXLIB327409P3g12b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4587986
BLAST score
                  456
E value
                  0.0e + 00
Match length
                  460
```

```
100
% identity
                  Arabidopsis thaliana ABA-regulated gene cluster, complete
NCBI Description
                  sequence
Seq. No.
                  121588
                  7009 1.R1010
Contig ID
5'-most EST
                  LIB22-035-Q1-E1-A4
                  BLASTN
Method
NCBI GI
                  g2618677
BLAST score
                  543
                  0.0e+00
E value
Match length
                  663
% identity
                  96
NCBI Description
                  Arabidopsis thaliana BAC F21B7 chromosome 1, complete
                  sequence [Arabidopsis thaliana]
Seq. No.
                  121589
                  7010 1.R1010
Contig ID
5'-most EST
                  LIB23-006-Q1-E1-D4
Method
                  BLASTN
NCBI GI
                  q2828278
BLAST score
                  495
E value
                  0.0e+00
Match length
                  806
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16
NCBI Description
                  (ESSAII project)
Seq. No.
                  121590
Contig ID
                  7012 1.R1010
5'-most EST
                  LIB22-035-Q1-E1-A8
Method
                  BLASTX
                  g3176690
NCBI GI
BLAST score
                  893
E value
                  1.0e-99
Match length
                  239
% identity
                  83
                  (AC003671) Similar to ubiquitin ligase gb_D63905 from S.
NCBI Description
                  cerevisiae. EST gb R65295 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  121591
                  7015 1.R1010
Contig ID
5'-most EST
                  jC-atXP104CE10G4T7b1
                  BLASTX
Method
NCBI GI
                  g4835234
BLAST score
                  377
                  3.0e-48
E value
                  184
Match length
                  57
% identity
NCBI Description
                  (AL049862) putative cold acclimation protein [Arabidopsis
                  thaliana]
                  121592 .
Seq. No.
Contig ID
                  7015 2.R1010
5'-most EST
                  jC-atXP96C249E12T7b1
```

```
g4006858
NCBI GI
BLAST score
                  89
                  2.8e-02
E value
Match length
                  132
                   48
% identity
                   (Z99707) cold acclimation protein homolog [Arabidopsis
NCBI Description
                  thaliana]
                  121593
Seq. No.
                   7015 3.R1010
Contig ID
                   jC-atXLIB327409P3g09b1
5'-most EST
                  BLASTX
Method
                  q4006858
NCBI GI
BLAST score
                   326
                   6.0e-30
E value
Match length
                  175
                   47
% identity
                   (Z99707) cold acclimation protein homolog [Arabidopsis
NCBI Description
                  thaliana
                  121594
Seq. No.
Contig ID
                  7015 4.R1010
5'-most EST
                   jC-atXP12C103F6T7d2
Method ·
                  BLASTX
                  g4006858 ...
NCBI GI
BLAST score
                  110
E value
                  8.0e-42
Match length
                  184
                   54
% identity
                  (Z99707) cold acclimation protein homolog [Arabidopsis
NCBI Description
                  thaliana]
                  121595
Seq. No.
                  7017 1.R1010
Contig ID
                  LIB25-067-Q1-E1-D8
5'-most EST
Seq. No.
                   121596
                   7020 1.R1010
Contig ID
5'-most EST
                  LIB22-039-Q1-E1-E1
                   BLASTX
Method
                   q3834325
NCBI GI
BLAST score
                   564
E value
                   5.0e-58
                   142
Match length
% identity
                   (AC005679) Strong similarity to gb AF067141 gamma-glutamyl
NCBI Description
                  hydrolase from Arabidopsis thaliana. ESTs gb R83955,
                   gb T45062, gb T22220, gb AA586207, gb AI099851 and
                   gb AI00672 come from this gene. [Arabidopsis thaliana]
                   121597
Seq. No.
                   7020 2.R1010
Contig ID
5'-most EST
                  LIB23-040-Q1-E1-G4
Method
                   BLASTX
NCBI GI
                   q3834325
BLAST score
                   229
E value
                   1.0e-28
```

Method

NCBI GI

```
Match length
                   97
                   79
% identity
                   (AC005679) Strong similarity to gb AF067141 gamma-glutamyl
NCBI Description
                  hydrolase from Arabidopsis thaliana. ESTs gb R83955,
                   gb T45062, gb T22220, gb AA586207, gb AI09985\overline{1} and
                   gb AI00672 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   121598
                   7028 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327409P4g02b1
Method
                   BLASTN
NCBI GI
                  q2582640
BLAST score
                   59
E value
                   2.0e-24
Match length
                   66
                   99
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                   factor, RSp40
                   121599
Seq. No.
                   7030 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327409P1g11b1
Method
                  BLASTX
                  g1370186
NCBI GI
                   454
BLAST score
                   2.0e-99
E value
                   201
Match length
% identity
                   90
                  (Z73942) RAB7C [Lotus japonicus]
NCBI Description
                   121600
Seq. No.
                   7030 2.R1010
Contig ID
5'-most EST
                   jC-atXP100C251H17T7b1
Method
                   BLASTX
NCBI GI
                   q1370186
BLAST score
                   1009
                   1.0e-110
E value
                   206
Match length
% identity
                   92
                  (Z73942) RAB7C [Lotus japonicus]
NCBI Description
Seq. No.
                   121601
Contig ID
                   7030 3.R1010
5'-most EST
                   jC-atXLIB327437P4f08a2
                   BLASTX
Method
NCBI GI
                  q1370182
BLAST score
                   147
E value
                   7.0e-37
                  147
Match length
% identity
                   67
NCBI Description
                  (Z73940) RAB7A [Lotus japonicus]
                  121602
Seq. No.
Contig ID
                  7030 4.R1010
```

13485

jC-atXP39C159L23T7d1

BLASTX

q1370186

```
BLAST score
                  462
E value
                  2.0e-55
Match length
                  114
% identity
                  98
                  (Z73942) RAB7C [Lotus japonicus]
NCBI Description
                  121603
Seq. No.
                  7030 5.R1010
Contig ID
                  LIB25-093-Q1-E1-D10
5'-most EST
                  BLASTX
Method
                  g4545231
NCBI GI
BLAST score
                  331
                  7.0e-67
E value
Match length
                  147
% identity
                  88
                  (AF116243) RAS-related GTP-binding protein [Gossypium
NCBI Description
                  hirsutum]
                  121604
Seq. No.
Contig ID
                  7032 1.R1010
                  jC-atXLIB327409P1q07b1
5'-most EST
Method
                  BLASTN
                  g2582640
NCBI GI
BLAST score
                  69
E value
                  4.0e-30
                  77
Match length
% identity
                  97
NCBI Description
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
                  factor, RSp40
Seq. No.
                  121605
                  7033 1.R1010
Contig ID
5'-most EST
                  jC-atXP113C230L3T7032a2
                  BLASTN
Method
NCBI GI
                  q4263694
BLAST score
                  374
E value
                  0.0e + 00
Match length
                  652
                  98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F22D22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  121606
Seq. No.
                  .7033 3.R1010
Contig ID
                  g1217353
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4263710
BLAST score
                  929
                  1.0e-100
E value
                  208
Match length
% identity
                  89
                  (AC006223) putative pur-alpha transcriptional activator
NCBI Description
                  protein [Arabidopsis thaliana]
                  121607
Seq. No.
Contig ID
                  7039 2.R1010
```

jC-atXLIB327409P2q04b1

% identity

```
BLASTN
Method
                   g3063690
NCBI GI
                   222
BLAST score
                   1.0e-121
E value
                   395
Match length
                   98
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
                   (ESSAII project)
                   121608
Seq. No.
                   7041 1.R1010
Contig ID
5'-most EST
                   jC-atXLIB327404P2c09b1
Method
                   BLASTX
                   g1076660
NCBI GI
BLAST score
                   387
                   3.0e-37
E value
Match length
                   120
% identity
                   68
NCBI Description
                   D13F(MYBST1) protein - potato >gi 786426 bbs 159122
                   (S74753) MybSt1=Myb-related transcriptional activator
                   {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                   leaf, Peptide, 342 aa] [Solanum tuberosum]
Seq. No.
                   121609
                   7041 2.R1010
Contig ID
5'-most EST
                   g2759482
Method
                   BLASTX
NCBI GI
                   g1076660
BLAST score
                   212
                   7.0e-17
E value
Match length
                   44
                   89
% identity
                   D13F(MYBST1) protein - potato >gi 786426 bbs 159122
NCBI Description
                   (S74753) MybSt1=Myb-related transcriptional activator
                   {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                   leaf, Peptide, 342 aa] [Solanum tuberosum]
Seq. No.
                   121610
Contig ID
                   7044 1.R1010
5'-most EST
                   jC-atXLIB327409P3f10b1
Method
                   BLASTX
NCBI GI
                   g2809246
BLAST score
                   252
                   2.0e-21 ·
E value
Match length
                   80
% identity
                   56
NCBI Description
                   (AC002560) F2401.15 [Arabidopsis thaliana]
                   121611
Seq. No.
                   7045 1.R1010
Contig ID
                   jC-a\overline{t}XLIB327409P4f08b1
5'-most EST
Method
                   BLASTX
                  g2244814
NCBI GI
BLAST score
                   592
                   3.0e-61
E value
Match length
                  154
```

```
NCBI Description (Z97336) protein kinase [Arabidopsis thaliana]
                  121612
Seq. No.
                  7045 2.R1010
Contig ID
                  LIB35-039-Q1-E1-H5
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2244814
BLAST score
                  402
E value
                  4.0e-39
Match length
                  123
                  69
% identity
NCBI Description
                  (Z97336) protein kinase [Arabidopsis thaliana]
                  121613
Seq. No.
                  7047 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327409P3f09b1
                  121614
Seq. No.
                  7047 2.R1010
Contig ID
5'-most EST
                  g935113
Method
                  BLASTN
NCBI GI
                  g3264774
BLAST score
                  320
E value
                  1.0e-180
Match length
                  434
% identity
                  99
                  Arabidopsis thaliana BAC T8A17 chromosome IV, complete
NCBI Description
                  sequence [Arabidopsis thaliana]
Seq. No.
                  121615
                  7051_1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327409P3f08b1
Method
                  BLASTN
NCBI GI
                  g3461834
BLAST score
                  266
E value
                  1.0e-148
Match length
                  555
% identity *
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T9I4 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  121616
Seq. No.
                  7055 1.R1010
Contig ID
5'-most EST
                  jC-alxLIB327435P3h03b1
Method
                  BLASTN
                . g4757417
NCBI GI
BLAST score
                  229
E value
                  1.0e-125
Match length
                  488
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  T30G6, complete sequence
                  121617
Seq. No.
Contig ID
                  7059 1.R1010
5'-most EST
                  LIB24-042-Q1-E1-C8
```

Contig ID

```
NCBI GI
                   g2392769
BLAST score
                   272
E value
                   2.0e-23
Match length
                   173
% identity
                   46
NCBI Description
                   (AC002534) putative histone deacetylase [Arabidopsis
                   thaliana]
                   121618
Seq. No.
                   7061 1.R1010
Contig ID
5'-most EST
                   jC-alXLIB327436P1h12b1
Method
                   BLASTX
NCBI GI
                   g1408294
BLAST score
                   246
                   2.0e-20
E value
                   184
Match length
% identity
                   33
NCBI Description
                   (U61983) benzyl alcohol dehydrogenase [Acinetobacter
                   calcoaceticus]
                   121619
Seq. No.
                   7061_2.R1010
Contig ID
5'-most EST
                   jC-atXLIB327409P4f02b1
Method
                   BLASTX
NCBI GI
                   g2213499
BLAST score
                   189
E value
                   5.0e-14
Match length
                   148
% identity
                   36
NCBI Description
                  (Z97050) adhE [Mycobacterium tuberculosis]
                   121620
Seq. No.
                   7061 3.R1010
Contig ID
5'-most EST
                   g2749645
Method
                   BLASTN
NCBI GI
                   g2264306
BLAST score
                   385
E value
                   0.0e + 00
Match length
                   445
                   97
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBK5, complete sequence [Arabidopsis thaliana]
                   121621
Seq. No.
Contig ID
                   7061 4.R1010
5'-most EST
                   g259<del>6</del>917
Method
                   BLASTN
                   g2264306
NCBI GI
BLAST score
                   88
E value
                   9.0e-42
Match length
                   335
% identity
                   97
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBK5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   121622
```

7062 1.R1010

Contig ID

```
5'-most EST
               jC-atXLIB327409P3f01b1
Method
                  BLASTX
NCBI GI :
                  q4432844
BLAST score
                  330
                  3.0e-41
E value
                  91
Match length
                  89
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
                  121623
Seq. No.
                  7063 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327409P4f04b1
Method
                  BLASTX
                  g4454039
NCBI GI
BLAST score
                  335
E value
                 -7.0e-44
Match length
                  197
                  54
% identity
                  (AL035394) putative Na+/H+-exchanging protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  121624
                  7065 1.R1010
Contig ID
5'-most EST
                  LIB3234-087-Q1-K1-G6
Method
                  BLASTN
                  g3860243
NCBI GI
BLAST score
                  362
E value
                  0.0e + 00
                  378
Match length
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F15K20 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  121625
Seq. No.
                  7066 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327409P1f08b1
Method
                  BLASTX
NCBI GI
                  g3252807
BLAST score
                  298
E value
                  1.0e-26
Match length
                  142
% identity
                  46
NCBI Description
                 (AC004705) hypothetical protein [Arabidopsis thaliana]
                  121626
Seq. No.
                  7069 1.R1010
Contig ID
5'-most EST
                  g2748346
Method
                  BLASTX
NCBI GI
                  g2244772
BLAST score
                  232
E value
                  1.0e-144
Match length
                  300
% identity
                  89
NCBI Description (297335) transport protein [Arabidopsis thaliana]
Seq. No.
                  121627
```

7073 1.R1010

```
5'-most EST
                   jC-atXLIB327409P1f09b1
Method
                   BLASTX
NCBI GI
                  g4454464
BLAST score
                   519
                   6.0e-84
E value
Match length
                  271
% identity
                   61
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
                  121628
Seq. No.
Contig ID
                  7073 3.R1010
5'-most EST
                  g2393289
Method
                  BLASTX
NCBI GI
                  q4454464
BLAST score
                  259
E value
                  3.0e-22
Match length
                  61
% identity
                  80
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
                  121629
Seq. No.
                  7076 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327409P1f04b1
                  BLASTX
Method
                  g2980793
NCBI GI
BLAST score
                  200
E value
                  3.0e-15
Match length
                  109
% identity
                  37
NCBI Description
                  (AL022197) putative protein [Arabidopsis thaliana]
                  121630
Seq. No.
Contig ID
                  7076 2.R1010
5'-most EST
                  jC-atXLIB327408P1f02b1
Method
                  BLASTX
NCBI GI
                  g1076316
BLAST score
                  274
E value
                  6.0e-24
Match length
                  70
% identity
                  61
NCBI Description
                  drought-induced protein Di19 - Arabidopsis thaliana
                  >gi_469110_emb_CAA55321 (X78584) Di19 [Arabidopsis
                  thaliana]
Seq. No.
                  121631
Contig ID
                  7079_1.R1010
5'-most EST
                  LIB25-006-Q1-E1-C10
Method
                  BLASTX
                  g3924603
NCBI GI
BLAST score
                  484
                  9.0e-49
E value.
Match length
                  142
% identity
                  70
NCBI Description
                  (AF069442) putative WD-repeat protein [Arabidopsis
                  thaliana]
```

13491

121632

Seq. No.

E value

0.0e + 00

```
Contig ID
                  7080 1.R1010
5'-most EST
                  LIB3176-042-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q4587556
BLAST score
                  1317
                  1.0e-146
E value
                  249
Match length
% identity
                  98
                  (AC006577) Similar to gi_1653162 (p)ppGpp
NCBI Description
                  3-pyrophosphohydrolase f\overline{r}om Synechocystis sp genome
                  gb_D90911. EST gb_W43807 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  121633
                  7081 1.R1010
Contig ID
5'-most EST
                  LIB24-088-Q1-E1-B6
                  BLASTX
Method
                  q2245110
NCBI GI
BLAST score
                  274
                  9.0e-24
E value
Match length
                  157
                  85
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  121634
                  7082 1.R1010
Contig ID
                  LIB22-035-Q1-E1-H8
5'-most EST
Method
                  BLASTX
                  q4454464
NCBI GI
BLAST score
                  473
                  2.0e-47
E value
                  119
Match length
                  71
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                  121635
Seq. No.
                  7082_2.R1010
Contig ID
5'-most EST
                  g473290
                  121636
Seq. No.
Contig ID
                  7082 3.R1010
5'-most EST
                  g473348
Method
                  BLASTN
NCBI GI
                  g2462264
BLAST score
                  34
E value
                  2.0e-09
Match length
                  34
                  100
% identity
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.
                  121637
                  7086 1.R1010
Contig ID
5'-most EST
                  jC-alX22036Q1E1A07b1
Method
                  BLASTN
NCBI GI
                  q4455168
BLAST score
                  427
```

```
431
Match length
% identity
                   100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10
                   (ESSAII project)
Seq. No.
                   121638
Contig ID
                   7087 1.R1010
                   jC-atXLIB327409P2f08b1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2582640
BLAST score
                   67
E value
                   5.0e-29
Match length
                   74
                   99
% identity
                  Arabidopsis thaliana mRNA for arginine/serine-rich splicing
NCBI Description
                  factor, RSp40
                   121639
Seq. No.
Contig ID
                   7089 1.R1010
5'-most EST
                   g1215927
Method
                   BLASTX
NCBI GI
                   g2059326
BLAST score
                   232
E value
                   8.0e-19
Match length
                   197
% identity
                   32
                  (D67067) thymic epithelial cell surface antigen [Mus
NCBI Description
                  musculus]
                   121640
Seq. No.
Contig ID
                   7090 1.R1010
5'-most EST
                   jC-atXLIB327409P2f06b1
                   BLASTX
Method
NCBI GI
                   g3367522
BLAST score
                   776
E value
                   7.0e-83
Match length
                   155
% identity
                   99
                   (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  121641
Seq. No.
Contig ID
                  7094 1.R1010
5'-most EST
                   jC-atXLIB327409P4f01b1
Method
                  BLASTX
NCBI GI
                  g1730621
BLAST score
                  534
E value
                   4.0e-54
Match length
                  202
% identity
                  53
NCBI Description
                  HYPOTHETICAL 48.1 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION
                  >gi_630106_pir__S48817 hypothetical protein YML079w - yeast
                   (Saccharomyces cerevisiae) >gi_587531_emb_CAA86498_
                   (Z46373) orf, len: 423, CAI: 0.18, 27.4% identity in 307 aa
```

overlap with S36201 S36201 hypothetical protein 1 - Rhizobium leguminosarum [Saccharomyces cerevisiae]

% identity

```
121642
Seq. No.
Contig ID
                  7096 1.R1010
5'-most EST
                  jC-atXLIB327409P3f02b1
Seq. No.
                   121643 -
                  7098 1.R1010
Contig ID
                  LIB3176-109-P1-K1-B8
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4490704
BLAST score
                  1274
E value
                  1.0e-141
                  262
Match length
% identity
                   95
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
Seq. No.
                  121644
                  7107 1.R1010
Contig ID
5'-most EST
                  jC-atXLIB327409P1g05b1
Method
                  BLASTX
NCBI GI
                  q4580471
BLAST score
                  540
E value
                   4.0e-90
Match length
                  331
% identity
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
                  121645
Seq. No.
Contig ID
                  7110 1.R1010
5'-most EST
                  jC-atXLIB327406P4f10b2
Method
                  BLASTX
NCBI GI
                  q3643594
BLAST score
                  741
E value
                  8.0e-79
Match length
                  141
% identity
                  100
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                  121646
Contig ID
                  7110 2.R1010
5'-most EST
                  LIB22-036-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  g3643594
BLAST score
                  365
E value
                  1.0e-34
Match length
                  73
% identity
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                  121647
Contig ID
                  7112 1.R1010
                  jC-atXLIB327409P2g10b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4262222
BLAST score
                  648
                  6.0e-68
E value
                  146
Match length
```

Seq. No.

```
NCBI Description (AC006200) putative RNA helicase A, 3' partial [Arabidopsis
                   thaliana]
Seq. No.
                  121648
Contig ID
                  7115 1.R1010
                   jC-atXLIB327409P3g01b1
5'-most EST
                  BLASTX
Method
                  g3033375
NCBI GI
BLAST score
                  472
                   3.0e-47
E value
Match length
                  155
% identity
                   60
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  121649
                  7115 2.R1010
Contig ID
5'-most EST
                  g930528
Method
                  BLASTX
NCBI GI
                  g4587532
BLAST score
                  73
                   5.0e-36
E value
Match length
                  129
% identity
NCBI Description
                   (AC007060) Strong similarity to F19I3.2 gi 3033375 putative
                  berberine bridge enzyme from Arabidopsis thaliana BAC
                  gb AC004238. This gene
                  121650
Seq. No.
Contig ID
                  7116 1.R1010
                  LIB22-085-Q1-E2-D10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4583544
BLAST score
                  493
E value
                  1.0e-49
Match length
                  100
% identity
                  91
                  (Z95637) acyl-CoA:1-acylglycerol-3-phosphate
NCBI Description
                  acyltransferase [Brassica napus]
                  121651
Seq. No.
Contig ID
                  7116 2.R1010
                  LIB3176-062-P1-K1-F6
5'-most EST
Method
                  BLASTX
                  g4583544
NCBI GI
BLAST score
                  129
                  9.0e-67
E value
Match length
                  135
% identity
                  86
                  (Z95637) acyl-CoA:1-acylglycerol-3-phosphate
NCBI Description
                  acyltransferase [Brassica napus]
Seq. No.
                  121652
                  7119 1.R1010
Contig ID
                  LIB3168-010-P1-K1-D3
5'-most EST
```

Contig ID

7120 1.R1010

```
5'-most EST
                   jC-atXLIB327409P4g10b1
                   BLASTN
Method
NCBI GI
                   g4757403
BLAST score
                   457
                   0.0e+00
E value
Match length
                   457
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJL12, complete sequence
Seq. No.
                   121654
Contig ID
                   7121 1.R1010
5'-most EST
                  jC-atXLIB327416P4c08b1
Method
                   BLASTX
                  g2735017
NCBI GI
BLAST score
                   144
E value
                   8.0e-09
Match length
                   122
% identity
                  (U82481) KI domain interacting kinase 1 [Zea mays]
NCBI Description
                   121655
Seq. No.
Contig ID
                   7122 1.R1010
5'-most EST
                   jC-atXLIB327409P4g08b1
Method
                   BLASTX
NCBI GI
                   q3482919
BLAST score
                   371
E value
                   3.0e-35
Match length
                   161
                   51
% identity
                  (AC003970) Putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   121656
Contig ID
                   7124 1.R1010
5'-most EST
                   jC-atXLIB327409P4g09b1
Method
                   BLASTX
NCBI GI
                   g4539294
BLAST score
                   247
E value
                   7.0e-21
Match length
                   120
% identity
                  (AL049480) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   121657
Contig ID
                   7125 2.R1010
5'-most EST
                  LIB3168-070-P1-K1-F7
Method
                  BLASTX
                   g4262250
NCBI GI
BLAST score
                   636
E value
                   2.0e-66
Match length
                  126
% identity
                   100
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                   121658
Seq. No.
                  7128 1.R1010
Contig ID
```

Seq. No.

```
5'-most EST
                   jC-atXP52C181L17T7d2
                   BLASTX
Method
                   g3785982
NCBI GI
BLAST score
                   818
                   1.0e-87
E value
Match length
                   151
% identity
                   99
                   (AC005560) putative major latex protein [Arabidopsis
NCBI Description
                   thaliana]
                   121659
Seq. No.
Contig ID
                   7128 2.R1010
5'-most EST
                   g2758703
Method
                   BLASTX
NCBI GI
                   g3785981
BLAST score
                   394
E value
                   2.0e-82
Match length
                   151
% identity
                   94
                  (AC005560) putative major latex protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   121660
                   7128_3.R1010
Contig ID
                   g2758523
5'-most EST
Method
                  BLASTX
                  g2244762
NCBI GI
BLAST score
                   338
E value
                   1.0e-36
Match length
                   113
% identity
                   77
NCBI Description
                  (Z97335) major latex protein [Arabidopsis thaliana]
Seq. No.
                   121661.
Contig ID
                   7131_1.R1010
5'-most EST
                  g934747
                  BLASTN
Method
                   q2924651
NCBI GI
BLAST score
                   763
E value
                   0.0e + 00
Match length
                   783
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K2A18, complete sequence [Arabidopsis thaliana]
                   121662
Seq. No.
Contig ID
                   7132 1.R1010
5'-most EST
                   jC-alXLIB327434P3b02b1
Method
                  BLASTX
NCBI GI
                  q3063449
BLAST score
                  1438
E value
                  1.0e-160
Match length
                  407
% identity ·
                . . 61
NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana]
```

```
Contig ID
                  7132 2.R1010
                  LIB3175-081-P1-K1-A6
5'-most EST
Method
                  BLASTX ·
NCBI GI
                  q3063449
BLAST score
                  527
                  1.0e-54
E value
Match length
                  140
% identity
                  80
                  (AC003981) F22013.11 [Arabidopsis thaliana]
NCBI Description
                  121664
Seq. No.
                  7135 1.R1010
Contig ID
5'-most EST
                  g934994
Seq. No.
                  121665
                  7136 1.R1010
Contig ID
                  jC-atXLIB327409P3e10b1
5'-most EST
                  BLASTX
Method
                  g2073478.
NCBI GI
BLAST score
                  175
                  2.0e-12
E value
Match length
                  76
                  53
% identity
NCBI Description
                  (Y11784) DNA polymerase I [Rickettsia prowazekii]
                  >gi 3861304 emb CAA15203 (AJ235273) DNA POLYMERASE I
                  (polA) [Rickettsia prowazekii]
                  121666
Seq. No.
Contig ID
                  7137 1.R1010
                  LIB3168-051-P1-K1-G2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4185141
BLAST score
                  585
E value
                  1.0e-60
Match length
                  122
% identity
NCBI Description
                  (AC005724) putative calmodulin-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  121667
Contig ID
                  7139 1.R1010
5'-most EST
                  jC-atXLIB327426P2f11b1
Method
                  BLASTX
NCBI GI
                  q461812
BLAST score
                  291
E value
                  6.0e-26
Match length
                  114
% identity
                  46
                  CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
NCBI Description
                  GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)
                  Cytochrome P-450 protein [Catharanthus roseus]
                  >gi 445604 prf 1909351A cytochrome P450 [Catharanthus
                  roseus]
Seq. No.
                  121668
                  7139 2.R1010
Contig ID
5'-most EST
                  jC-atXP83CG3E2T7014a1
```

NCBI Description

121673

7142 2.R1010

LIB23-008-Q1-E1-H4

Seq. No.

Contig ID 5'-most EST

```
BLASTX
Method
NCBI GI
                   g461812
                   232
BLAST score
                   1.0e-21
E value
                   144
Match length
                   40
% identity
NCBI Description
                  CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
                   GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)
                  Cytochrome P-450 protein [Catharanthus roseus]
                  >gi_445604_prf__1909351A cytochrome P450 [Catharanthus
                   roseus]
Seq. No.
                   121669
                   7139 3.R1010
Contig ID
5'-most EST
                   q315\overline{2}94
Method
                  BLASTX
NCBI GI
                   q461812
BLAST score
                   168
E value
                   2.0e-39
Match length
                   198
                   51
% identity
NCBI Description CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
                  GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)
                   Cytochrome P-450 protein [Catharanthus roseus]
                 >gi 445604_prf__1909351A cytochrome P450 [Catharanthus
                   roseus]
                   121670
Seq. No.
Contig ID
                   7139 5.R1010
                  g2597055
5'-most EST
Method
                  BLASTN
                  g4220637
NCBI GI
BLAST score
                   72
E value
                  4.0e-32
Match length
                   395
                   17
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MIE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   121671
                   7141_1.R1010
Contig ID
                  LIB3176-034-P1-K1-D10
5'-most EST
Seq. No.
                   121672
Contig ID
                   7142_1.R1010
                   jC-atXLIB327420P1g02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1209756
                   706
BLAST score
E value
                  1.0e-138
Match length
                   377
% identity
                   65
```

13499

(U43629) integral membrane protein [Beta vulgaris]

% identity





```
Method
                   BLASTX
NCBI GI
                   q1209756
BLAST score
                   713
E value
                   4.0e-75
Match length
                   281
                   66
% identity
NCBI Description
                  (U43629) integral membrane protein [Beta vulgaris]
                   121674
Seq. No.
Contig ID
                   7143 1.R1010
5'-most EST
                   jC-atXLIB327409P2f05b1
                   121675
Seq. No.
                   7144 1.R1010
Contig ID
                   jC-atXLIB327409P3h07b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2642154
BLAST score
                   635
E value
                   8.0e-66
                   301
Match length
% identity
NCBI Description
                   (AC003000) unknown protein [Arabidopsis thaliana]
                   >gi_3790595 (AF079186) RING-H2 finger protein RHC2a
                   [Arabidopsis thaliana]
                   121676
Seq. No.
                   7144 3.R1010
Contig ID
                  jC-aTXLIB327409P3h07a1
5'-most EST
Method
                   BLASTN
NCBI GI
                  g4589410
BLAST score
                   536
E value
                   0.0e + 00
Match length
                   588
                   97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F2015, complete sequence
                   121677
Seq. No.
Contig ID
                  7146 1.R1010
5'-most EST
                  LIB22-037-Q1-E1-B5
Method
                  BLASTX
NCBI GI
                  q4262174
BLAST score
                  2587
E value
                  0.0e + 00
Match length
                   477
                  100
% identity
NCBI Description
                  (AC005508) 9058 [Arabidopsis thaliana]
                  121678
Seq. No.
Contig ID
                  7146 3.R1010
5'-most EST
                  LIB22-085-Q1-E1-G3
Method
                  BLASTX
NCBI GI
                  g4262174
BLAST score
                  350
E value
                  6.0e-33
Match length
                  70
```